Regulation of the Hepatitis B virus replication and gene expression by the multi-functional protein TARDBP

Grace Naswa Makokha, Hiromi Abe-Chayama, Sajeda Chowdhury, C. Nelson Hayes, Masataka Tsuge, Tadahiko Yoshima, Yuji Ishida, Yizhou Zhang, Takuro Uchida, Chise Tateno, Rie Akiyama, Kazuaki Chayama.

SUPPLEMENTAL FIGURE LEGENDS

Figure S1. TARDBP knock-in donor plasmids. The sequences of left and right homology arm of TARDBP (A), TARDBP puro-DD knock-in cassette (B), and TARDBP bla-DD knock-in cassette (C).

Figure S2. Over-expression of TARDBP in NTCP-HepG2/TARDBP knock-out (Tar KO) cells. (A) Western blotting was performed on NTCP parent cells and NTCP Tar KO cells treated with or without Shield1 (500nM and 1000nM). (B) The pcDNA-FLAG TARDBP plasmid was transfected into NTCP-Tar KO cells for exogenous expression. The cells were harvested at days 0, 3, 6, and 9 after transfection for western blotting analysis. The amount of protein expressed at each time point was detected using anti-TARDBP antibody. GAPDH was used as a loading control.

Figure S3. The EMSA probes from the HBV core promoter region. The sequences of the 12 probes (6-sense and 6-antisense) constructed from the entire core promoter region of nt1613-1849 of the HBV genome. The probes were labeled as sense (S) probes 1-6 and anti-sense (AS) probes 1-6 in a consecutive manner, starting from the C-terminal region backwards to the N-terminus.

Figure S4. TARDBP binds to a sequence within the HBV core promoter (A) The 12 probes were subjected to EMSA with 2μg of a GST tagged TARDBP as follows: S probe 1 alone (lane 1), S probes 1-6 with TARDBP protein (lanes 2-7), AS probes 1-6 with protein (lanes 8-13), and a re-probe of S probe 3 (lanes 14-15). (B) The two probes that showed possible binding to TARDBP in (A) based on the presence of a shifted band (S probe 3 and AS probe 1) were re-subjected to EMSA in the presence or absence of protein together with the corresponding unlabeled probe as a specific competitor and detected by short exposure (left panel) and a long exposure (right panel). (C) Four short fragments of about 24-28 bp labeled s1-s4 were constructed from AS probe 1 (WT). The nucleotide sequence and position of each fragment in the HBV genome is shown. (D) Each of the probes in C was subjected to EMSA in the presence or absence of the TARDBP protein as follows: WT alone (lane 1), WT plus protein (lane 2), s1 alone (lane 3), s1 plus protein (lane 4), s2 alone (lane 5), s2 plus protein (lane 6), s3 alone (lane 7), s3 plus protein (lane 8), s4 alone (lane 9), and s4 plus protein (lane 10). The location of the free probe, the TARDBP-DNA complex (shifted probe), and the putative secondary structure is indicated by an arrow.

Figure S5. TARDBP failed to precipitate HBV cccDNA. Immunoprecipitation was performed on nuclear protein derived from chimeric mice frozen tissue using the anti-rabbit (negative control), anti-TARDBP and anti-HBc (positive control) antibodies. The amount of cccDNA captured by the beads (antibody) was quantified. Prior to quantification, the DNA was pretreated with T5 exonuclease to digest all DNA other than cccDNA. The values are presented as a ratio (%) of DNA quantified in the pellet versus that detected in the supernatant of the immunoprecipitated samples.

Figure S6. Prediction of TARDBP RNA-binding domains in the HBV transcriptome. (A) Because TARDBP is well known to bind preferentially to UG-rich regions of RNA, we tried to identify potential TARDBP HBV RNA binding sites by examining the HBV genome for conserved TG-repeats. To identify potential TARDBP HBV RNA binding sites, HBV genotype C genome alignments were downloaded from HBVdb (https://hbvdb.ibcp.fr/HBVdb/; accessed on 2016/12/20). In this Jalview genome alignment, thymine was colored in green and guanine was colored in orange, indicating that the HBV genome contains a number of clusters of T or G nucleotides. However, when we performed a regular expression search for (TG)+ repeats, we found few conserved TG stretches with more than two repeats, e.g., the short pattern outlined in red, suggesting that it would be difficult to determine the TARDBP RNA binding site using only a regular expression search. (B) However, published TARDBP RNA binding site motifs suggest that while most patterns contain a core pattern of about 6 TG repeats, the nucleotide profile at each position is somewhat flexible. Therefore, we downloaded the 11 experimentally determined TARDBP RNA-binding motifs from the RBPDB database of RNA-binding protein specificities (http://rbpdb.ccbr.utoronto.ca/index.php; accessed on 2018/11/01) and performed a fuzzy search (http://www.bioinformatics.org/sms2/fuzzy_search_dna.html; reference sequence = KR819180.1, match = 5, mismatch = -1, and gap = -5) to find the highest scoring matches for each pattern without over-penalizing for mismatches. (C) Fuzzy matches were exported in BED format and uploaded to the NCBI Graphics panel for HBV reference sequence KR819180.1. We observed a number of matches within the X transcript overlapping the core promoter/enhancer II region (yellow) and found other clusters within the S and core transcripts, as well as a match is downstream of the polyadenylation site (blue). These results suggest that TARDBP might interact with HBV transcripts within the 3’ non-coding regions shared by all transcripts and might interact with HBV RNA in the same region as the DNA binding site in the core promoter/enhancer II region.

Figure S7-S14. Full length blots used to generate main figures.

SUPPLEMENTAL TABLES AND FIGURES

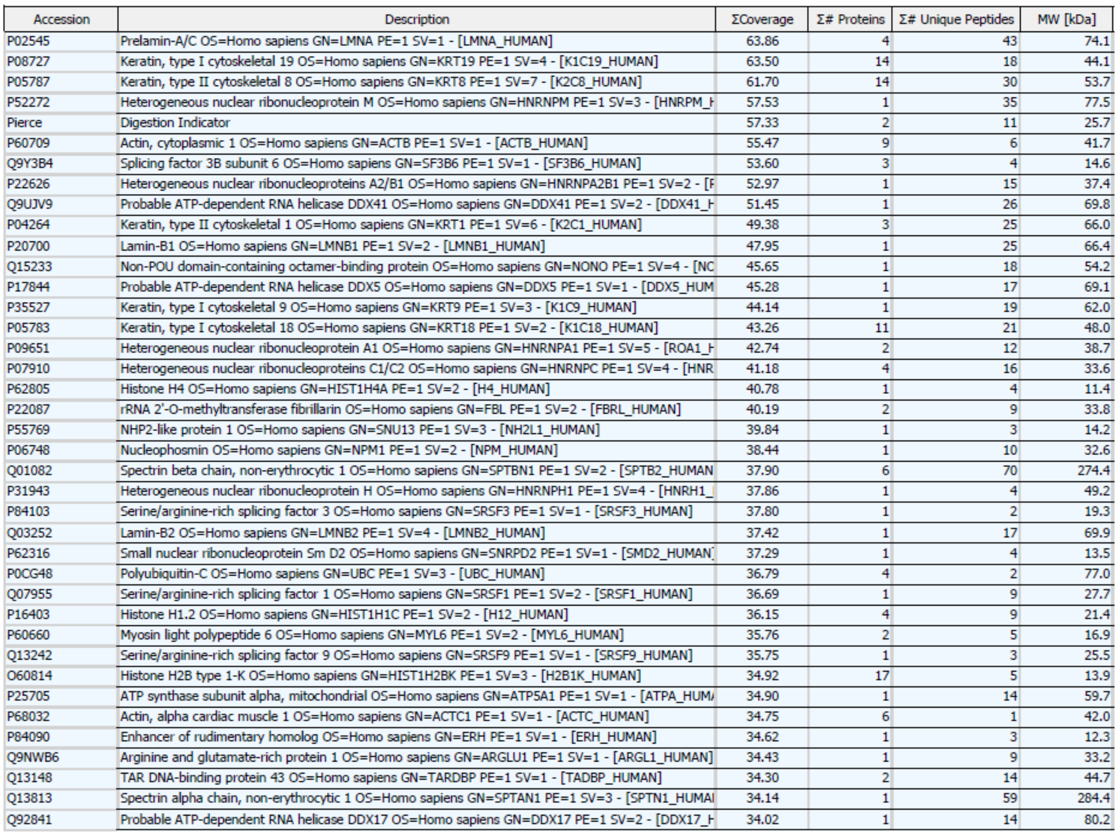
Table S1. PCR primer sequences.

PCR primer	
Name	Sequence (5' to 3')
LHA1F	GTTCTTTACACCTGGTTCACTGCCC
RHA2R	GAGGCAGAGAGAAGGATAAGACCAG
LHA2F	GAGGAACAGAGGGAAACTTTTCTCCTG
RHA3R	CAGATCGACTACTAACAGCACACTACTTC
DDF	GAAGATGGAAAGAAAGTCGATTCCTC
DDR	GGCACCATAGGCATAATCTGGAG
puroF2	ACCACCAGGGCAAGGGTCTG
puroR1	AAGCCGAGCCGCTCGTAGAAG
blaF1	GCTGGCAACCTGACTTGTATCGTC
blaR1	CACTGTCCTTCACTATGGCTTTG

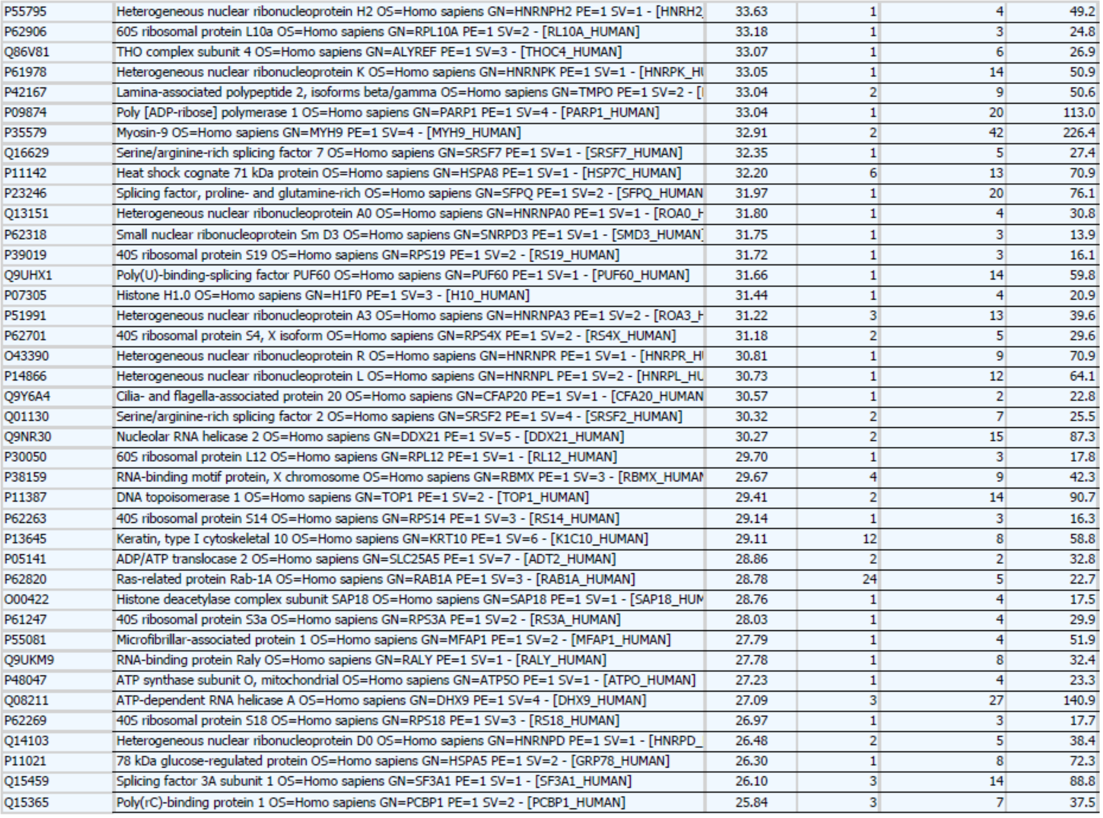
Table S2. PCR primer sets and product sizes.

PCR analysis of knock-in clones Genomic DNA		
Forward primer	Reverse primer	product size (bp)
LHA2F	RHA3R	2389 + 2188
LHA2F	DDR	1444 + 1243
LHA2F	puroR1	1053
LHA2F	blaR1	860
DDF	RHA3R	1106
puroF2	RHA3R	1466
blaF1	RHA3R	1453

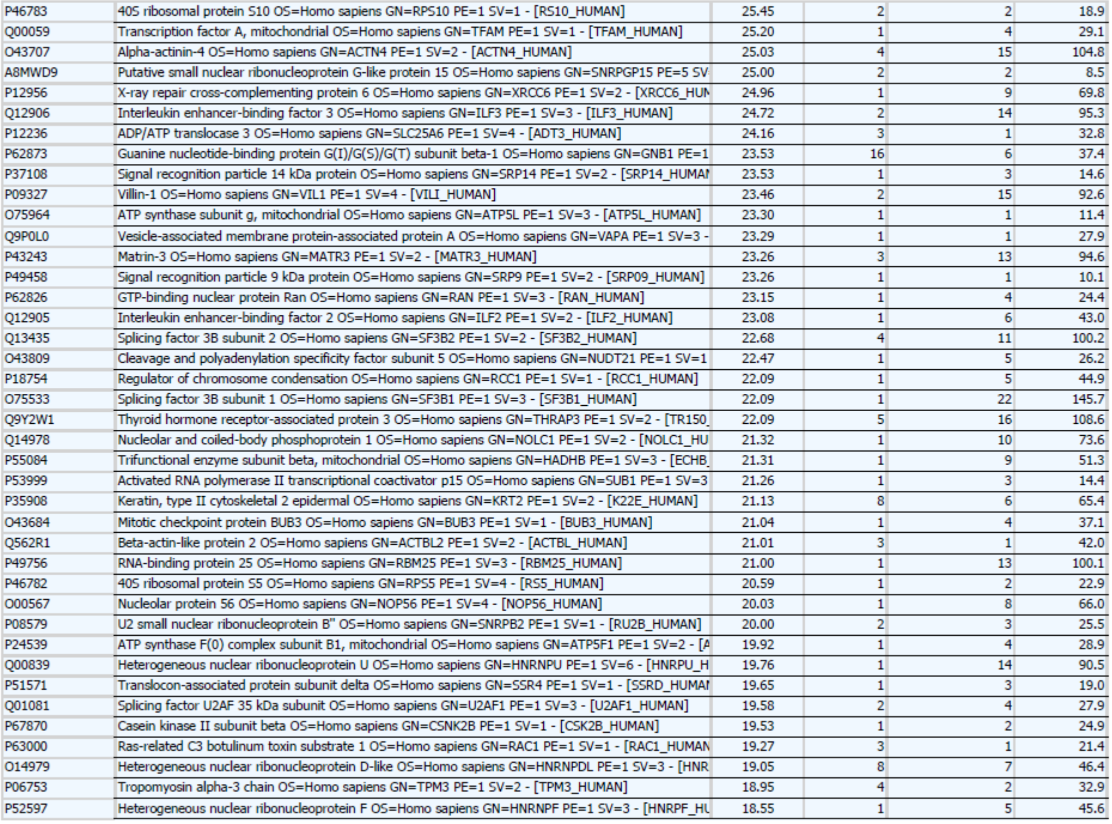
Table S3. List of candidate proteins co-immunoprecipitated with TARDBP and identified by mass spectrometry analysis.



Accession	Description	ΣCoverage	Σ# Proteins	Σ# Unique Peptides	MW [kDa]
P02545	Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1 - [LMNA_HUMAN]	63.86	4	43	74.1
P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	63.50	14	18	44.1
P05787	Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7 - [K2C8_HUMAN]	61.70	14	30	53.7
P52272	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3 - [HNRPM_	57.53	1	35	77.5
Pierce	Digestion Indicator	57.33	2	11	25.7
P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]	55.47	9	6	41.7
Q9Y3B4	Splicing factor 3B subunit 6 OS=Homo sapiens GN=SF3B6 PE=1 SV=1 - [SF3B6_HUMAN]	53.60	3	4	14.6
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [	52.97	1	15	37.4
Q9UJV9	Probable ATP-dependent RNA helicase DDX41 OS=Homo sapiens GN=DDX41 PE=1 SV=2 - [DDX41_	51.45	1	26	69.8
P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K2C1_HUMAN]	49.38	3	25	66.0
P20700	Lamin-B1 OS=Homo sapiens GN=LMNB1 PE=1 SV=2 - [LMNB1_HUMAN]	47.95	1	25	66.4
Q15233	Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4 - [NC	45.65	1	18	54.2
P17844	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 - [DDX5_HUM	45.28	1	17	69.1
P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN]	44.14	1	19	62.0
P05783	Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=2 - [K1C18_HUMAN]	43.26	11	21	48.0
P09651	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=5 - [ROA1_	42.74	2	12	38.7
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=4 - [HNR	41.18	4	16	33.6
P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 - [H4_HUMAN]	40.78	1	4	11.4
P22087	rRNA 2'-O-methyltransferase fibrillarin OS=Homo sapiens GN=FBL PE=1 SV=2 - [FBRL_HUMAN]	40.19	2	9	33.8
P55769	NHP2-like protein 1 OS=Homo sapiens GN=SNU13 PE=1 SV=3 - [NH2L1_HUMAN]	39.84	1	3	14.2
P06748	Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2 - [NPM_HUMAN]	38.44	1	10	32.6
Q01082	Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2 - [SPTB2_HUMAN	37.90	6	70	274.4
P31943	Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4 - [HNRH1_	37.86	1	4	49.2
P84103	Serine/arginine-rich splicing factor 3 OS=Homo sapiens GN=SRSF3 PE=1 SV=1 - [SRSF3_HUMAN]	37.80	1	2	19.3
Q03252	Lamin-B2 OS=Homo sapiens GN=LMNB2 PE=1 SV=4 - [LMNB2_HUMAN]	37.42	1	17	69.9
P62316	Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=1 SV=1 - [SMD2_HUMAN]	37.29	1	4	13.5
P0CG48	Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=3 - [UBC_HUMAN]	36.79	4	2	77.0
Q07955	Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2 - [SRSF1_HUMAN]	36.69	1	9	27.7
P16403	Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2 - [H12_HUMAN]	36.15	4	9	21.4
P60660	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2 - [MYL6_HUMAN]	35.76	2	5	16.9
Q13242	Serine/arginine-rich splicing factor 9 OS=Homo sapiens GN=SRSF9 PE=1 SV=1 - [SRSF9_HUMAN]	35.75	1	3	25.5
O60814	Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3 - [H2B1K_HUMAN]	34.92	17	5	13.9
P25705	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 - [ATPA_HUM	34.90	1	14	59.7
P68032	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]	34.75	6	1	42.0
P84090	Enhancer of rudimentary homolog OS=Homo sapiens GN=ERH PE=1 SV=1 - [ERH_HUMAN]	34.62	1	3	12.3
Q9NWB6	Arginine and glutamate-rich protein 1 OS=Homo sapiens GN=ARGLU1 PE=1 SV=1 - [ARGL1_HUMAN]	34.43	1	9	33.2
Q13148	TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1 - [TADBP_HUMAN]	34.30	2	14	44.7
Q13813	Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3 - [SPTN1_HUMA	34.14	1	59	284.4
Q92841	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2 - [DDX17_	34.02	1	14	80.2



P55795	Heterogeneous nuclear ribonucleoprotein H2 OS=Homo sapiens GN=HNRNPH2 PE=1 SV=1 - [HNRH2	33.63	1	4	49.2
P62906	60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2 - [RL10A_HUMAN]	33.18	1	3	24.8
Q86V81	THO complex subunit 4 OS=Homo sapiens GN=ALYREF PE=1 SV=3 - [THOC4_HUMAN]	33.07	1	6	26.9
P61978	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1 - [HNRPK_H	33.05	1	14	50.9
P42167	Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=2 - [	33.04	2	9	50.6
P09874	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4 - [PARP1_HUMAN]	33.04	1	20	113.0
P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN]	32.91	2	42	226.4
Q16629	Serine/arginine-rich splicing factor 7 OS=Homo sapiens GN=SRSF7 PE=1 SV=1 - [SRSF7_HUMAN]	32.35	1	5	27.4
P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1 - [HSP7C_HUMAN]	32.20	6	13	70.9
P23246	Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2 - [SFPQ_HUMAN	31.97	1	20	76.1
Q13151	Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1 - [ROA0_H	31.80	1	4	30.8
P62318	Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens GN=SNRPD3 PE=1 SV=1 - [SMD3_HUMAN	31.75	1	3	13.9
P39019	40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2 - [RS19_HUMAN]	31.72	1	3	16.1
Q9UHX1	Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens GN=PUF60 PE=1 SV=1 - [PUF60_HUMAN]	31.66	1	14	59.8
P07305	Histone H1.0 OS=Homo sapiens GN=H1F0 PE=1 SV=3 - [H10_HUMAN]	31.44	1	4	20.9
P51991	Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2 - [ROA3_H	31.22	3	13	39.6
P62701	40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2 - [RS4X_HUMAN]	31.18	2	5	29.6
O43390	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1 - [HNRPR_H	30.81	1	9	70.9
P14866	Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2 - [HNRPL_HU	30.73	1	12	64.1
Q9Y6A4	Cilia- and flagella-associated protein 20 OS=Homo sapiens GN=CFAP20 PE=1 SV=1 - [CFA20_HUMAN	30.57	1	2	22.8
Q01130	Serine/arginine-rich splicing factor 2 OS=Homo sapiens GN=SRSF2 PE=1 SV=4 - [SRSF2_HUMAN]	30.32	2	7	25.5
Q9NR30	Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5 - [DDX21_HUMAN]	30.27	2	15	87.3
P30050	60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 - [RL12_HUMAN]	29.70	1	3	17.8
P38159	RNA-binding motif protein, X chromosome OS=Homo sapiens GN=RBMX PE=1 SV=3 - [RBMX_HUMAN	29.67	4	9	42.3
P11387	DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2 - [TOP1_HUMAN]	29.41	2	14	90.7
P62263	40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3 - [RS14_HUMAN]	29.14	1	3	16.3
P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN]	29.11	12	8	58.8
P05141	ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 - [ADT2_HUMAN]	28.86	2	2	32.8
P62820	Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3 - [RAB1A_HUMAN]	28.78	24	5	22.7
O00422	Histone deacetylase complex subunit SAP18 OS=Homo sapiens GN=SAP18 PE=1 SV=1 - [SAP18_HUM	28.76	1	4	17.5
P61247	40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 - [RS3A_HUMAN]	28.03	1	4	29.9
P55081	Microfibrillar-associated protein 1 OS=Homo sapiens GN=MFAP1 PE=1 SV=2 - [MFAP1_HUMAN]	27.79	1	4	51.9
Q9UKM9	RNA-binding protein Raly OS=Homo sapiens GN=RALY PE=1 SV=1 - [RALY_HUMAN]	27.78	1	8	32.4
P48047	ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1 - [ATPO_HUMAN]	27.23	1	4	23.3
Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9_HUMAN]	27.09	3	27	140.9
P62269	40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3 - [RS18_HUMAN]	26.97	1	3	17.7
Q14103	Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1 - [HNRPD_	26.48	2	5	38.4
P11021	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2 - [GRP78_HUMAN]	26.30	1	8	72.3
Q15459	Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1 - [SF3A1_HUMAN]	26.10	3	14	88.8
Q15365	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2 - [PCBP1_HUMAN]	25.84	3	7	37.5



P46783	40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1 - [RS10_HUMAN]	25.45	2	2	18.9
Q00059	Transcription factor A, mitochondrial OS=Homo sapiens GN=TFAM PE=1 SV=1 - [TFAM_HUMAN]	25.20	1	4	29.1
O43707	Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2 - [ACTN4_HUMAN]	25.03	4	15	104.8
A8MWD9	Putative small nuclear ribonucleoprotein G-like protein 15 OS=Homo sapiens GN=SNRPGP15 PE=5 SV	25.00	2	2	8.5
P12956	X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2 - [XRCC6_HUM	24.96	1	9	69.8
Q12906	Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3 - [ILF3_HUMAN]	24.72	2	14	95.3
P12236	ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4 - [ADT3_HUMAN]	24.16	3	1	32.8
P62873	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1	23.53	16	6	37.4
P37108	Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=1 SV=2 - [SRP14_HUMAN	23.53	1	3	14.6
P09327	Villin-1 OS=Homo sapiens GN=VIL1 PE=1 SV=4 - [VILI_HUMAN]	23.46	2	15	92.6
O75964	ATP synthase subunit g, mitochondrial OS=Homo sapiens GN=ATP5L PE=1 SV=3 - [ATP5L_HUMAN]	23.30	1	1	11.4
Q9P0L0	Vesicle-associated membrane protein-associated protein A OS=Homo sapiens GN=VAPA PE=1 SV=3 -	23.29	1	1	27.9
P43243	Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2 - [MATR3_HUMAN]	23.26	3	13	94.6
P49458	Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2 - [SRP09_HUMAN]	23.26	1	1	10.1
P62826	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3 - [RAN_HUMAN]	23.15	1	4	24.4
Q12905	Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2 - [ILF2_HUMAN]	23.08	1	6	43.0
Q13435	Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=1 SV=2 - [SF3B2_HUMAN]	22.68	4	11	100.2
O43809	Cleavage and polyadenylation specificity factor subunit 5 OS=Homo sapiens GN=NUDT21 PE=1 SV=1	22.47	1	5	26.2
P18754	Regulator of chromosome condensation OS=Homo sapiens GN=RCC1 PE=1 SV=1 - [RCC1_HUMAN]	22.09	1	5	44.9
O75533	Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3 - [SF3B1_HUMAN]	22.09	1	22	145.7
Q9Y2W1	Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2 - [TR150_	22.09	5	16	108.6
Q14978	Nucleolar and coiled-body phosphoprotein 1 OS=Homo sapiens GN=NOLC1 PE=1 SV=2 - [NOLC1_HU	21.32	1	10	73.6
P55084	Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3 - [ECHB_	21.31	1	9	51.3
P53999	Activated RNA polymerase II transcriptional coactivator p15 OS=Homo sapiens GN=SUB1 PE=1 SV=3	21.26	1	3	14.4
P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2 - [K22E_HUMAN]	21.13	8	6	65.4
O43684	Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 PE=1 SV=1 - [BUB3_HUMAN]	21.04	1	4	37.1
Q562R1	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2 - [ACTBL_HUMAN]	21.01	3	1	42.0
P49756	RNA-binding protein 25 OS=Homo sapiens GN=RBM25 PE=1 SV=3 - [RBM25_HUMAN]	21.00	1	13	100.1
P46782	40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4 - [RS5_HUMAN]	20.59	1	2	22.9
O00567	Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 - [NOP56_HUMAN]	20.03	1	8	66.0
P08579	U2 small nuclear ribonucleoprotein B'' OS=Homo sapiens GN=SNRPB2 PE=1 SV=1 - [RU2B_HUMAN]	20.00	2	3	25.5
P24539	ATP synthase F(0) complex subunit B1, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2 - [A	19.92	1	4	28.9
Q00839	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6 - [HNRPU_H	19.76	1	14	90.5
P51571	Translocon-associated protein subunit delta OS=Homo sapiens GN=SSR4 PE=1 SV=1 - [SSRD_HUMAN	19.65	1	3	19.0
Q01081	Splicing factor U2AF 35 kDa subunit OS=Homo sapiens GN=U2AF1 PE=1 SV=3 - [U2AF1_HUMAN]	19.58	2	4	27.9
P67870	Casein kinase II subunit beta OS=Homo sapiens GN=CSNK2B PE=1 SV=1 - [CSK2B_HUMAN]	19.53	1	2	24.9
P63000	Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1 - [RAC1_HUMAN	19.27	3	1	21.4
O14979	Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRNPDL PE=1 SV=3 - [HNR	19.05	8	7	46.4
P06753	Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=2 - [TPM3_HUMAN]	18.95	4	2	32.9
P52597	Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3 - [HNRPF_HU	18.55	1	5	45.6

Q08945	FACT complex subunit SSRP1 OS=Homo sapiens GN=SSRP1 PE=1 SV=1 - [SSRP1_HUMAN]	18.48	1	9	81.0
P19338	Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3 - [NUCL_HUMAN]	18.31	2	11	76.6
P27487	Dipeptidyl peptidase 4 OS=Homo sapiens GN=DPP4 PE=1 SV=2 - [DPP4_HUMAN]	18.15	1	9	88.2
Q96I25	Splicing factor 45 OS=Homo sapiens GN=RBM17 PE=1 SV=1 - [SPF45_HUMAN]	17.96	1	5	44.9
P40939	Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2 - [ECH	17.82	1	9	82.9
Q13247	Serine/arginine-rich splicing factor 6 OS=Homo sapiens GN=SRSF6 PE=1 SV=2 - [SRSF6_HUMAN]	17.73	1	3	39.6
P06576	ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3 - [ATPB_HUMAN	17.58	1	7	56.5
Q12874	Splicing factor 3A subunit 3 OS=Homo sapiens GN=SF3A3 PE=1 SV=1 - [SF3A3_HUMAN]	17.37	1	4	58.8
Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=	17.16	3	6	48.2
Q07020	60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2 - [RL18_HUMAN]	17.02	1	2	21.6
O94906	Pre-mRNA-processing factor 6 OS=Homo sapiens GN=PRPF6 PE=1 SV=1 - [PRP6_HUMAN]	17.00	1	10	106.9
P10809	60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2 - [CH60_HUMAN	16.93	1	4	61.0
Q15393	Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4 - [SF3B3_HUMAN]	16.68	3	14	135.5
Q15029	116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=1 SV=1 -	16.67	1	11	109.4
Q9H307	Pinin OS=Homo sapiens GN=PNN PE=1 SV=4 - [PININ_HUMAN]	16.60	1	8	81.6
O60506	Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2 - [HNRPQ_H	16.37	1	3	69.6
P13010	X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3 - [XRCC5_HU	16.12	2	8	82.7
O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15	16.10	1	11	90.9
Q13595	Transformer-2 protein homolog alpha OS=Homo sapiens GN=TRA2A PE=1 SV=1 - [TRA2A_HUMAN]	15.96	1	4	32.7
Q15717	ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1 PE=1 SV=2 - [ELAV1_HUMAN]	15.95	1	4	36.1
Q6P2Q9	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2 - [PRP8_HUMAN]	15.93	1	21	273.4
Q15287	RNA-binding protein with serine-rich domain 1 OS=Homo sapiens GN=RNPS1 PE=1 SV=1 - [RNPS1_H	15.74	1	2	34.2
P13987	CD59 glycoprotein OS=Homo sapiens GN=CD59 PE=1 SV=1 - [CD59_HUMAN]	15.63	1	1	14.2
O96019	Actin-like protein 6A OS=Homo sapiens GN=ACTL6A PE=1 SV=1 - [ACL6A_HUMAN]	15.62	2	5	47.4
P35659	Protein DEK OS=Homo sapiens GN=DEK PE=1 SV=1 - [DEK_HUMAN]	15.47	1	3	42.6
P35232	Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1 - [PHB_HUMAN]	15.44	1	4	29.8
P62277	40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2 - [RS13_HUMAN]	15.23	1	2	17.2
Q9NYF8	Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=2 - [BCLF1_HUMAN]	15.22	1	9	106.1
P68104	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 - [EF1A1_HUMAN]	15.15	3	6	50.1
P05023	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1 -	15.05	5	9	112.8
P17096	High mobility group protein HMG-I/HMG-Y OS=Homo sapiens GN=HMGA1 PE=1 SV=3 - [HMGA1_HU	14.95	1	1	11.7
P05386	60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1 - [RLA1_HUMAN]	14.91	2	1	11.5
Q9UBB9	Tuftelin-interacting protein 11 OS=Homo sapiens GN=TFIP11 PE=1 SV=1 - [TFP11_HUMAN]	14.81	1	6	96.8
Q13185	Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4 - [CBX3_HUMAN]	14.75	1	1	20.8
P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1 - [TBA1B_HUMAN]	14.63	7	3	50.1
P09661	U2 small nuclear ribonucleoprotein A' OS=Homo sapiens GN=SNRPA1 PE=1 SV=2 - [RU2A_HUMAN]	14.51	1	3	28.4
P38919	Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4 - [IF4A3_HUMAN]	14.36	1	2	46.8
P04843	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1	14.33	1	9	68.5
P62273	40S ribosomal protein S29 OS=Homo sapiens GN=RPS29 PE=1 SV=2 - [RS29_HUMAN]	14.29	1	1	6.7
Q13838	Spliceosome RNA helicase DDX39B OS=Homo sapiens GN=DDX39B PE=1 SV=1 - [DX39B_HUMAN]	14.25	2	3	49.0

P62995	Transformer-2 protein homolog beta OS=Homo sapiens GN=TRA2B PE=1 SV=1 - [TRA2B_HUMAN]	14.24	1	3	33.6
Q9Y5B9	FACT complex subunit SPT16 OS=Homo sapiens GN=SUPT16H PE=1 SV=1 - [SP16H_HUMAN]	14.23	1	9	119.8
Q9Y2X3	Nucleolar protein 58 OS=Homo sapiens GN=NOP58 PE=1 SV=1 - [NOP58_HUMAN]	14.18	1	4	59.5
Q6NXT2	Histone H3.3C OS=Homo sapiens GN=H3F3C PE=1 SV=3 - [H3C_HUMAN]	14.07	5	1	15.2
O60264	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS	14.07	1	5	121.8
O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2 -	14.00	1	27	244.4
P35637	RNA-binding protein FUS OS=Homo sapiens GN=FUS PE=1 SV=1 - [FUS_HUMAN]	13.88	2	7	53.4
A0A0B4J2D9	Immunoglobulin kappa variable 1D-13 OS=Homo sapiens GN=IGKV1D-13 PE=3 SV=1 - [KVD13_HUM	13.68	1	1	12.6
P35580	Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3 - [MYH10_HUMAN]	13.61	1	8	228.9
P62829	60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1 - [RL23_HUMAN]	13.57	1	2	14.9
P26599	Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1 - [PTBP1_HUMAN]	13.56	5	7	57.2
P17480	Nucleolar transcription factor 1 OS=Homo sapiens GN=UBTF PE=1 SV=1 - [UBF1_HUMAN]	13.48	1	2	89.4
Q99459	Cell division cycle 5-like protein OS=Homo sapiens GN=CDC5L PE=1 SV=2 - [CDC5L_HUMAN]	13.47	1	7	92.2
P26368	Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4 - [U2AF2_HUMAN]	13.47	7	6	53.5
P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4 - [HS90B_HUMAN]	13.40	8	8	83.2
P68400	Casein kinase II subunit alpha OS=Homo sapiens GN=CSNK2A1 PE=1 SV=1 - [CSK21_HUMAN]	13.30	4	2	45.1
P31942	Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens GN=HNRNPH3 PE=1 SV=2 - [HNRH3	13.29	1	1	36.9
P08754	Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3 - [G	13.28	11	1	40.5
P16401	Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3 - [H15_HUMAN]	13.27	1	1	22.6
Q08170	Serine/arginine-rich splicing factor 4 OS=Homo sapiens GN=SRSF4 PE=1 SV=2 - [SRSF4_HUMAN]	13.16	1	3	56.6
P31930	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3 - [QC	13.13	1	3	52.6
Q99623	Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2 - [PHB2_HUMAN]	13.04	1	2	33.3
P62304	Small nuclear ribonucleoprotein E OS=Homo sapiens GN=SNRPE PE=1 SV=1 - [RUXE_HUMAN]	13.04	1	1	10.8
O96000	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 OS=Homo sapiens GN=NDUFB10 P	12.79	1	2	20.8
P49755	Transmembrane emp24 domain-containing protein 10 OS=Homo sapiens GN=TMED10 PE=1 SV=2 - [	12.79	1	1	25.0
Q8TA86	Retinitis pigmentosa 9 protein OS=Homo sapiens GN=RP9 PE=1 SV=2 - [RP9_HUMAN]	12.67	1	2	26.1
P07437	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]	12.61	4	2	49.6
P08621	U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens GN=SNRNP70 PE=1 SV=2 - [RU17_HU	12.59	1	4	51.5
Q14498	RNA-binding protein 39 OS=Homo sapiens GN=RBM39 PE=1 SV=2 - [RBM39_HUMAN]	12.45	1	5	59.3
P19105	Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2 - [ML12A_HUMAN]	12.28	2	2	19.8
Q9Y6C9	Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1 - [MTCH2_HUMAN]	12.21	1	2	33.3
Q9H0D6	5'-3' exoribonuclease 2 OS=Homo sapiens GN=XRN2 PE=1 SV=1 - [XRN2_HUMAN]	12.21	1	4	108.5
Q07065	Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2 - [CKAP4_HUMAN]	12.13	1	3	66.0
Q00610	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5 - [CLH1_HUMAN]	12.12	2	12	191.5
Q01780	Exosome component 10 OS=Homo sapiens GN=EXOSC10 PE=1 SV=2 - [EXOSX_HUMAN]	12.09	1	7	100.8
P36542	ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1 - [ATPG_HU	12.08	1	1	33.0
Q96EU6	Ribosomal RNA processing protein 36 homolog OS=Homo sapiens GN=RRP36 PE=1 SV=1 - [RRP36_H	11.97	1	2	29.8
P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1	11.93	3	3	37.2
P02533	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4 - [K1C14_HUMAN]	11.86	14	1	51.5
O75400	Pre-mRNA-processing factor 40 homolog A OS=Homo sapiens GN=PRPF40A PE=1 SV=2 - [PR40A_HU	11.70	1	8	108.7

P62249	40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2 - [RS16_HUMAN]	11.64	1	2	16.4
P61106	Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4 - [RAB14_HUMAN]	11.63	16	1	23.9
Q86X95	Corepressor interacting with RBPJ 1 OS=Homo sapiens GN=CIR1 PE=1 SV=1 - [CIR1_HUMAN]	11.56	1	3	52.3
P45880	Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2 - [VD	11.22	2	1	31.5
P11166	Solute carrier family 2, facilitated glucose transporter member 1 OS=Homo sapiens GN=SLC2A1 PE=1	11.18	1	4	54.0
Q9Y265	RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 - [RUVB1_HUMAN]	11.18	1	4	50.2
P04899	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3 - [	10.99	11	1	40.4
Q8WWI1	LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=3 - [LMO7_HUMAN]	10.99	1	10	192.6
P62314	Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens GN=SNRPD1 PE=1 SV=1 - [SMD1_HUMAN]	10.92	1	1	13.3
Q9ULV4	Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1 - [COR1C_HUMAN]	10.76	3	3	53.2
O95292	Vesicle-associated membrane protein-associated protein B/C OS=Homo sapiens GN=VAPB PE=1 SV=	10.70	1	1	27.2
Q13243	Serine/arginine-rich splicing factor 5 OS=Homo sapiens GN=SRSF5 PE=1 SV=1 - [SRSF5_HUMAN]	10.66	1	1	31.2
Q13547	Histone deacetylase 1 OS=Homo sapiens GN=HDAC1 PE=1 SV=1 - [HDAC1_HUMAN]	10.58	2	2	55.1
P55265	Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR PE=1 SV=4 - [DSR	10.52	1	9	136.0
Q9Y3T9	Nucleolar complex protein 2 homolog OS=Homo sapiens GN=NOC2L PE=1 SV=4 - [NOC2L_HUMAN]	10.28	1	4	84.9
Q8N1F7	Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2 - [NUP93_HUMAN]	10.26	1	6	93.4
Q9BY77	Polymerase delta-interacting protein 3 OS=Homo sapiens GN=POLDIP3 PE=1 SV=2 - [PDIP3_HUMAN	10.21	1	2	46.1
P78527	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_	10.17	2	30	468.8
P35268	60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2 - [RL22_HUMAN]	10.16	1	1	14.8
Q8NCQ2	Uncharacterized protein CSNK1G2-AS1 OS=Homo sapiens GN=CSNK1G2-AS1 PE=2 SV=2 - [CNAS1_H	10.14	1	1	16.1
P63244	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Homo sapiens GN=GNB2L1 PE=1 SV=3 -	10.09	1	2	35.1
Q9UKV3	Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens GN=ACIN1 PE=1 SV=2 -	10.07	1	10	151.8
P63173	60S ribosomal protein L38 OS=Homo sapiens GN=RPL38 PE=1 SV=2 - [RL38_HUMAN]	10.00	1	1	8.2
Q14690	Protein RRP5 homolog OS=Homo sapiens GN=PDCD11 PE=1 SV=3 - [RRP5_HUMAN]	9.99	1	14	208.6
P04350	Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 - [TBB4A_HUMAN]	9.91	3	1	49.6
P21796	Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2 - [VD	9.89	2	2	30.8
Q9Y5B6	PAX3- and PAX7-binding protein 1 OS=Homo sapiens GN=PAXBP1 PE=1 SV=2 - [PAXB1_HUMAN]	9.71	1	5	104.7
Q00325	Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2 - [MPCP_HUMA	9.67	1	3	40.1
P49916	DNA ligase 3 OS=Homo sapiens GN=LIG3 PE=1 SV=2 - [DNLI3_HUMAN]	9.61	1	5	112.8
Q8N684	Cleavage and polyadenylation specificity factor subunit 7 OS=Homo sapiens GN=CPSF7 PE=1 SV=1 -	9.55	1	4	52.0
P42677	40S ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=1 SV=3 - [RS27_HUMAN]	9.52	2	1	9.5
Q9BZE4	Nucleolar GTP-binding protein 1 OS=Homo sapiens GN=GTPBP4 PE=1 SV=3 - [NOG1_HUMAN]	9.46	1	3	73.9
O75934	Pre-mRNA-splicing factor SPF27 OS=Homo sapiens GN=BCAS2 PE=1 SV=1 - [SPF27_HUMAN]	9.33	1	2	26.1
P62306	Small nuclear ribonucleoprotein F OS=Homo sapiens GN=SNRPF PE=1 SV=1 - [RUXF_HUMAN]	9.30	1	1	9.7
Q14151	Scaffold attachment factor B2 OS=Homo sapiens GN=SAFB2 PE=1 SV=1 - [SAFB2_HUMAN]	9.23	7	2	107.4
Q07021	Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Homo sapiens GN=C1	9.22	1	1	31.3
O00541	Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 - [PESC_HUMAN]	9.18	1	3	68.0
Q15424	Scaffold attachment factor B1 OS=Homo sapiens GN=SAFB PE=1 SV=4 - [SAFB1_HUMAN]	9.18	7	1	102.6
Q9P013	Spliceosome-associated protein CWC15 homolog OS=Homo sapiens GN=CWC15 PE=1 SV=2 - [CWC1	9.17	1	1	26.6
O95235	Kinesin-like protein KIF20A OS=Homo sapiens GN=KIF20A PE=1 SV=1 - [KI20A_HUMAN]	8.99	13	5	100.2

P62913	60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2 - [RL11_HUMAN]	8.99	1	1	20.2
P28370	Probable global transcription activator SNF2L1 OS=Homo sapiens GN=SMARCA1 PE=1 SV=2 - [SMCA	8.92	1	1	122.5
O43795	Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B PE=1 SV=3 - [MYO1B_HUMAN]	8.89	2	5	131.9
P13647	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3 - [K2C5_HUMAN]	8.81	8	1	62.3
Q96DI7	U5 small nuclear ribonucleoprotein 40 kDa protein OS=Homo sapiens GN=SNRNP40 PE=1 SV=1 - [SN	8.68	5	2	39.3
Q13573	SNW domain-containing protein 1 OS=Homo sapiens GN=SNW1 PE=1 SV=1 - [SNW1_HUMAN]	8.58	1	5	61.5
Q9UMS4	Pre-mRNA-processing factor 19 OS=Homo sapiens GN=PRPF19 PE=1 SV=1 - [PRP19_HUMAN]	8.53	1	3	55.1
P27824	Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2 - [CALX_HUMAN]	8.45	1	4	67.5
O43172	U4/U6 small nuclear ribonucleoprotein Prp4 OS=Homo sapiens GN=PRPF4 PE=1 SV=2 - [PRP4_HUMA	8.43	5	1	58.4
Q8WXF1	Paraspeckle component 1 OS=Homo sapiens GN=PSPC1 PE=1 SV=1 - [PSPC1_HUMAN]	8.41	1	1	58.7
P30049	ATP synthase subunit delta, mitochondrial OS=Homo sapiens GN=ATP5D PE=1 SV=2 - [ATPD_HUMA	8.33	1	1	17.5
Q15428	Splicing factor 3A subunit 2 OS=Homo sapiens GN=SF3A2 PE=1 SV=2 - [SF3A2_HUMAN]	8.19	1	3	49.2
Q9NV31	U3 small nucleolar ribonucleoprotein protein IMP3 OS=Homo sapiens GN=IMP3 PE=1 SV=1 - [IMP3_	8.15	1	1	21.8
Q13263	Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5 - [TIF1B_HUMAN	8.02	2	4	88.5
Q13123	Protein Red OS=Homo sapiens GN=IK PE=1 SV=3 - [RED_HUMAN]	7.90	1	2	65.6
P23284	Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=2 - [PPIB_HUMAN]	7.87	1	1	23.7
P42285	Superkiller viralicidic activity 2-like 2 OS=Homo sapiens GN=SKIV2L2 PE=1 SV=3 - [SK2L2_HUMAN]	7.87	1	5	117.7
Q9BQG0	Myb-binding protein 1A OS=Homo sapiens GN=MYBBP1A PE=1 SV=2 - [MBB1A_HUMAN]	7.61	1	5	148.8
Q9HD64	X antigen family member 1 OS=Homo sapiens GN=XAGE1A PE=2 SV=3 - [XAGE1_HUMAN]	7.41	2	1	9.1
Q9Y383	Putative RNA-binding protein Luc7-like 2 OS=Homo sapiens GN=LUC7L2 PE=1 SV=2 - [LC7L2_HUMAN	7.40	2	2	46.5
P52434	DNA-directed RNA polymerases I, II, and III subunit RPABC3 OS=Homo sapiens GN=POLR2H PE=1 S	7.33	1	1	17.1
Q9NVP1	ATP-dependent RNA helicase DDX18 OS=Homo sapiens GN=DDX18 PE=1 SV=2 - [DDX18_HUMAN]	7.31	1	4	75.4
P35222	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 - [CTNB1_HUMAN]	7.30	2	3	85.4
P62899	60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1 - [RL31_HUMAN]	7.20	1	1	14.5
P15880	40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2 - [RS2_HUMAN]	7.17	1	1	31.3
A6NIZ1	Ras-related protein Rap-1b-like protein OS=Homo sapiens PE=2 SV=1 - [RP1BL_HUMAN]	7.07	2	1	20.9
P0C0S5	Histone H2A.Z OS=Homo sapiens GN=H2AFZ PE=1 SV=2 - [H2AZ_HUMAN]	7.03	15	1	13.5
P42704	Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3 -	6.96	1	8	157.8
P62244	40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=2 - [RS15A_HUMAN]	6.92	1	1	14.8
Q5JTV8	Torsin-1A-interacting protein 1 OS=Homo sapiens GN=TOR1AIP1 PE=1 SV=2 - [TOIP1_HUMAN]	6.86	1	3	66.2
Q9Y230	RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3 - [RUVB2_HUMAN]	6.70	1	2	51.1
P20042	Eukaryotic translation initiation factor 2 subunit 2 OS=Homo sapiens GN=EIF2S2 PE=1 SV=2 - [IF2B_	6.61	1	2	38.4
O43818	U3 small nucleolar RNA-interacting protein 2 OS=Homo sapiens GN=RRP9 PE=1 SV=1 - [U3IP2_HUM	6.53	1	2	51.8
P13073	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens GN=COX4I1 PE=1 SV=1	6.51	1	1	19.6
O75396	Vesicle-trafficking protein SEC22b OS=Homo sapiens GN=SEC22B PE=1 SV=4 - [SC22B_HUMAN]	6.51	1	1	24.6
O95232	Luc7-like protein 3 OS=Homo sapiens GN=LUC7L3 PE=1 SV=2 - [LC7L3_HUMAN]	6.48	1	1	51.4
P21127	Cyclin-dependent kinase 11B OS=Homo sapiens GN=CDK11B PE=1 SV=3 - [CD11B_HUMAN]	6.42	2	3	92.7
P53985	Monocarboxylate transporter 1 OS=Homo sapiens GN=SLC16A1 PE=1 SV=3 - [MOT1_HUMAN]	6.40	1	1	53.9
O15160	DNA-directed RNA polymerases I and III subunit RPAC1 OS=Homo sapiens GN=POLR1C PE=1 SV=1 -	6.36	1	2	39.2
Q16643	Drebrin OS=Homo sapiens GN=DBN1 PE=1 SV=4 - [DREB_HUMAN]	6.32	1	2	71.4

Q9H5V9	UPF0428 protein CXorf56 OS=Homo sapiens GN=CXorf56 PE=1 SV=1 - [CX056_HUMAN]	6.31	1	1	25.6
P14678	Small nuclear ribonucleoprotein-associated proteins B and B' OS=Homo sapiens GN=SNRPB PE=1 SV=	6.25	2	1	24.6
P52292	Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1 - [IMA1_HUMAN]	6.24	1	2	57.8
P61586	Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1 - [RHOA_HUMAN]	6.22	1	1	21.8
P53007	Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2 - [TXTP_	6.11	1	1	34.0
O14519	Cyclin-dependent kinase 2-associated protein 1 OS=Homo sapiens GN=CDK2AP1 PE=1 SV=1 - [CDKA	6.09	2	1	12.4
P38646	Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2 - [GRP75_HUMAN]	6.04	1	2	73.6
Q86YZ3	Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2 - [HORN_HUMAN]	6.04	1	4	282.2
A0A0C4DH42	Immunoglobulin heavy variable 3-66 OS=Homo sapiens GN=IGHV3-66 PE=3 SV=1 - [HV366_HUMAN	6.03	23	1	12.7
P00387	NADH-cytochrome b5 reductase 3 OS=Homo sapiens GN=CYB5R3 PE=1 SV=3 - [NB5R3_HUMAN]	5.98	1	2	34.2
Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13 PE=1 SV=2 -	5.93	2	2	74.1
P39656	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=	5.92	1	2	50.8
Q9H6R4	Nucleolar protein 6 OS=Homo sapiens GN=NOL6 PE=1 SV=2 - [NOL6_HUMAN]	5.85	1	4	127.5
Q2TAY7	WD40 repeat-containing protein SMU1 OS=Homo sapiens GN=SMU1 PE=1 SV=2 - [SMU1_HUMAN]	5.85	1	2	57.5
P25490	Transcriptional repressor protein YY1 OS=Homo sapiens GN=YY1 PE=1 SV=2 - [TYY1_HUMAN]	5.80	2	1	44.7
Q13601	KRR1 small subunit processome component homolog OS=Homo sapiens GN=KRR1 PE=1 SV=4 - [KRR	5.77	1	1	43.6
P62760	Visinin-like protein 1 OS=Homo sapiens GN=VSNL1 PE=1 SV=2 - [VISL1_HUMAN]	5.76	1	1	22.1
P22695	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3 - [QC	5.74	1	2	48.4
O60832	H/ACA ribonucleoprotein complex subunit 4 OS=Homo sapiens GN=DKC1 PE=1 SV=3 - [DKC1_HUMA	5.64	1	1	57.6
Q15392	Delta(24)-sterol reductase OS=Homo sapiens GN=DHCR24 PE=1 SV=2 - [DHC24_HUMAN]	5.62	1	3	60.1
P10092	Calcitonin gene-related peptide 2 OS=Homo sapiens GN=CALCB PE=1 SV=1 - [CALCB_HUMAN]	5.51	2	1	13.7
P11940	Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2 - [PABP1_HUMAN]	5.50	2	1	70.6
P41235	Hepatocyte nuclear factor 4-alpha OS=Homo sapiens GN=HNF4A PE=1 SV=3 - [HNF4A_HUMAN]	5.49	2	2	52.8
Q9BXP5	Serrate RNA effector molecule homolog OS=Homo sapiens GN=SRRT PE=1 SV=1 - [SRRT_HUMAN]	5.48	1	3	100.6
Q9H0A0	N-acetyltransferase 10 OS=Homo sapiens GN=NAT10 PE=1 SV=2 - [NAT10_HUMAN]	5.46	1	3	115.7
O00515	Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=2 - [LAD1_HUMAN]	5.42	1	2	57.1
Q3ZCQ8	Mitochondrial import inner membrane translocase subunit TIM50 OS=Homo sapiens GN=TIMM50 PE=	5.38	1	2	39.6
P27482	Calmodulin-like protein 3 OS=Homo sapiens GN=CALML3 PE=1 SV=2 - [CALL3_HUMAN]	5.37	2	1	16.9
P35998	26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3 - [PRS7_HUMAN]	5.31	1	1	48.6
P11169	Solute carrier family 2, facilitated glucose transporter member 3 OS=Homo sapiens GN=SLC2A3 PE=2	5.24	2	2	53.9
P51532	Transcription activator BRG1 OS=Homo sapiens GN=SMARCA4 PE=1 SV=2 - [SMCA4_HUMAN]	5.22	3	5	184.5
P18887	DNA repair protein XRCC1 OS=Homo sapiens GN=XRCC1 PE=1 SV=2 - [XRCC1_HUMAN]	5.21	1	3	69.4
P51654	Glypican-3 OS=Homo sapiens GN=GPC3 PE=1 SV=1 - [GPC3_HUMAN]	5.17	1	1	65.5
P36578	60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 - [RL4_HUMAN]	5.15	13	1	47.7
Q9H5K3	Protein O-mannose kinase OS=Homo sapiens GN=POMK PE=1 SV=1 - [SG196_HUMAN]	5.14	1	1	40.0
Q9H5Z1	Probable ATP-dependent RNA helicase DHX35 OS=Homo sapiens GN=DHX35 PE=1 SV=2 - [DHX35_H	5.12	1	2	78.9
Q99578	GTP-binding protein Rit2 OS=Homo sapiens GN=RIT2 PE=1 SV=1 - [RIT2_HUMAN]	5.07	1	1	24.7
Q9H0S4	Probable ATP-dependent RNA helicase DDX47 OS=Homo sapiens GN=DDX47 PE=1 SV=1 - [DDX47_H	5.05	1	2	50.6
O94905	Erlin-2 OS=Homo sapiens GN=ERLIN2 PE=1 SV=1 - [ERLN2_HUMAN]	5.01	2	1	37.8
Q14684	Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B PE=1 SV=3 - [RRP1B_	5.01	1	2	84.4
Q9P2I0	Cleavage and polyadenylation specificity factor subunit 2 OS=Homo sapiens GN=CPSF2 PE=1 SV=2 -	4.99	1	2	88.4
Q7L014	Probable ATP-dependent RNA helicase DDX46 OS=Homo sapiens GN=DDX46 PE=1 SV=2 - [DDX46_H	4.95	1	2	117.3
O75489	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Homo sapiens GN=NDUFS	4.92	1	1	30.2
O15523	ATP-dependent RNA helicase DDX3Y OS=Homo sapiens GN=DDX3Y PE=1 SV=2 - [DDX3Y_HUMAN]	4.85	2	1	73.1
Q9UJZ1	Stomatin-like protein 2, mitochondrial OS=Homo sapiens GN=STOML2 PE=1 SV=1 - [STML2_HUMAN]	4.78	1	1	38.5
P04156	Major prion protein OS=Homo sapiens GN=PRNP PE=1 SV=1 - [PRIO_HUMAN]	4.74	1	1	27.6
Q01844	RNA-binding protein EWS OS=Homo sapiens GN=EWSR1 PE=1 SV=1 - [EWS_HUMAN]	4.73	1	2	68.4
P50402	Emerin OS=Homo sapiens GN=EMD PE=1 SV=1 - [EMD_HUMAN]	4.72	1	1	29.0
Q09028	Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 PE=1 SV=3 - [RBBP4_HUMAN]	4.71	2	1	47.6
Q8WXX5	DnaJ homolog subfamily C member 9 OS=Homo sapiens GN=DNAJC9 PE=1 SV=1 - [DNJC9_HUMAN]	4.62	1	1	29.9
P84098	60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1 - [RL19_HUMAN]	4.59	1	1	23.5
P56747	Claudin-6 OS=Homo sapiens GN=CLDN6 PE=1 SV=2 - [CLD6_HUMAN]	4.55	1	1	23.3
Q92922	SWI/SNF complex subunit SMARCC1 OS=Homo sapiens GN=SMARCC1 PE=1 SV=3 - [SMRC1_HUMAN	4.52	2	3	122.8
P0DOX5	Immunoglobulin gamma-1 heavy chain OS=Homo sapiens PE=1 SV=1 - [IGG1_HUMAN]	4.45	5	1	49.3
Q8N163	Cell cycle and apoptosis regulator protein 2 OS=Homo sapiens GN=CCAR2 PE=1 SV=2 - [CCAR2_HUM	4.44	1	2	102.8
Q9BRX9	WD repeat domain-containing protein 83 OS=Homo sapiens GN=WDR83 PE=1 SV=1 - [WDR83_HUM	4.44	1	1	34.3
Q96J88	Epithelial-stromal interaction protein 1 OS=Homo sapiens GN=EPSTI1 PE=2 SV=2 - [ESIP1_HUMAN]	4.40	1	1	36.8
P11388	DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3 - [TOP2A_HUMAN]	4.38	2	4	174.3
P19784	Casein kinase II subunit alpha' OS=Homo sapiens GN=CSNK2A2 PE=1 SV=1 - [CSK22_HUMAN]	4.29	3	1	41.2
Q14980	Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [NUMA1_HUMAN]	4.26	1	2	238.1
Q9GZL7	Ribosome biogenesis protein WDR12 OS=Homo sapiens GN=WDR12 PE=1 SV=2 - [WDR12_HUMAN]	4.26	1	1	47.7
P38432	Coilin OS=Homo sapiens GN=COIL PE=1 SV=1 - [COIL_HUMAN]	4.17	1	1	62.6
Q9NY12	H/ACA ribonucleoprotein complex subunit 1 OS=Homo sapiens GN=GAR1 PE=1 SV=1 - [GAR1_HUMA	4.15	1	1	22.3
Q96HS1	Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Homo sapiens GN=PGAM5 PE=1 SV=	4.15	1	1	32.0
O95639	Cleavage and polyadenylation specificity factor subunit 4 OS=Homo sapiens GN=CPSF4 PE=1 SV=1 -	4.09	1	1	30.2
Q14683	Structural maintenance of chromosomes protein 1A OS=Homo sapiens GN=SMC1A PE=1 SV=2 - [SMC	4.06	1	2	143.1
Q10570	Cleavage and polyadenylation specificity factor subunit 1 OS=Homo sapiens GN=CPSF1 PE=1 SV=2 -	3.95	1	3	160.8
Q06587	E3 ubiquitin-protein ligase RING1 OS=Homo sapiens GN=RING1 PE=1 SV=2 - [RING1_HUMAN]	3.94	1	1	42.4
Q53GS9	U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens GN=USP39 PE=1 SV=2 - [SNUT2_HUMAN	3.89	1	2	65.3
P43307	Translocon-associated protein subunit alpha OS=Homo sapiens GN=SSR1 PE=1 SV=3 - [SSRA_HUMA	3.85	1	1	32.2
P46977	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=	3.83	1	2	80.5
P05198	Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3 - [IF2A_	3.81	1	1	36.1
P17676	CCAAT/enhancer-binding protein beta OS=Homo sapiens GN=CEBPB PE=1 SV=2 - [CEBPB_HUMAN]	3.77	1	1	36.1
P00367	Glutamate dehydrogenase 1, mitochondrial OS=Homo sapiens GN=GLUD1 PE=1 SV=2 - [DHE3_HUM	3.76	2	1	61.4
Q03701	CCAAT/enhancer-binding protein zeta OS=Homo sapiens GN=CEBPZ PE=1 SV=3 - [CEBPZ_HUMAN]	3.70	1	2	120.9
O00767	Acyl-CoA desaturase OS=Homo sapiens GN=SCD PE=1 SV=2 - [ACOD_HUMAN]	3.62	1	1	41.5
Q9BUJ2	Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1 PE=1 SV	3.62	1	1	95.7
Q5SSJ5	Heterochromatin protein 1-binding protein 3 OS=Homo sapiens GN=HP1BP3 PE=1 SV=1 - [HP1B3_HU	3.62	1	2	61.2
Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV	3.61	1	1	85.1
Q9UHR5	SAP30-binding protein OS=Homo sapiens GN=SAP30BP PE=1 SV=1 - [S30BP_HUMAN]	3.57	1	1	33.8

Q9UIG0	Tyrosine-protein kinase BAZ1B OS=Homo sapiens GN=BAZ1B PE=1 SV=2 - [BAZ1B_HUMAN]	3.51	1	5	170.8
P04234	T-cell surface glycoprotein CD3 delta chain OS=Homo sapiens GN=CD3D PE=1 SV=1 - [CD3D_HUMAN	3.51	1	1	18.9
Q12996	Cleavage stimulation factor subunit 3 OS=Homo sapiens GN=CSTF3 PE=1 SV=1 - [CSTF3_HUMAN]	3.49	1	1	82.9
Q96G21	U3 small nucleolar ribonucleoprotein protein IMP4 OS=Homo sapiens GN=IMP4 PE=1 SV=1 - [IMP4_H	3.44	1	1	33.7
O94776	Metastasis-associated protein MTA2 OS=Homo sapiens GN=MTA2 PE=1 SV=1 - [MTA2_HUMAN]	3.44	3	1	75.0
O75694	Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=1 SV=1 - [NU155_HUMAN]	3.38	1	4	155.1
Q12824	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1 OS=	3.38	1	1	44.1
O95218	Zinc finger Ran-binding domain-containing protein 2 OS=Homo sapiens GN=ZRANB2 PE=1 SV=2 - [ZR	3.33	1	1	37.4
Q14254	Flotillin-2 OS=Homo sapiens GN=FLOT2 PE=1 SV=2 - [FLOT2_HUMAN]	3.27	1	1	47.0
Q69YZ2	Transmembrane protein 200B OS=Homo sapiens GN=TMEM200B PE=2 SV=1 - [T200B_HUMAN]	3.26	1	1	32.7
P05455	Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2 - [LA_HUMAN]	3.19	1	1	46.8
Q9UDY2	Tight junction protein ZO-2 OS=Homo sapiens GN=TJP2 PE=1 SV=2 - [ZO2_HUMAN]	3.19	1	2	133.9
Q969G3	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=	3.16	1	1	46.6
Q9HAY6	Beta,beta-carotene 15,15'-dioxygenase OS=Homo sapiens GN=BCO1 PE=1 SV=1 - [BCDO1_HUMAN]	3.11	17	1	62.6
Q92499	ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2 - [DDX1_HUMAN]	3.11	1	1	82.4
P63010	AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=1 SV=1 - [AP2B1_HUMAN]	3.09	1	3	104.5
Q92945	Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4 - [FUBP2_HUMAN	3.09	1	2	73.1
Q14CX7	N-alpha-acetyltransferase 25, NatB auxiliary subunit OS=Homo sapiens GN=NAA25 PE=1 SV=1 - [NAA	3.09	18	1	112.2
O75369	Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2 - [FLNB_HUMAN]	3.07	1	5	278.0
Q8IX12	Cell division cycle and apoptosis regulator protein 1 OS=Homo sapiens GN=CCAR1 PE=1 SV=2 - [CCA	3.04	1	1	132.7
Q9BY49	Peroxisomal trans-2-enoyl-CoA reductase OS=Homo sapiens GN=PECR PE=1 SV=2 - [PECR_HUMAN]	2.97	1	1	32.5
Q9HCS7	Pre-mRNA-splicing factor SYF1 OS=Homo sapiens GN=XAB2 PE=1 SV=2 - [SYF1_HUMAN]	2.92	1	1	99.9
O60716	Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1 - [CTND1_HUMAN]	2.89	1	2	108.1
Q14839	Chromodomain-helicase-DNA-binding protein 4 OS=Homo sapiens GN=CHD4 PE=1 SV=2 - [CHD4_HU	2.88	2	3	217.9
Q8WTT2	Nucleolar complex protein 3 homolog OS=Homo sapiens GN=NOC3L PE=1 SV=1 - [NOC3L_HUMAN]	2.88	2	2	92.5
Q5JTH9	RRP12-like protein OS=Homo sapiens GN=RRP12 PE=1 SV=2 - [RRP12_HUMAN]	2.85	1	2	143.6
Q9NVI7	ATPase family AAA domain-containing protein 3A OS=Homo sapiens GN=ATAD3A PE=1 SV=2 - [ATD3	2.84	1	1	71.3
Q86YP4	Transcriptional repressor p66-alpha OS=Homo sapiens GN=GATAD2A PE=1 SV=1 - [P66A_HUMAN]	2.84	1	1	68.0
P26373	60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4 - [RL13_HUMAN]	2.84	1	1	24.2
O15427	Monocarboxylate transporter 4 OS=Homo sapiens GN=SLC16A3 PE=1 SV=1 - [MOT4_HUMAN]	2.80	1	1	49.4
Q09161	Nuclear cap-binding protein subunit 1 OS=Homo sapiens GN=NCBP1 PE=1 SV=1 - [NCBP1_HUMAN]	2.78	1	1	91.8
Q9Y4W6	AFG3-like protein 2 OS=Homo sapiens GN=AFG3L2 PE=1 SV=2 - [AFG32_HUMAN]	2.76	1	2	88.5
Q99959	Plakophilin-2 OS=Homo sapiens GN=PKP2 PE=1 SV=2 - [PKP2_HUMAN]	2.72	1	1	97.4
Q9H0U3	Magnesium transporter protein 1 OS=Homo sapiens GN=MAGT1 PE=1 SV=1 - [MAGT1_HUMAN]	2.69	1	1	38.0
O43395	U4/U6 small nuclear ribonucleoprotein Prp3 OS=Homo sapiens GN=PRPF3 PE=1 SV=2 - [PRPF3_HUM	2.64	1	2	77.5
Q5T9A4	ATPase family AAA domain-containing protein 3B OS=Homo sapiens GN=ATAD3B PE=1 SV=1 - [ATD3	2.62	1	1	72.5
Q8WWY3	U4/U6 small nuclear ribonucleoprotein Prp31 OS=Homo sapiens GN=PRPF31 PE=1 SV=2 - [PRP31_HU	2.61	1	1	55.4
P21333	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4 - [FLNA_HUMAN]	2.53	1	1	280.6
Q13200	26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3 - [PSMD	2.53	1	2	100.1
Q8TED0	U3 small nucleolar RNA-associated protein 15 homolog OS=Homo sapiens GN=UTP15 PE=1 SV=3 - [U	2.51	1	1	58.4
P35249	Replication factor C subunit 4 OS=Homo sapiens GN=RFC4 PE=1 SV=2 - [RFC4_HUMAN]	2.48	1	1	39.7
Q9Y3B9	RRP15-like protein OS=Homo sapiens GN=RRP15 PE=1 SV=2 - [RRP15_HUMAN]	2.48	1	1	31.5
Q9C0J8	pre-mRNA 3' end processing protein WDR33 OS=Homo sapiens GN=WDR33 PE=1 SV=2 - [WDR33_H	2.47	7	1	145.8
Q92786	Prospero homeobox protein 1 OS=Homo sapiens GN=PROX1 PE=1 SV=2 - [PROX1_HUMAN]	2.44	1	1	83.2
Q0VFZ6	Coiled-coil domain-containing protein 173 OS=Homo sapiens GN=CCDC173 PE=2 SV=2 - [CC173_HUM	2.36	1	1	66.4
Q6UN15	Pre-mRNA 3'-end-processing factor FIP1 OS=Homo sapiens GN=FIP1L1 PE=1 SV=1 - [FIP1_HUMAN]	2.36	1	1	66.5
Q86XP3	ATP-dependent RNA helicase DDX42 OS=Homo sapiens GN=DDX42 PE=1 SV=1 - [DDX42_HUMAN]	2.35	1	1	102.9
Q15059	Bromodomain-containing protein 3 OS=Homo sapiens GN=BRD3 PE=1 SV=1 - [BRD3_HUMAN]	2.34	3	2	79.5
Q6IPR3	tRNA wybutosine-synthesizing protein 3 homolog OS=Homo sapiens GN=TYW3 PE=2 SV=2 - [TYW3_	2.32	1	1	29.8
P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1 - [	2.30	2	2	114.7
Q13492	Phosphatidylinositol-binding clathrin assembly protein OS=Homo sapiens GN=PICALM PE=1 SV=2 - [P	2.30	1	1	70.7
Q9Y4C8	Probable RNA-binding protein 19 OS=Homo sapiens GN=RBM19 PE=1 SV=3 - [RBM19_HUMAN]	2.29	1	2	107.3
Q96GQ7	Probable ATP-dependent RNA helicase DDX27 OS=Homo sapiens GN=DDX27 PE=1 SV=2 - [DDX27_H	2.26	1	1	89.8
O00159	Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4 - [MYO1C_HUMAN]	2.26	1	1	121.6
P04844	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens GN=RPN2	2.22	1	1	69.2
Q9BUQ8	Probable ATP-dependent RNA helicase DDX23 OS=Homo sapiens GN=DDX23 PE=1 SV=3 - [DDX23_H	2.20	1	1	95.5
Q9UKF6	Cleavage and polyadenylation specificity factor subunit 3 OS=Homo sapiens GN=CPSF3 PE=1 SV=1 -	2.19	1	1	77.4
O94973	AP-2 complex subunit alpha-2 OS=Homo sapiens GN=AP2A2 PE=1 SV=2 - [AP2A2_HUMAN]	2.13	2	1	103.9
P46087	Probable 28S rRNA (cytosine(4447)-C(5))-methyltransferase OS=Homo sapiens GN=NOP2 PE=1 SV=2	2.09	1	1	89.2
P46013	Antigen KI-67 OS=Homo sapiens GN=MKI67 PE=1 SV=2 - [KI67_HUMAN]	2.06	1	1	358.5
P49792	E3 SUMO-protein ligase RanBP2 OS=Homo sapiens GN=RANBP2 PE=1 SV=2 - [RBP2_HUMAN]	2.02	5	4	358.0
Q16630	Cleavage and polyadenylation specificity factor subunit 6 OS=Homo sapiens GN=CPSF6 PE=1 SV=2 -	2.00	1	1	59.2
Q96FV9	THO complex subunit 1 OS=Homo sapiens GN=THOC1 PE=1 SV=1 - [THOC1_HUMAN]	1.98	1	1	75.6
Q14739	Lamin-B receptor OS=Homo sapiens GN=LBR PE=1 SV=2 - [LBR_HUMAN]	1.95	1	1	70.7
Q15042	Rab3 GTPase-activating protein catalytic subunit OS=Homo sapiens GN=RAB3GAP1 PE=1 SV=3 - [RB3	1.94	1	2	110.5
O14647	Chromodomain-helicase-DNA-binding protein 2 OS=Homo sapiens GN=CHD2 PE=1 SV=2 - [CHD2_HU	1.91	2	1	211.2
P39900	Macrophage metalloelastase OS=Homo sapiens GN=MMP12 PE=1 SV=1 - [MMP12_HUMAN]	1.91	1	1	54.0
O75955	Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3 - [FLOT1_HUMAN]	1.87	1	1	47.3
Q13427	Peptidyl-prolyl cis-trans isomerase G OS=Homo sapiens GN=PPIG PE=1 SV=2 - [PPIG_HUMAN]	1.86	1	1	88.6
Q8TEM1	Nuclear pore membrane glycoprotein 210 OS=Homo sapiens GN=NUP210 PE=1 SV=3 - [PO210_HUM	1.85	1	2	205.0
Q15389	Angiopoietin-1 OS=Homo sapiens GN=ANGPT1 PE=1 SV=2 - [ANGP1_HUMAN]	1.81	1	1	57.5
P16435	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2 - [NCPR_HUMAN]	1.77	1	1	76.6
P12270	Nucleoprotein TPR OS=Homo sapiens GN=TPR PE=1 SV=3 - [TPR_HUMAN]	1.74	1	1	267.1
O00505	Importin subunit alpha-4 OS=Homo sapiens GN=KPNA3 PE=1 SV=2 - [IMA4_HUMAN]	1.73	1	1	57.8
Q13206	Probable ATP-dependent RNA helicase DDX10 OS=Homo sapiens GN=DDX10 PE=1 SV=2 - [DDX10_H	1.71	1	1	100.8
Q9GZU2	Paternally-expressed gene 3 protein OS=Homo sapiens GN=PEG3 PE=1 SV=1 - [PEG3_HUMAN]	1.70	1	1	180.7
Q96KR1	Zinc finger RNA-binding protein OS=Homo sapiens GN=ZFR PE=1 SV=2 - [ZFR_HUMAN]	1.68	1	1	116.9
Q9BQ04	RNA-binding protein 4B OS=Homo sapiens GN=RBM4B PE=1 SV=1 - [RBM4B_HUMAN]	1.67	2	1	40.1
O14776	Transcription elongation regulator 1 OS=Homo sapiens GN=TCERG1 PE=1 SV=2 - [TCRG1_HUMAN]	1.64	1	1	123.8
Q12788	Transducin beta-like protein 3 OS=Homo sapiens GN=TBL3 PE=1 SV=2 - [TBL3_HUMAN]	1.61	1	1	89.0

Q13428	Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=3 - [TCOF_HUMAN]	1.61	1	1	152.0
Q9ULW0	Targeting protein for Xklp2 OS=Homo sapiens GN=TPX2 PE=1 SV=2 - [TPX2_HUMAN]	1.61	1	1	85.6
Q86U86	Protein polybromo-1 OS=Homo sapiens GN=PBRM1 PE=1 SV=1 - [PB1_HUMAN]	1.60	1	1	192.8
Q15637	Splicing factor 1 OS=Homo sapiens GN=SF1 PE=1 SV=4 - [SF01_HUMAN]	1.56	1	1	68.3
P17735	Tyrosine aminotransferase OS=Homo sapiens GN=TAT PE=1 SV=1 - [ATTY_HUMAN]	1.54	1	1	50.4
P33991	DNA replication licensing factor MCM4 OS=Homo sapiens GN=MCM4 PE=1 SV=5 - [MCM4_HUMAN]	1.51	1	1	96.5
Q92797	Symplekin OS=Homo sapiens GN=SYMPK PE=1 SV=2 - [SYMPK_HUMAN]	1.49	1	1	141.1
Q9NY61	Protein AATF OS=Homo sapiens GN=AATF PE=1 SV=1 - [AATF_HUMAN]	1.43	1	1	63.1
Q86SQ6	Adhesion G protein-coupled receptor A1 OS=Homo sapiens GN=ADGRA1 PE=2 SV=3 - [AGRA1_HUMA	1.43	1	1	60.8
Q9BVJ6	U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens GN=UTP14A PE=1 SV=1	1.43	1	1	87.9
Q9BZJ0	Crooked neck-like protein 1 OS=Homo sapiens GN=CRNKL1 PE=1 SV=4 - [CRNL1_HUMAN]	1.42	1	1	100.4
Q9UQE7	Structural maintenance of chromosomes protein 3 OS=Homo sapiens GN=SMC3 PE=1 SV=2 - [SMC3_	1.40	1	1	141.5
P42701	Interleukin-12 receptor subunit beta-1 OS=Homo sapiens GN=IL12RB1 PE=1 SV=1 - [I12R1_HUMAN]	1.36	1	1	73.1
Q96NH3	Protein broad-minded OS=Homo sapiens GN=TBC1D32 PE=2 SV=4 - [BROMI_HUMAN]	1.35	6	1	144.7
Q9Y5Q0	Fatty acid desaturase 3 OS=Homo sapiens GN=FADS3 PE=2 SV=1 - [FADS3_HUMAN]	1.35	1	1	51.1
Q92851	Caspase-10 OS=Homo sapiens GN=CASP10 PE=1 SV=3 - [CASPA_HUMAN]	1.34	1	1	58.9
Q9BRR9	Rho GTPase-activating protein 9 OS=Homo sapiens GN=ARHGAP9 PE=1 SV=2 - [RHG09_HUMAN]	1.33	1	1	83.2
Q8NFH3	Nucleoporin Nup43 OS=Homo sapiens GN=NUP43 PE=1 SV=1 - [NUP43_HUMAN]	1.32	3	1	42.1
Q8TAM2	Tetratricopeptide repeat protein 8 OS=Homo sapiens GN=TTC8 PE=1 SV=2 - [TTC8_HUMAN]	1.29	1	1	61.5
Q9H6N6	Putative uncharacterized protein MYH16 OS=Homo sapiens GN=MYH16 PE=1 SV=2 - [MYH16_HUMA	1.28	3	1	128.2
Q00266	S-adenosylmethionine synthase isoform type-1 OS=Homo sapiens GN=MAT1A PE=1 SV=2 - [METK1_	1.27	3	1	43.6
Q9Y6W6	Dual specificity protein phosphatase 10 OS=Homo sapiens GN=DUSP10 PE=1 SV=1 - [DUS10_HUMAN	1.24	1	1	52.6
P57740	Nuclear pore complex protein Nup107 OS=Homo sapiens GN=NUP107 PE=1 SV=1 - [NU107_HUMAN]	1.19	1	1	106.3
Q9NQW1	Protein transport protein Sec31B OS=Homo sapiens GN=SEC31B PE=1 SV=1 - [SC31B_HUMAN]	1.19	2	1	128.6
Q15051	IQ calmodulin-binding motif-containing protein 1 OS=Homo sapiens GN=IQCB1 PE=1 SV=1 - [IQCB1_	1.17	1	1	68.9
Q68DV7	E3 ubiquitin-protein ligase RNF43 OS=Homo sapiens GN=RNF43 PE=1 SV=1 - [RNF43_HUMAN]	1.15	1	1	85.7
O75691	Small subunit processome component 20 homolog OS=Homo sapiens GN=UTP20 PE=1 SV=3 - [UTP2	1.15	1	1	318.2
P01024	Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2 - [CO3_HUMAN]	1.14	1	1	187.0
Q92621	Nuclear pore complex protein Nup205 OS=Homo sapiens GN=NUP205 PE=1 SV=3 - [NU205_HUMAN]	1.14	1	1	227.8
Q92484	Acid sphingomyelinase-like phosphodiesterase 3a OS=Homo sapiens GN=SMPDL3A PE=1 SV=2 - [ASM	1.10	1	1	51.2
Q6PI77	Protein BHLHb9 OS=Homo sapiens GN=BHLHB9 PE=2 SV=1 - [BHLH9_HUMAN]	1.10	1	1	60.3
P49761	Dual specificity protein kinase CLK3 OS=Homo sapiens GN=CLK3 PE=1 SV=3 - [CLK3_HUMAN]	1.10	1	1	73.5
Q9H2P0	Activity-dependent neuroprotector homeobox protein OS=Homo sapiens GN=ADNP PE=1 SV=1 - [AD	1.09	1	1	123.5
P02751	Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4 - [FINC_HUMAN]	1.09	1	2	262.5
Q9BVP2	Guanine nucleotide-binding protein-like 3 OS=Homo sapiens GN=GNL3 PE=1 SV=2 - [GNL3_HUMAN]	1.09	1	1	62.0
Q5UIP0	Telomere-associated protein RIF1 OS=Homo sapiens GN=RIF1 PE=1 SV=2 - [RIF1_HUMAN]	1.09	1	1	274.3
Q8IXK0	Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 PE=1 SV=1 - [PHC2_HUMAN]	1.05	1	1	90.7
Q8WUM0	Nuclear pore complex protein Nup133 OS=Homo sapiens GN=NUP133 PE=1 SV=2 - [NU133_HUMAN]	1.04	1	1	128.9
Q3MJ13	WD repeat-containing protein 72 OS=Homo sapiens GN=WDR72 PE=2 SV=2 - [WDR72_HUMAN]	1.00	1	1	123.3
O15078	Centrosomal protein of 290 kDa OS=Homo sapiens GN=CEP290 PE=1 SV=2 - [CE290_HUMAN]	0.93	2	1	290.2

A8K2U0	Alpha-2-macroglobulin-like protein 1 OS=Homo sapiens GN=A2ML1 PE=1 SV=3 - [A2ML1_HUMAN]	0.89	1	1	161.0
P49790	Nuclear pore complex protein Nup153 OS=Homo sapiens GN=NUP153 PE=1 SV=2 - [NU153_HUMAN]	0.88	1	1	153.8
Q9H2G4	Testis-specific Y-encoded-like protein 2 OS=Homo sapiens GN=TSPYL2 PE=1 SV=1 - [TSYL2_HUMAN]	0.87	1	1	79.4
Q9C0G6	Dynein heavy chain 6, axonemal OS=Homo sapiens GN=DNAH6 PE=1 SV=3 - [DYH6_HUMAN]	0.84	1	1	475.7
P26358	DNA (cytosine-5)-methyltransferase 1 OS=Homo sapiens GN=DNMT1 PE=1 SV=2 - [DNMT1_HUMAN]	0.74	1	1	183.0
Q07157	Tight junction protein ZO-1 OS=Homo sapiens GN=TJP1 PE=1 SV=3 - [ZO1_HUMAN]	0.69	1	1	195.3
Q8NFU7	Methylcytosine dioxygenase TET1 OS=Homo sapiens GN=TET1 PE=1 SV=2 - [TET1_HUMAN]	0.66	1	1	235.2
Q14571	Inositol 1,4,5-trisphosphate receptor type 2 OS=Homo sapiens GN=ITPR2 PE=1 SV=2 - [ITPR2_HUMA	0.63	1	1	307.9
Q9NYQ6	Cadherin EGF LAG seven-pass G-type receptor 1 OS=Homo sapiens GN=CELSR1 PE=1 SV=1 - [CELR1	0.56	1	1	329.3
P51610	Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2 - [HCFC1_HUMAN]	0.54	1	1	208.6
O15067	Phosphoribosylformylglycinamidine synthase OS=Homo sapiens GN=PFAS PE=1 SV=4 - [PUR4_HUMA	0.45	2	1	144.6
Q15154	Pericentriolar material 1 protein OS=Homo sapiens GN=PCM1 PE=1 SV=4 - [PCM1_HUMAN]	0.30	1	1	228.4
Q8WXX0	Dynein heavy chain 7, axonemal OS=Homo sapiens GN=DNAH7 PE=1 SV=2 - [DYH7_HUMAN]	0.17	1	1	460.9

Figure S1 A. TARDBP left and right arms (1220 bp).

(Black: Left arm of TARDBP, Black: Right arm of TARDBP, Black: gRNA, White: PAM)

GTTCTTTACACCTGGTTCACTGCCCATATTCAGTCTTCAGGTTCAGCTGATGGATCGC
TTGCTTAGGAAAATCGACTGGGACCTATCACGCCCATGCCTCAGCCAGTTAGGCTCC
TCCTCTGCCTTCAGGATTACTTAACGACTAACCCGATTGTCATAAAATAGCTACTGTTT
ATTGTTCCCTTGCATACCCTAGCTTGTAACCAGCAAGCCACGTTGGACTCACAGTTAC
AGTTTCAGTACCTGACGCATCATAAGCCTTCAGGGAAAGTTTTTTGAATGAATGAAC
TGGCGAGGCATCACATTTTGATAGGAAATCACTACCCTTACCTTCACCTCGTCATTTT
TCAGGGATAACCAATGCATATACGAATCCAGACAAGCATTTTTCTGGAAGTCAGAAC
TCTGACATGGTTTGGGTATTATCATTATAAGGAAACAGTTATTCTGACATGAATGTTGT
TCATTCATATCTCTTTTCTCTTTAGGAAAAGTAAAAGATGTCTGAATATATTCGGGTAA
guide 3
CCGAAGATGAGAACGATGAGCCCATTGAAATACCATCGGAAGACGATGGGACGGTG
guide 1
CTGCTCTCCACGGTTACAGCCCAGTTTCCAGGGGCGTGTGGGCTTCGCTACAGGAAT
CCAGTGTCTCAGTGTATGAGAGGTGTCCGGCTGGTAGAAGGAATTCTGCATGCCCCA
GATGCTGGCTGGGGAAATCTGGTGTATGTTGTCAACTATCCAAAAGGTTTGTTACCAT
TTGGTTTTTGTAATCATGCTGAAGTGTGTTCAGGTGTGTGTCTCATCCATGGATCTTA
GCCTCTTTTGGTGGCAGAATGTCTCCTGAAACTTAAGTATTTCCTTGAACTTCAGTGT
TAGACAAGTTTGGAAGACCACGAGTCTAAATTTATGGAAACTGGGGATTGTAGATCA
TTTTAAAAGAGAAAACAATGTATTTAAAAAATATCTGAATAAACTTTGCCAAGTTGAT
GATAAATTTCAGGAATCACTAAGAATGTTTTGTACATAAATCATTGTTGTAAATAGATT
CTTCTGAAGTGCTTCAGTGTTTGGATTTGATCATTGTCCTTTTGGTGTTACATCATTCA
TTCAGCAAATCTGAGTTCATTTTTTCCCTTAAATGAGCAAACAGTTGGAGTAGCCAA
ATCTTGAATTAGTGCAGTTCCAATTACAATTTCGAGGTTCTGGTCTTATCCTTCTCTCT
GCCTC

Figure S1 B.TARDBP puro-DD knock-in cassette (2252 bp).

(Black: Left arm of TARDBP, Blue: Puro, Orange: P2A, Red: DD-tag, Sky blue: 3xGGGGS, Black: Right arm of TARDBP, Black: point mutation site of PAM sequences)

GTTCTTTACACCTGGTTCACTGCCCATATTCAGTCTTCAGGTTCAGCTGATGGATCGC
TTGCTTAGGAAAATCGACTGGGACCTATCACGCCCATGCCTCAGCCAGTTAGGCTCC
TCCTCTGCCTTCAGGATTACTTAACGACTAACCCGATTGTCATAAAATAGCTACTGTTT
ATTGTTCCCTTGCATACCCTAGCTTGTAACCAGCAAGCCACGTTGGACTCACAGTTAC
AGTTTCAGTACCTGACGCATCATAAGCCTTCAGGGAAAGTTTTTTGAATGAATGAAC
TGGCGAGGCATCACATTTTGATAGGAAATCACTACCCTTACCTTCACCTCGTCATTTT
TCAGGGATAACCAATGCATATACGAATCCAGACAAGCATTTTTCTGGAAGTCAGAAC
TCTGACATGGTTTGGGTATTATCATTATAAGGAAACAGTTATTCTGACATGAATGTTGT
TCATTCATATCTCTTTTCTCTTTAGGAAAAGTAAAAGATGACCGAGTACAAGCCCACG
GTGCGCCTCGCCACCCGCGACGACGTCCCCAGGGCCGTACGCACCCTCGCCGCCGC
GTTCGCCGACTACCCCGCCACGCGCCACACCGTCGATCCGGACCGCCACATCGAGC
GGGTCACCGAGCTGCAAGAACTCTTCCTCACGCGCGTCGGGCTCGACATCGGCAAG
GTGTGGGTCGCGGACGACGGCGCCGCGGTGGCGGTCTGGACCACGCCGGAGAGCG
TCGAAGCGGGGGCGGTGTTCGCCGAGATCGGCCCGCGCATGGCCGAGTTGAGCGGT
TCCCGGCTGGCCGCGCAGCAACAGATGGAAGGCCTCCTGGCGCCGCACCGGCCCAA
GGAGCCCGCGTGGTTCCTGGCCACCGTCGGCGTCTCGCCCGACCACCAGGGCAAGG
GTCTGGGCAGCGCCGTCGTGCTCCCCGGAGTGGAGGCGGCCGAGCGCGCCGGGGT
GCCCGCCTTCCTGGAGACCTCCGCGCCCCGCAACCTCCCCTTCTACGAGCGGCTCGG
CTTCACCGTCACCGCCGACGTCGAGGTGCCCGAAGGACCGCGCACCTGGTGCATGA
CCCGCAAGCCCGGTGCCGGATCCGGAGCCACGAACTTCTCTCTGTTAAAGCAAGCA
GGAGACGTGGAAGAAAACCCCGGTCCCATGGGAGTGCAGGTGGAAACCATCTCCCC
AGGAGACGGGCGCACCTTCCCCAAGCGCGGCCAGACCTGTGTGGTGCACTACACCG
GGATGCTTGAAGATGGAAAGAAAGTCGATTCCTCCCGGGACAGAAACAAGCCCTTT
AAGTTTATGCTAGGCAAGCAGGAGGTGATCCGAGGCTGGGAAGAAGGGGTTGCCCA
GATGAGTGTGGGTCAGAGAGCCAAACTGACTATATCTCCAGATTATGCCTATGGTGCC
ACTGGGCACCCAGGCATCATCCCACCACATGCCACTCTCGTCTTCGATGTGGAGCTT
CTAAAACCGGAAGGTGGAGGTGGATCTGGTGGAGGTGGATCTGGTGGCGGCGGTTC
AATGTCTGAATATATTCGGGTAACCGAAGATGAGAACGATGAGCCCATTGAAATACC
ATCGGAAGACGATGGGACGGTGCTGCTCTCCACAGTTACAGCCCAGTTTCCAGGGG
CGTGTGGGCTTCGCTACAGAAATCCAGTGTCTCAGTGTATGAGAGGTGTCCGGCTGG
TAGAAGGAATTCTGCATGCCCCAGATGCTGGCTGGGGAAATCTGGTGTATGTTGTCA
ACTATCCAAAAGGTTTGTTACCATTTGGTTTTTGTAATCATGCTGAAGTGTGTTCAGG
TGTGTGTCTCATCCATGGATCTTAGCCTCTTTTGGTGGCAGAATGTCTCCTGAAACTT

AAGTATTTCCTTGAACTTCAGTGTTAGACAAGTTTGGAAGACCACGAGTCTAAATTT
ATGGAAACTGGGGATTGTAGATCATTTTAAAAGAGAAAACAATGTATTTAAAAAATAT
CTGAATAAACTTTGCCAAGTTGATGATAAATTTCAGGAATCACTAAGAATGTTTTGTA
CATAAATCATTGTTGTAAATAGATTCTTCTGAAGTGCTTCAGTGTTTGGATTTGATCAT
TGTCCTTTTGGTGTTACATCATTCATTCAGCAAATCTGAGTTCATTTTTTCCCTTAAAT
GAGCAAACAGTTGGAGTAGCCAAATCTTGAATTAGTGCAGTTCCAATTACAATTTCG
AGGTTCTGGTCTTATCCTTCTCTCTGCCTC

Figure S1 C.TARDBP bla-DD knock-in cassette (2051 bp).

(Black: Left arm of TARDBP, Blue: bla, Orange: P2A, Red: DD-tag, Sky blue: 3xGGGGS, Black: Right arm of TARDBP, Black: point mutation site of PAM sequences)

GTTCTTTACACCTGGTTCACTGCCCATATTCAGTCTTCAGGTTCAGCTGATGGATCGC
TTGCTTAGGAAAATCGACTGGGACCTATCACGCCCATGCCTCAGCCAGTTAGGCTCC
TCCTCTGCCTTCAGGATTACTTAACGACTAACCCGATTGTCATAAAATAGCTACTGTTT
ATTGTTCCCTTGCATACCCTAGCTTGTAACCAGCAAGCCACGTTGGACTCACAGTTAC
AGTTTCAGTACCTGACGCATCATAAGCCTTCAGGGAAAGTTTTTTGAATGAATGAAC
TGGCGAGGCATCACATTTTGATAGGAAATCACTACCCTTACCTTCACCTCGTCATTTT
TCAGGGATAACCAATGCATATACGAATCCAGACAAGCATTTTTCTGGAAGTCAGAAC
TCTGACATGGTTTGGGTATTATCATTATAAGGAAACAGTTATTCTGACATGAATGTTGT
TCATTCATATCTCTTTTCTCTTTAGGAAAAGTAAAAGATGGCCAAGCCTTTGTCTCAA
GAAGAATCCACCCTCATTGAAAGAGCAACGGCTACAATCAACAGCATCCCCATCTCT
GAAGACTACAGCGTCGCCAGCGCAGCTCTCTCTAGCGACGGCCGCATCTTCACTGGT
GTCAATGTATATCATTTTACTGGGGGACCTTGTGCAGAACTCGTGGTGCTGGGCACTG
CTGCTGCTGCGGCAGCTGGCAACCTGACTTGTATCGTCGCGATCGGAAATGAGAACA
GGGGCATCTTGAGCCCCTGCGGACGGTGCCGACAGGTGCTTCTCGATCTGCATCCTG
GGATCAAAGCCATAGTGAAGGACAGTGATGGACAGCCGACGGCAGTTGGGATTCGT
GAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCGGATCCGGAGCCACGAACTTCTCT
CTGTTAAAGCAAGCAGGAGACGTGGAAGAAAACCCCGGTCCCATGGGAGTGCAGG
TGGAAACCATCTCCCCAGGAGACGGGCGCACCTTCCCCAAGCGCGGCCAGACCTGT
GTGGTGCACTACACCGGGATGCTTGAAGATGGAAAGAAAGTCGATTCCTCCCGGGA
CAGAAACAAGCCCTTTAAGTTTATGCTAGGCAAGCAGGAGGTGATCCGAGGCTGGG
AAGAAGGGGTTGCCCAGATGAGTGTGGGTCAGAGAGCCAAACTGACTATATCTCCA
GATTATGCCTATGGTGCCACTGGGCACCCAGGCATCATCCCACCACATGCCACTCTCG
TCTTCGATGTGGAGCTTCTAAAACCGGAAGGTGGAGGTGGATCTGGTGGAGGTGGA
TCTGGTGGCGGCGGTTCAATGTCTGAATATATTCGGGTAACCGAAGATGAGAACGAT
GAGCCCATTGAAATACCATCGGAAGACGATGGGACGGTGCTGCTCTCCACAGTTACA
GCCCAGTTTCCAGGGGCGTGTGGGCTTCGCTACAGAAATCCAGTGTCTCAGTGTATG
AGAGGTGTCCGGCTGGTAGAAGGAATTCTGCATGCCCCAGATGCTGGCTGGGGAAA
TCTGGTGTATGTTGTCAACTATCCAAAAGGTTTGTTACCATTTGGTTTTTGTAATCATG
CTGAAGTGTGTTCAGGTGTGTGTCTCATCCATGGATCTTAGCCTCTTTTGGTGGCAGA
ATGTCTCCTGAAACTTAAGTATTTCCTTGAACTTCAGTGTTAGACAAGTTTGGAAGAC
CACGAGTCTAAATTTATGGAAACTGGGGATTGTAGATCATTTTAAAAGAGAAAACAA
TGTATTTAAAAAATATCTGAATAAACTTTGCCAAGTTGATGATAAATTTCAGGAATCA
CTAAGAATGTTTTGTACATAAATCATTGTTGTAAATAGATTCTTCTGAAGTGCTTCAGT

GTTTGGATTTGATCATTGTCCTTTTGGTGTTACATCATTCATTCAGCAAATCTGAGTTC
ATTTTTTCCCTTAAATGAGCAAACAGTTGGAGTAGCCAAATCTTGAATTAGTGCAGTT
CCAATTACAATTTCGAGGTTCTGGTCTTATCCTTCTCTCTGCCTC

Figure S2.

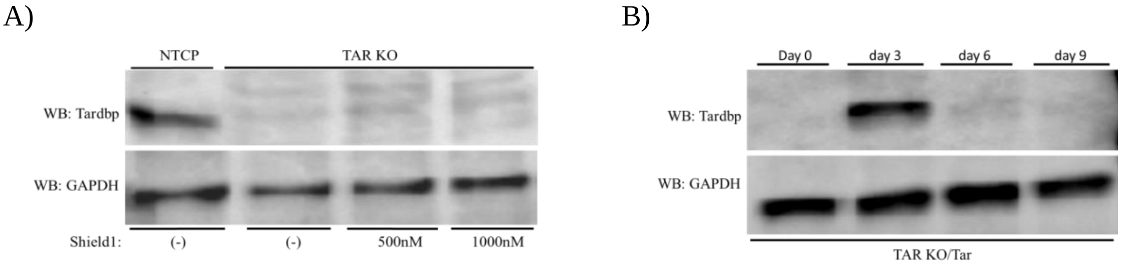

A)
NTCP
TAR KO
WB: Tardbp
WB: GAPDH
Shield1:
(-)
(-)
500nM
1000nM
B)
Day 0
day 3
day 6
day 9
WB: Tardbp
WB: GAPDH
TAR KO/Tar

Figure S3.

Probe 1 (1804-1849)
S TTCACCAGCACCATGCAACTTTTTCACCTCTGCCTAATCATCTCAT
AS ATGAGATGATTAGGCAGAGGTGAAAAAGTTGCATGGTGCTGGTGAA

Probe 2 (1765-1810)
S GTCTTTGTACTAGGAGGCTGTAGGCATAAATTGGTCTGTTCACCAG
AS CTGGTGAACAGACCAATTTATGCCTACAGCCTCCTAGTACAAAGAC

Probe 3 (1728-1773)
S AAGACTGGGAGGAGTTGGGGGAGGAGATTAGGTTAAAGGTCTTTGT
AS ACAAAGACCTTTAACCTAATCTCCTCCCCCAACTCCTCCCAGTCTT

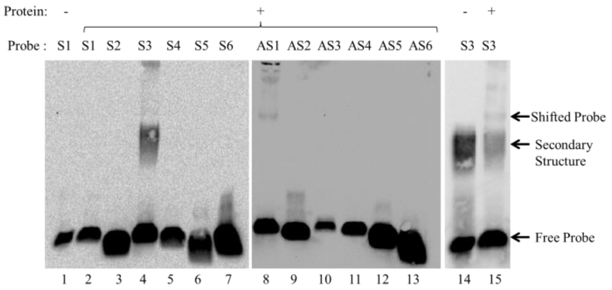
Probe 4 (1690-1735)
S GACCGACCTTGAGGCATACTTCAAAGACTGTGTGTTTAAAGACTGG
AS CCAGTCTTTAAACACACAGTCTTTGAAGTATGCCTCAAGGTCGGTC

Probe 5(1655-1700)
S CATAAGAGGACTCTTGGACTCTCAGCAATGTCAACGACCGACCTTG
AS CAAGGTCGGTCGTTGACATTGCTGAGAGTCCAAGAGTCCTCTTATG

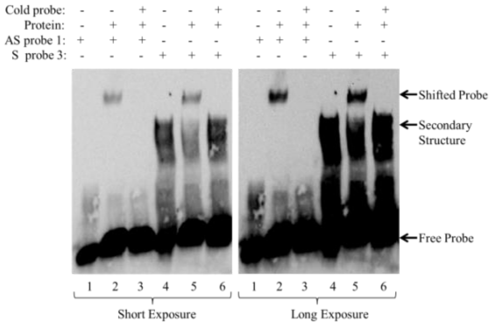
Probe 6 (1611-1657)
S TGGAGACCACCGTGAACGCCCGCCAGGTCTTGCCCAAGGTCTTACAT
AS ATGTAAGACCTTGGGCAAGACCTGGCGGGCGTTCACGGTGGTCTCCA

Figure S4.

A)



B)



C)

WT(1804-1849 ATGAGATGATTAGGCAGAGGTGAAAAAGTTGCATGGTGCTGGTGAA
s1 (1799-1825) ATGAACATGAGATGATTAGGCAGAGGTG
s2 (1822-1849) GGTGAAAAAGTTGCATGGTGCTGGTGAA
s3 (1818-1841) CAGAGGTGAAAAAGTTGCATGGTG
s4 (1828-1851) AAAGTTGCATGGTGCTGGTGAACA

D)

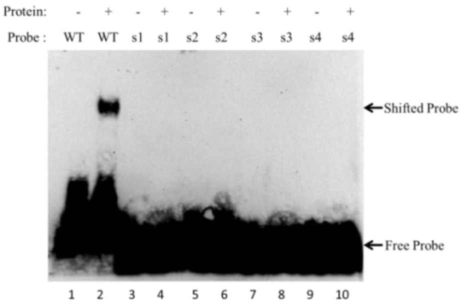


Figure S5.

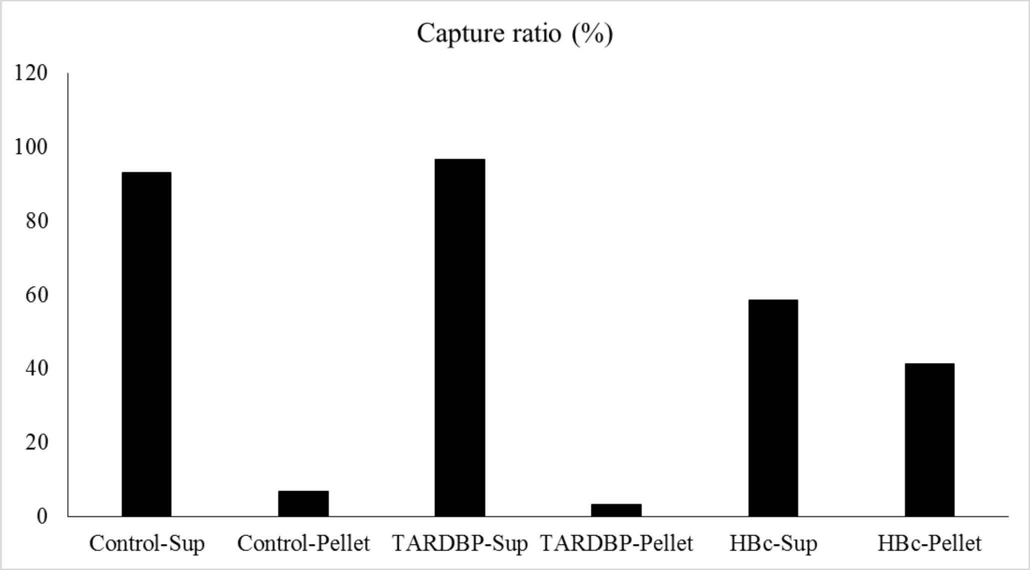
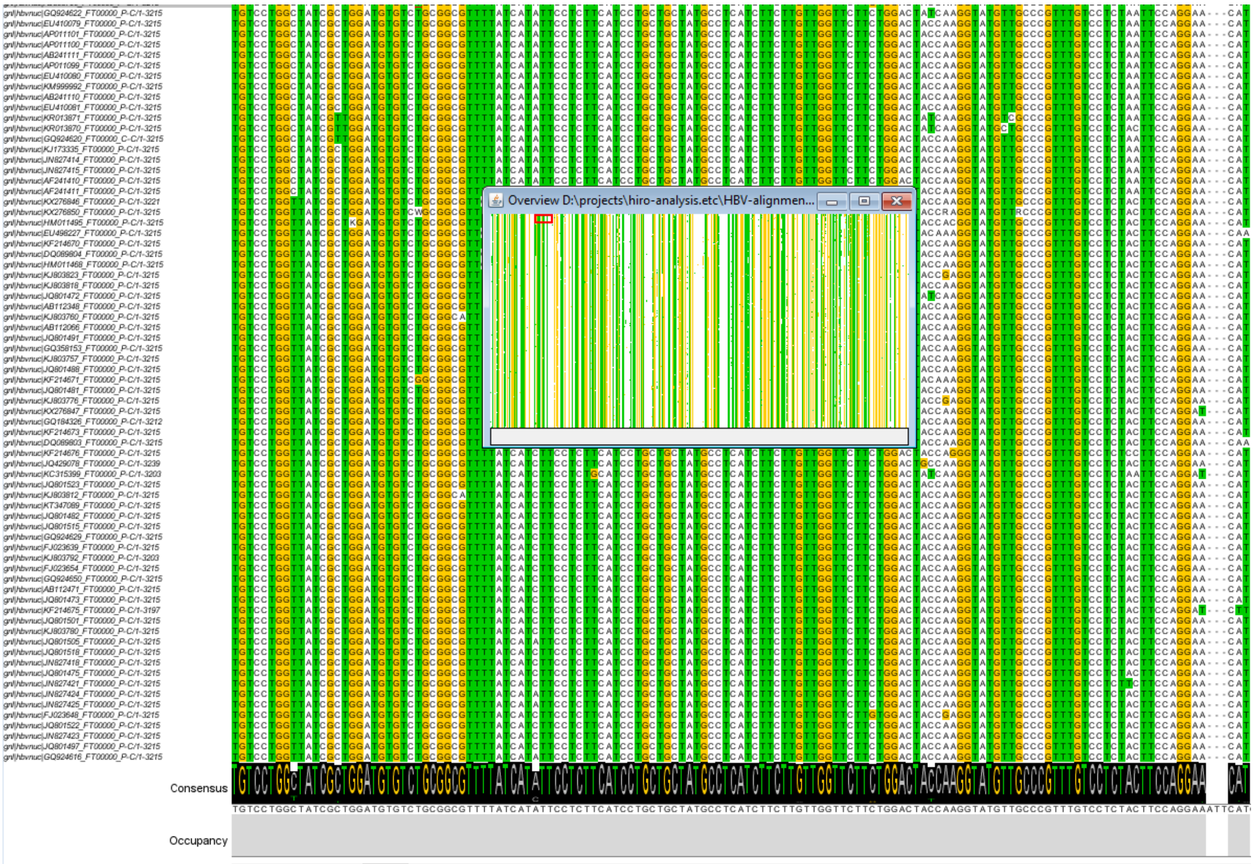
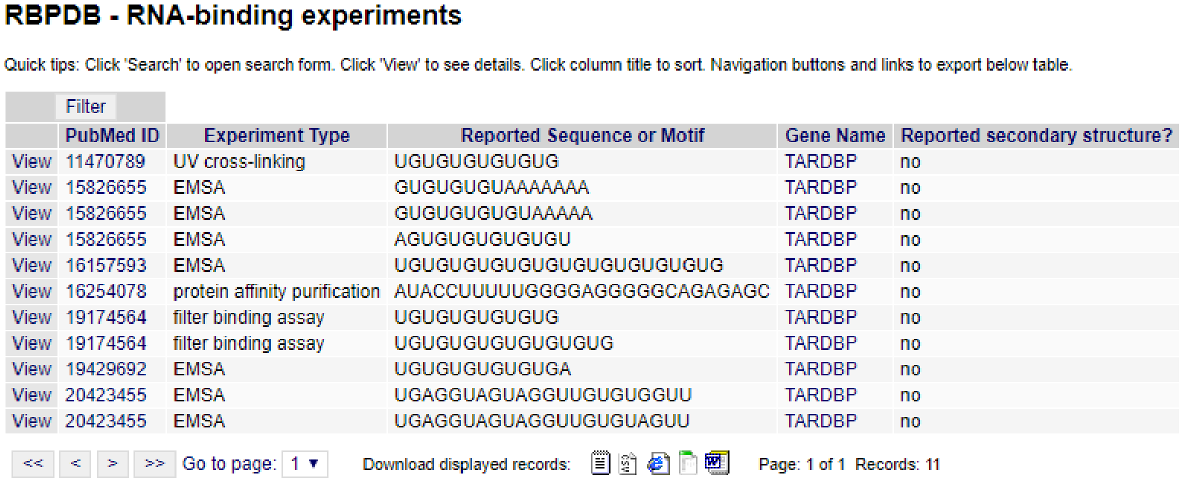

Capture ratio (%)
120
100
80
60
40
20
0
Control-Sup
Control-Pellet
TARDBP-Sup
TARDBP-Pellet
HBc-Sup
HBc-Pellet

Figure S6.

A)



B)



RBPDB - RNA-binding experiments

Quick tips: Click 'Search' to open search form. Click 'View' to see details. Click column title to sort. Navigation buttons and links to export below table.

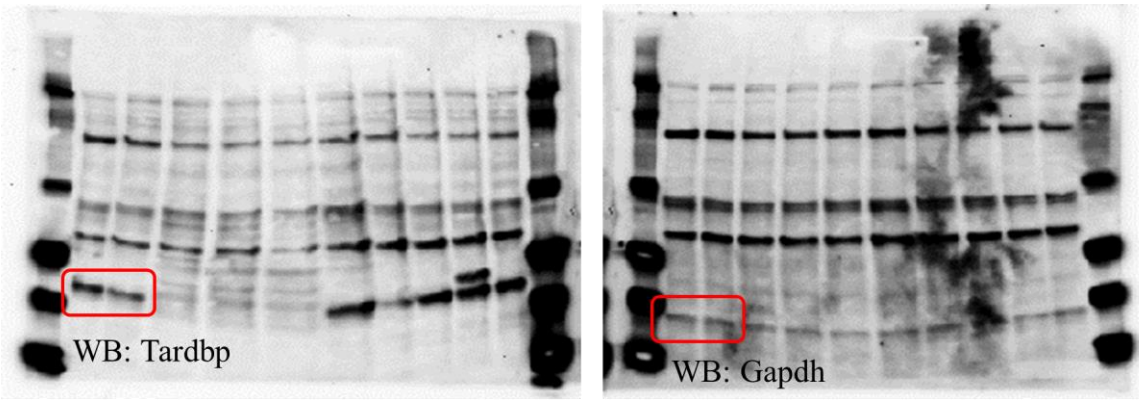
	PubMed ID	Experiment Type	Reported Sequence or Motif	Gene Name	Reported secondary structure?
View	11470789	UV cross-linking	UGUGUGUGUGUG	TARDBP	no
View	15826655	EMSA	GUGUGUGUAAAAAAA	TARDBP	no
View	15826655	EMSA	GUGUGUGUGUAAAAA	TARDBP	no
View	15826655	EMSA	AGUGUGUGUGUGU	TARDBP	no
View	16157593	EMSA	UGUGUGUGUGUGUGUGUGUGUG	TARDBP	no
View	16254078	protein affinity purification	AUACCUUUUUGGGGAGGGGGCAGAGAGC	TARDBP	no
View	19174564	filter binding assay	UGUGUGUGUGUG	TARDBP	no
View	19174564	filter binding assay	UGUGUGUGUGUGUGUG	TARDBP	no
View	19429692	EMSA	UGUGUGUGUGUGA	TARDBP	no
View	20423455	EMSA	UGAGGUAGUAGGUUGUGUGGUU	TARDBP	no
View	20423455	EMSA	UGAGGUAGUAGGUUGUGUAGUU	TARDBP	no

C)

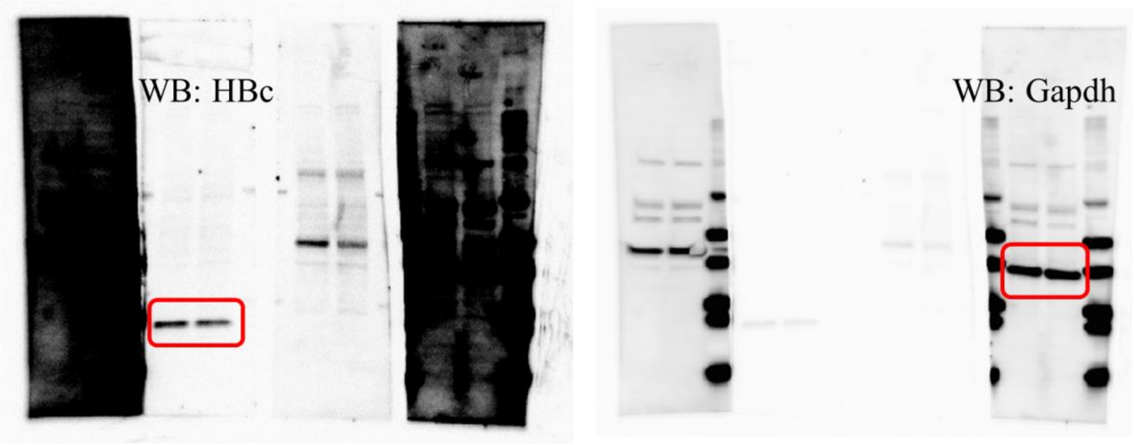

1
200
400
600
800
1 K
1,200
1,400
1,600
1,800
2 K
2,200
2,400
2,600
2,800
3 K
3,215
Genes
P
ALM26189.1
P
ALM26189.1
ALM26187.1
ALM26187.1
ALM26191.1
ALM26...
S
S
ALM26188.1
ALM26186.1
(U) matches.bed/TARDBP
match1
match2
match3
match4
match5
match6
match7
match8
match9
match10
match11
match12
match13
match14
match15
match16
match17
match18
match19
match20
match21
match22
match23
match24
match25
match26
match27
match28
match29
match30
match31
match32
match33
match34
match35
match36
match37
match38
match39
match40
match41
match42
match43
match44
match45
match46
match47

Figure S7.

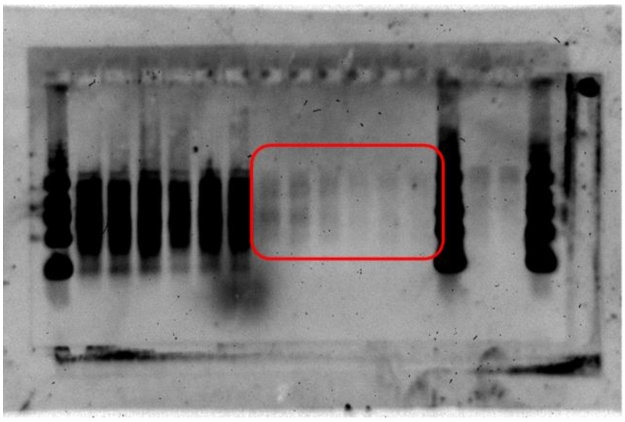
Full length blots for Fig. 1a



Full length blots for Fig. 1d



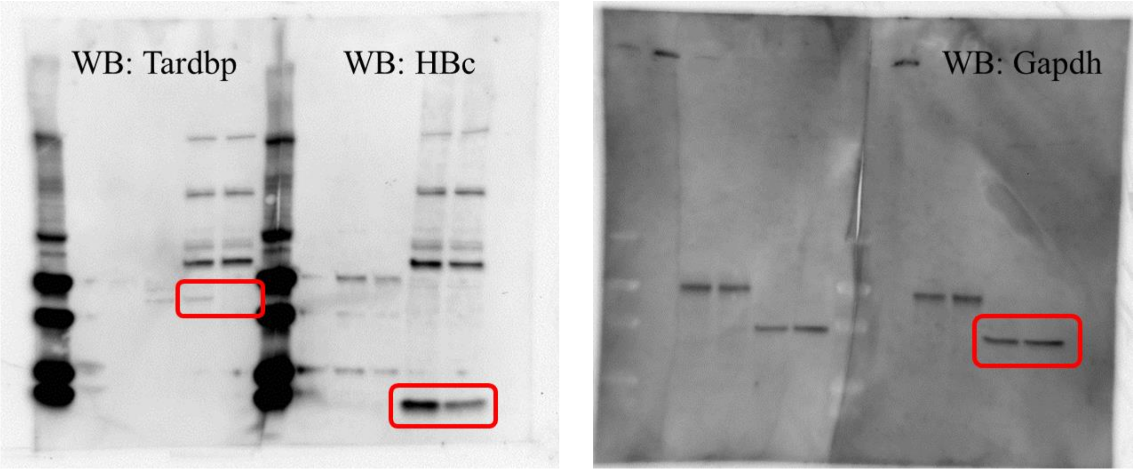
Full length blot for Fig. 1e



Supplementary data: Full length blots.
The red rectangles indicate the cropped portion of the images used in the figures of the manuscript.

Figure S8.

Full length blots for Fig. 2a



Full length blot for Fig. 2c

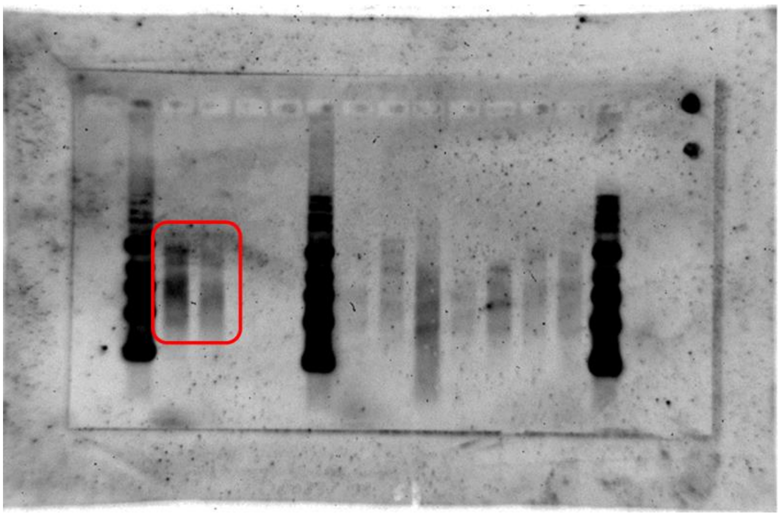
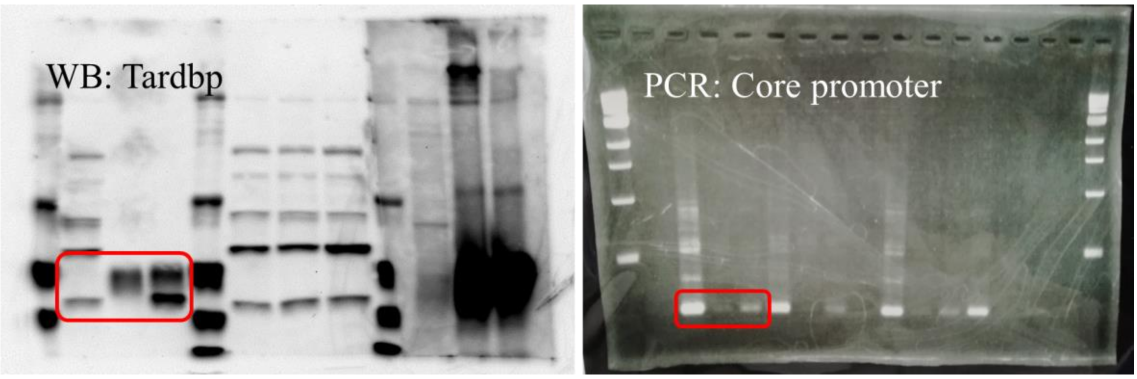


Figure S9.

Full length blots for Fig.3c



Full length blots for Fig. 3e

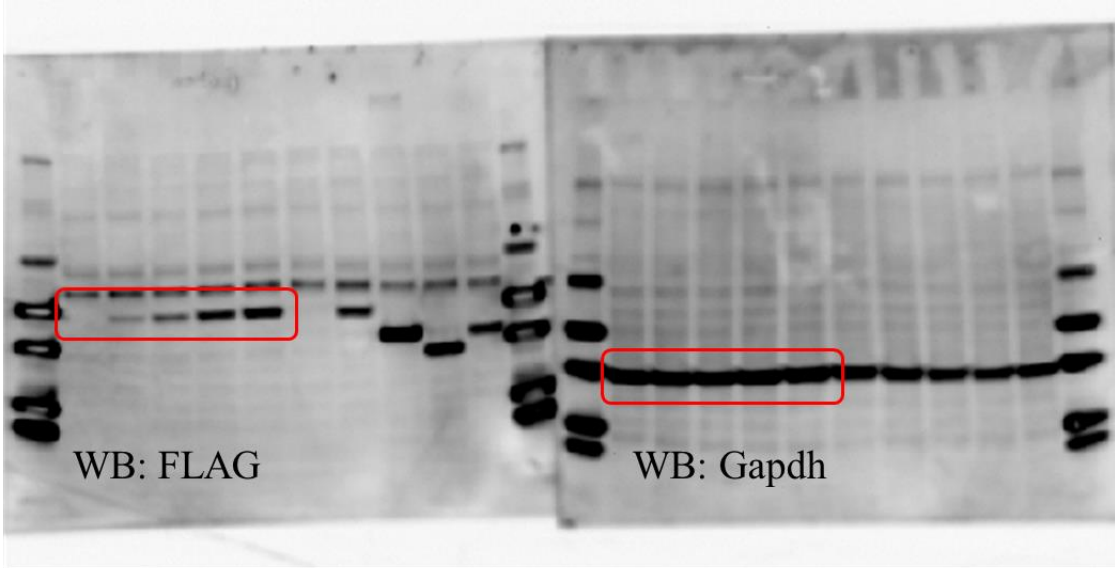
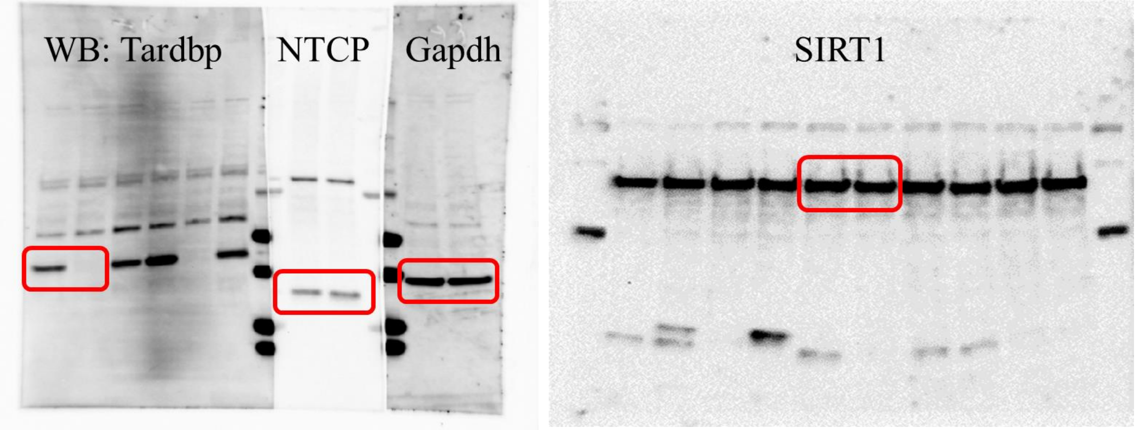


Figure S10.

Full length blots for Fig. 4b



Full length blots for Fig. 4c

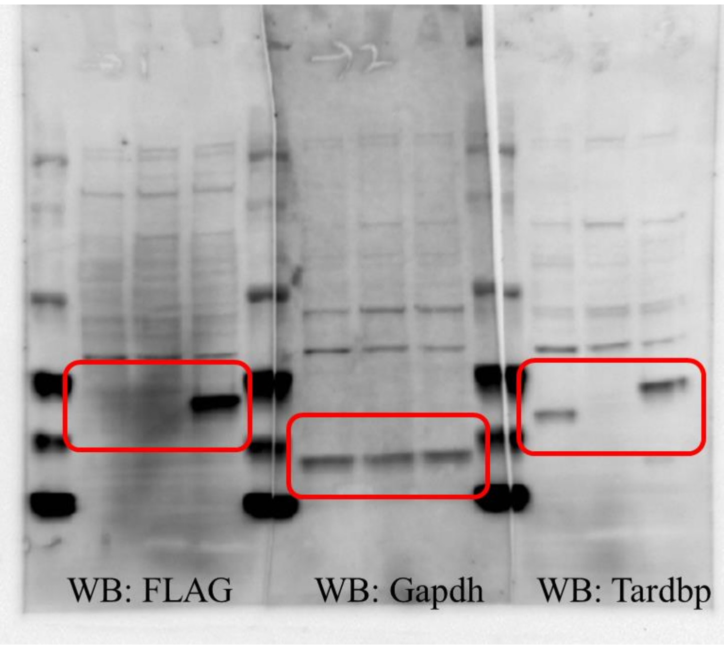


Figure S11.

Full length blots for Fig. 5b

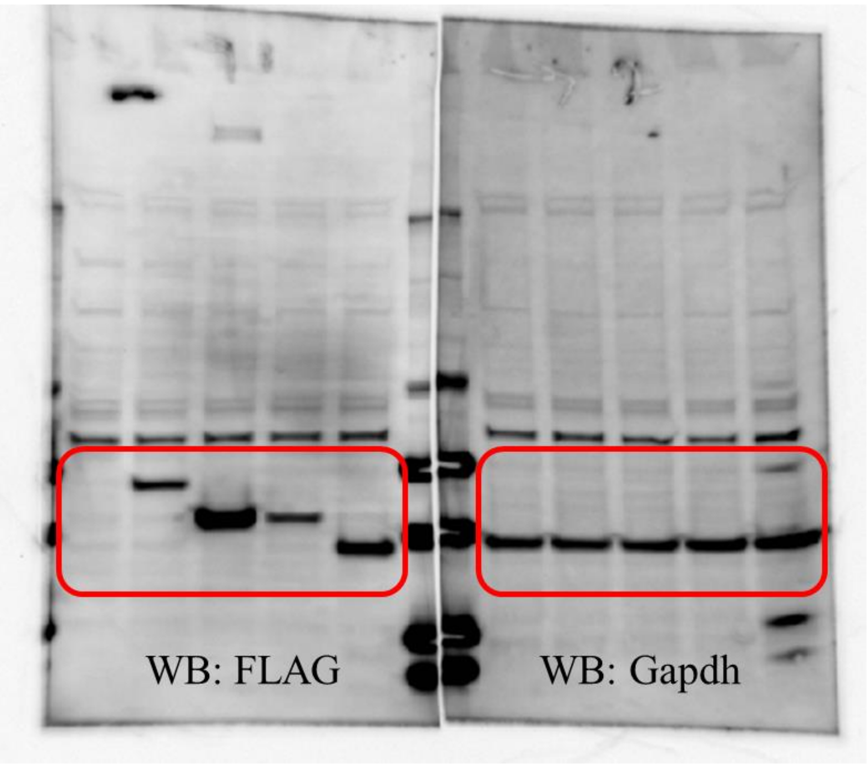
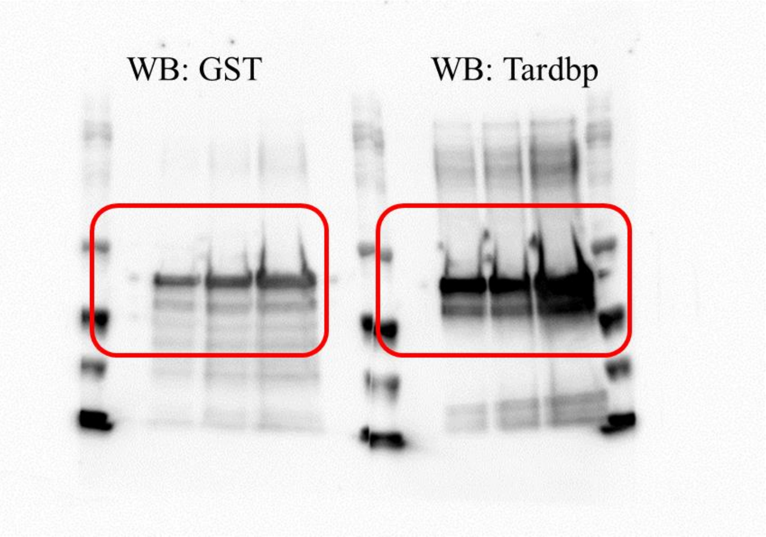
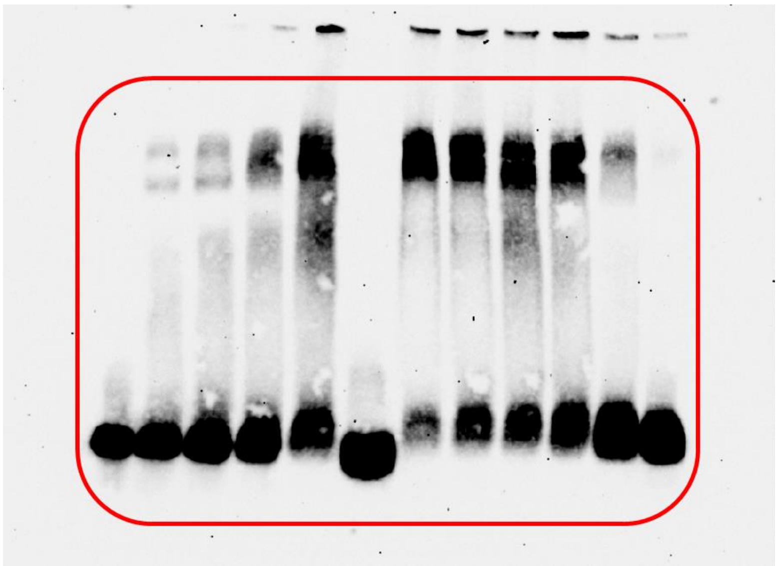


Figure S12.

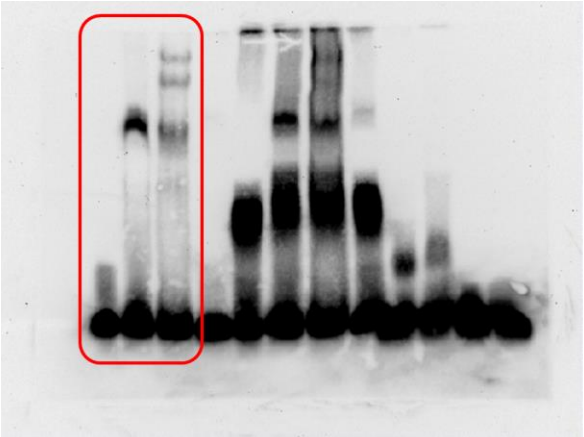
Full length blots for Fig. 6a



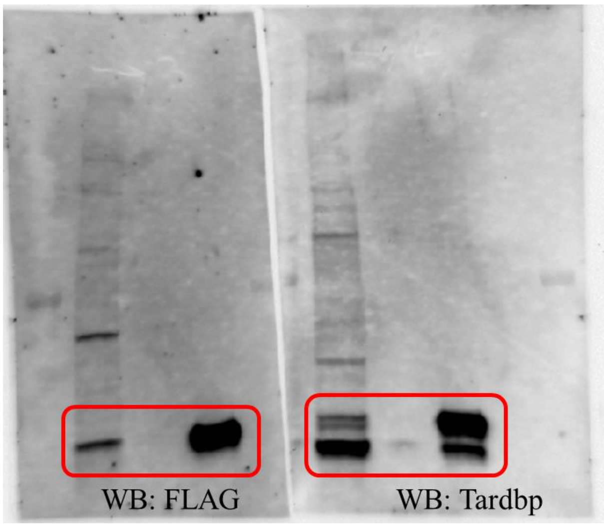
Full length blot for Fig. 6c



Full length blot Fig. 6d



Full length blots Fig. 6e



Full length blot Fig. 6f

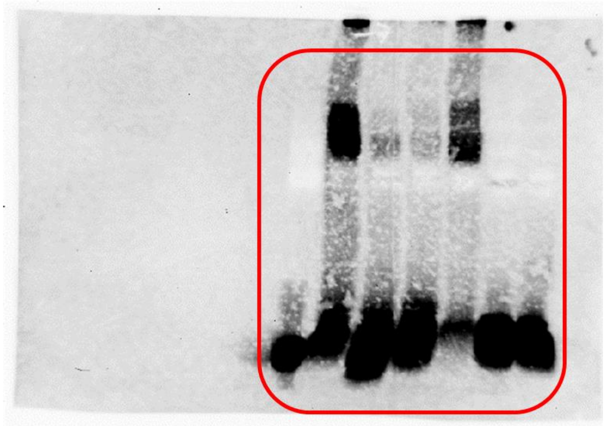


Figure S13.

Full length blots for Fig. 7c

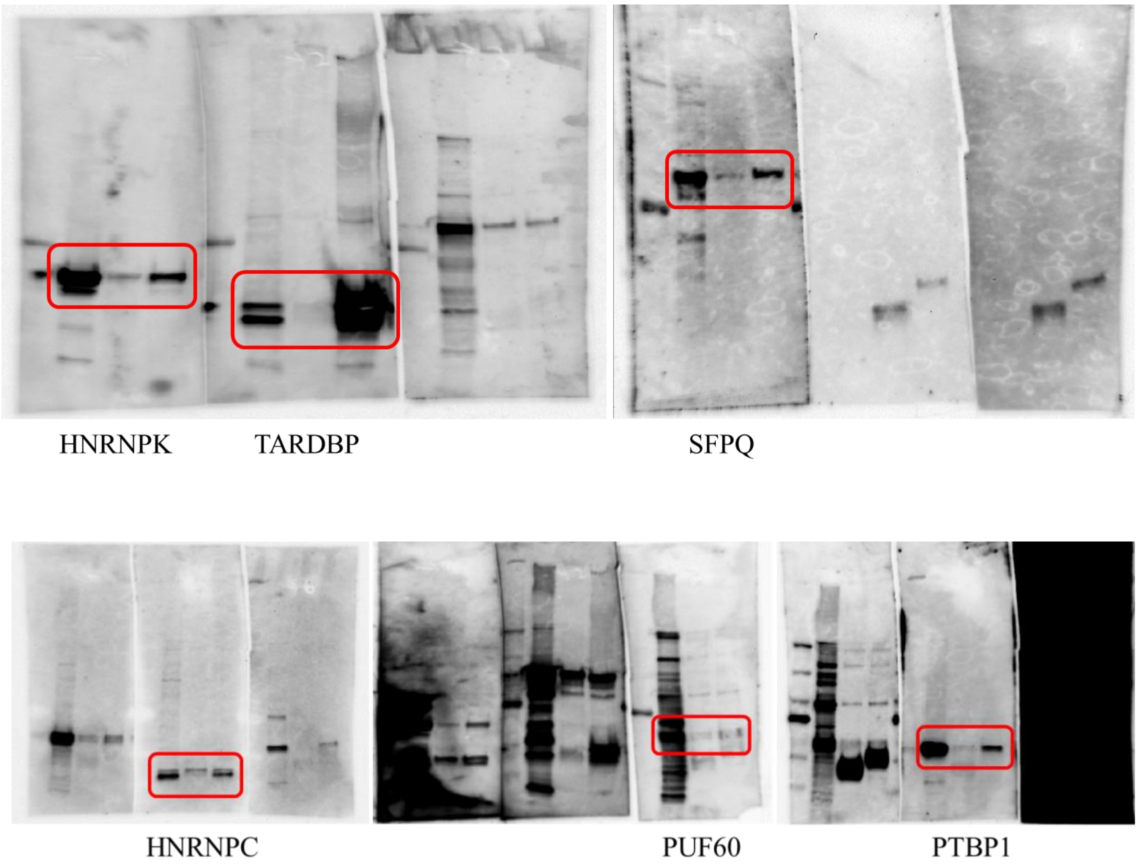
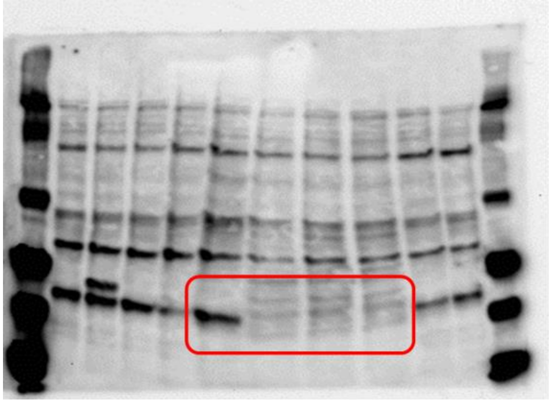
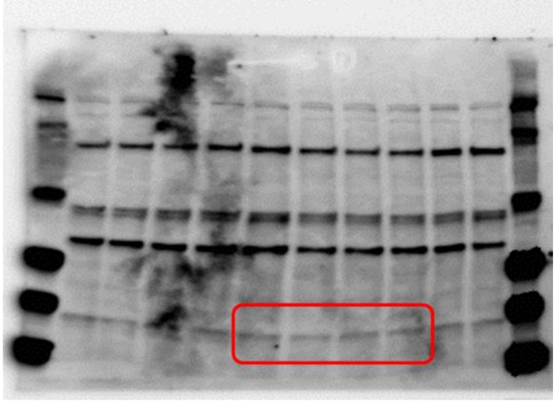


Figure S14.

Full length blots for Fig. S2a



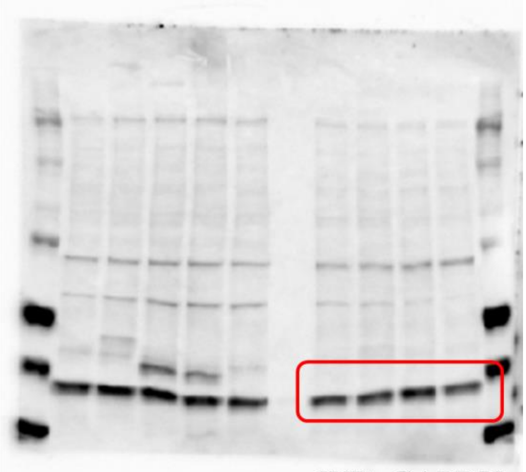
WB: Tardbp



WB: GAPDH

Full length blots for Fig. S2b

WB: Tardbp



WB: GAPDH