

Supplementary Data

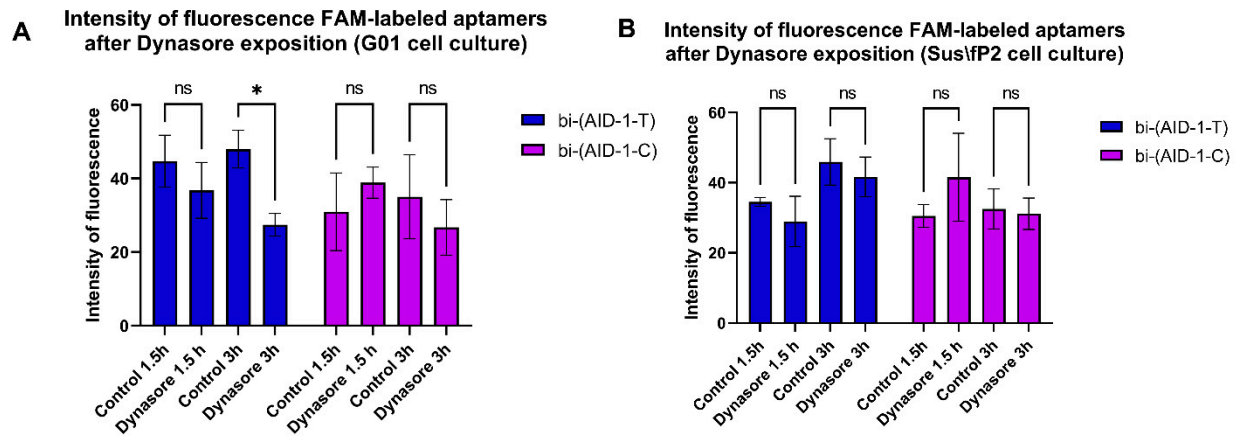


Figure S1. Fluorescence changes of FAM-labeled aptamers after Dynasore exposure

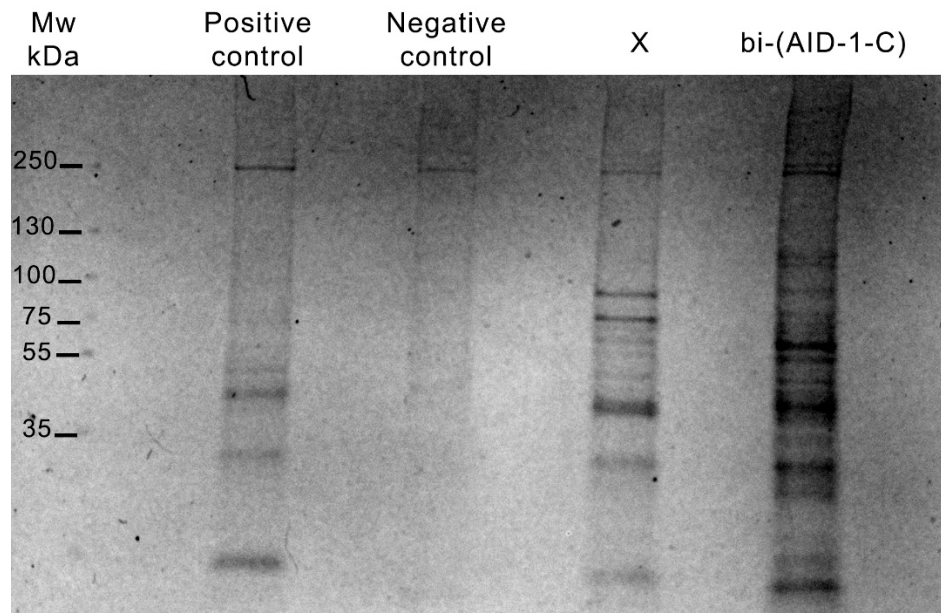


Figure S2. Full 4-20% PAGE electrophoresis of proteins obtained after incubation of cell lysates with biotin-labeled control oligonucleotide (positive control) and biotin-labeled bi-(AID-1-C) after the first column elution. The negative control contains oligonucleotide-untreated protein lysate after the first elution.

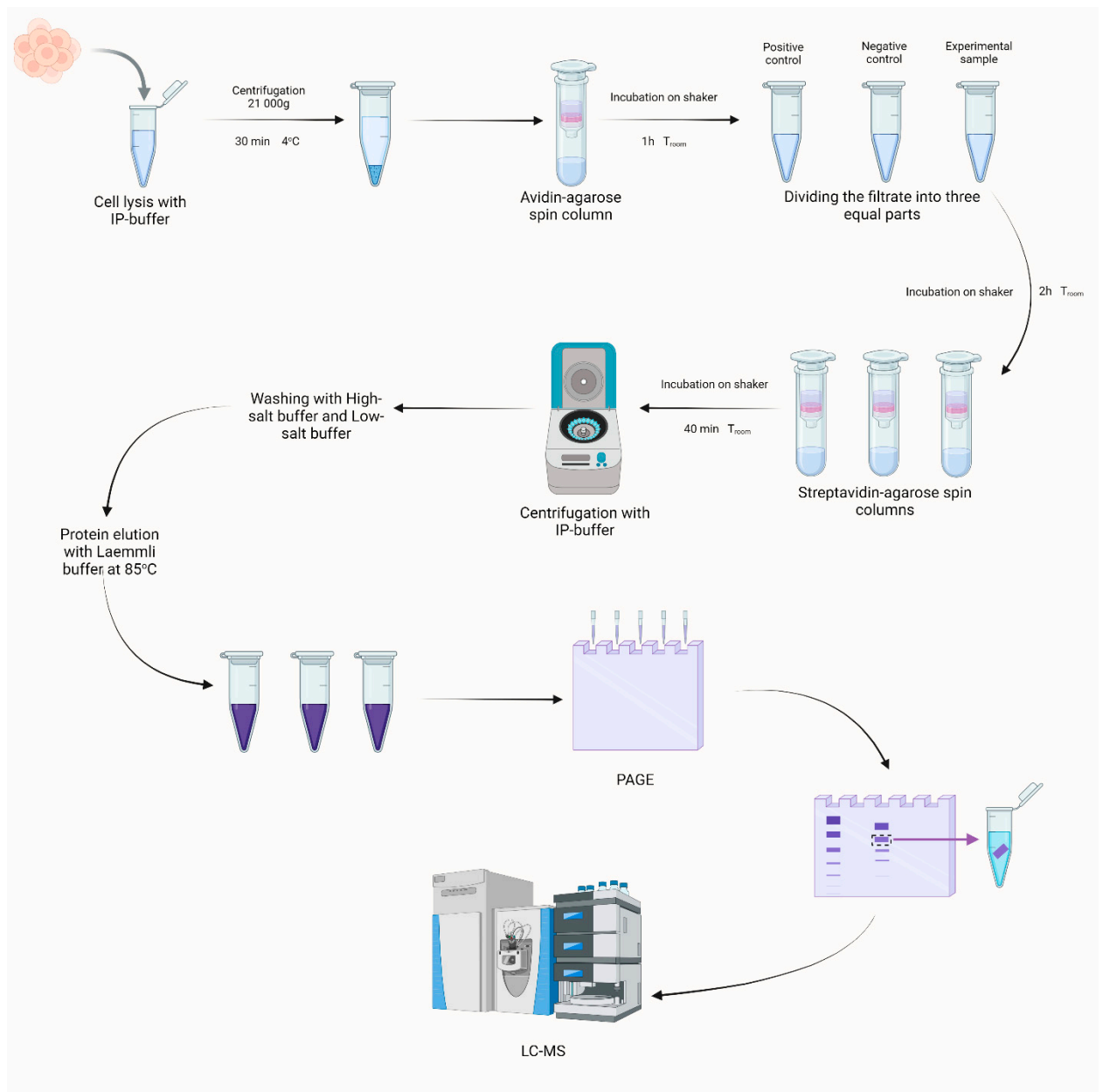


Figure S3. Assessment of aptamers specificity to the target protein. Created in BioRender. Pavlova, G. (2024) BioRender.com/t64u759

Table S1. Proteins specifically bound to biotin-labeled bi-(AID-1-T)

Protein ID	Accession	- 10 Ig P	Coverage (%)	Coverage (%) Sample 2	Area Sample 2	#Peptides	#Unique	#Spec Sample 2	PTM		Avg. Mass	Description
P09874	PARP1_HUMAN	219.24	36	36	1.60E+08	60	60	114	Carbamidomethylation	Oxidation (M)	Acetylation (Protein N-term)	113084 Poly [ADP-ribose] polymerase 1 OS=Homo sapiens OX=9606 GN=PARP1 PE=1 SV=4
Q9H2U1	DHX36_HUMAN	211.11	28	28	1.44E+08	47	47	101	Carbamidomethylation	Oxidation (M)	Acetylation (Protein N-term)	114760 ATP-dependent DNA/RNA helicase DHX36 OS=Homo

UMA N									hylati on			sapiens OX=9606 GN=DHX36 PE=1 SV=2
Q1 KM D3	HNR L2_H UMA N	16 6. 63	27	27	7.70E +07	29	29	92	Carb amid omet hylati on	Oxidation (M)	85105	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens OX=9606 GN=HNRNPUL2 PE=1 SV=1
P68 371	TBB4 B_H UMA N	12 5. 29	16	16	0	7	1	24	Carb amid omet hylati on	Oxidation (M)	49831	Tubulin beta-4B chain OS=Homo sapiens OX=9606 GN=TUBB4B PE=1 SV=1
Q07 157	ZO1_ HUM AN	11 9. 68	7	7	2.47E +06	15	13	18			19545 7	Tight junction protein ZO-1 OS=Homo sapiens OX=9606 GN=TJP1 PE=1 SV=3
P16 615	AT2A 2_HU MAN	11 4. 27	12	12	2.83E +06	14	14	16	Carb amid omet hylati on	Oxidation (M)	11475 7	Sarcoplasmic/endo plasmic reticulum calcium ATPase 2 OS=Homo sapiens OX=9606 GN=ATP2A2 PE=1 SV=1
Q9 UD Y2	ZO2_ HUM AN	11 2. 37	14	14	2.50E +06	21	19	24	Carb amid omet hylati on	Oxidation (M)	13395 8	Tight junction protein ZO-2 OS=Homo sapiens OX=9606 GN=TJP2 PE=1 SV=2
P08 621	RU17 _HU MAN	10 8. 03	19	19	1.86E +06	9	9	13			51557	U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens OX=9606 GN=SNRNP70 PE=1 SV=2
Q9 NR 30	DDX 21_H UMA N	10 4. 2	18	18	2.01E +06	15	12	17			87344	Nucleolar RNA helicase 2 OS=Homo sapiens OX=9606 GN=DDX21 PE=1 SV=5
Q12 797	ASP H_H UMA N	10 3. 01	17	17	3.38E +06	14	14	18	Carb amid omet hylati on	Oxidation (M)	85863	Aspartyl/asparagin yl beta-hydroxylase OS=Homo sapiens OX=9606 GN=ASPH PE=1 SV=3
Q8 N9 T8	KRI1 _HU MAN	10 1. 85	15	15	2.40E +06	10	10	12			82598	Protein KRI1 homolog OS=Homc sapiens OX=9606

											GN=KRI1 PE=1 SV=3
Q15 029	U5S1 _HU MAN	97 .7 2	9	9	2.36E +06	11	11	15		10943 6	116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens OX=9606 GN=EFTUD2 PE=1 SV=1
Q9 NZ B2	F120 A_H UMA N	95 .1 4	9	9	1.60E +06	11	10	11	Carbamidomethylation	12188 8	Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens OX=9606 GN=FAM120A PE=1 SV=2
O00 267	SPT5 H_H UMA N	94 .2 7	9	9	1.87E +06	12	12	15	Oxidation (M)	12100 0	Transcription elongation factor SPT5 OS=Homo sapiens OX=9606 GN=SUPT5H PE=1 SV=1
Q9 Y2 W1	TR15 0_HU MAN	93 .8 1	8	8	1.56E +06	9	9	11		10866 6	Thyroid hormone receptor-associated protein 3 OS=Homo sapiens OX=9606 GN=THRAP3 PE=1 SV=2
P11 498	PYC_ HUM AN	93 .5 5	6	6	2.05E +05	7	7	8	Carbamidomethylation	12963 4	Pyruvate carboxylase mitochondrial OS=Homo sapiens OX=9606 GN=PC PE=1 SV=2
Q16 531	DDB1 _HU MAN	91 .3 4	8	8	1.68E +06	10	10	12	Oxidation (M)	12696 8	DNA damage- binding protein 1 OS=Homo sapiens OX=9606 GN=DDB1 PE=1 SV=1
P02 786	TFR1 _HU MAN	90 .8 1	12	12	1.09E +06	9	9	9		84871	Transferrin receptor protein 1 OS=Homo sapiens OX=9606 GN=TFRC PE=1 SV=2
P05 067	A4_H UMA N	89 .0 8	11	11	3.32E +06	10	10	16	Carb amid omet hylati on	86943	Amyloid-beta precursor protein OS=Homo sapiens OX=9606 GN=APP PE=1 SV=3

Q16 643	DREB _HU MAN	88 .6 4	14	14	1.01E +06	9	9	10	Oxid ation (M)	Acetylation (Protein N-term)	71429	Drebrin OS=Homo sapiens OX=9606 GN=DBN1 PE=1 SV=4
O00 159	MYO 1C_H UMA N	88 .5 6	8	8	7.20E +05	9	9	9			12168 2	Unconventional myosin-Ic OS=Homo sapiens OX=9606 GN=MYO1C PE=1 SV=4
Q96 A65	EXO C4_H UMA N	87 .1 1	7	7	4.01E +05	6	6	8			11049 8	Exocyst complex component 4 OS=Homo sapiens OX=9606 GN=EXOC4 PE=1 SV=1
P28 370	SMC A1_H UMA N	86 .9	10	10	1.09E +06	13	13	13	Carbamidomethylation		12260 5	Probable global transcription activator SNF2L1 OS=Homo sapiens OX=9606 GN=SMARCA1 PE=1 SV=2
Q7 L2J 0	MEP CE_H UMA N	86 .2 7	7	7	7.11E +05	6	6	7	Oxidation (M)		74355	7SK snRNA methylphosphate capping enzyme OS=Homo sapiens OX=9606 GN=MEPCE PE=1 SV=1
P27 694	RFA1 _HU MAN	85 .7 6	16	16	1.09E +06	10	10	13			68138	Replication protein A 70 kDa DNA- binding subunit OS=Homo sapiens OX=9606 GN=RPA1 PE=1 SV=2
P35 222	CTN B1_H UMA N	84 .6 7	10	10	4.66E +05	9	8	11			85497	Catenin beta-1 OS=Homo sapiens OX=9606 GN=CTNNB1 PE=1 SV=1
Q9 BU F5	TBB6 _HU MAN	81 .1 7	10	10	2.81E +04	4	1	6	Carb amid omet hylati on	Oxidation (M)	49857	Tubulin beta-6 chain OS=Homo sapiens OX=9606 GN=TUBB6 PE=1 SV=1
P81 605	DCD _HU MAN	79 .7 4	42	42	2.73E +06	6	6	7			11284	Dermcidin OS=Homo sapiens OX=9606 GN=DCD PE=1 SV=2
P36 578	RL4_ HUM AN	79 .6 7	11	11	1.48E +06	5	5	6	Carb amid omet	Oxidation (M)	47697	60S ribosomal protein L4 OS=Homo sapiens

hylation										OX=9606 GN=RPL4 PE=1 SV=5
O00 469	PLO D2_H UMA N	79 .3 4	7	7	2.95E +05	5	5	6	84686	Procollagen-lysine 2-oxoglutarate 5- dioxygenase 2 OS=Homo sapiens OX=9606 GN=PLOD2 PE=1 SV=2
O00 203	AP3B 1_HU MAN	78 .7 6	4	4	2.74E +05	6	6	6	12132 0	AP-3 complex subunit beta-1 OS=Homo sapiens OX=9606 GN=AP3B1 PE=1 SV=3
Q8 NF Z0	FBH1 _HU MAN	77 .7 8	7	7	3.63E +05	7	7	11	11768 6	F-box DNA helicase 1 OS=Homo sapiens OX=9606 GN=FBH1 PE=1 SV=2
P35 606	COP B2_H UMA N	76 .1 4	8	8	4.72E +05	9	9	10	10248 7	Coatomer subunit beta' OS=Homo sapiens OX=9606 GN=COPB2 PE=1 SV=2
P21 127	CD11 B_H UMA N	75 .5	11	11	1.56E +06	10	10	11	92620	Carbamidomethylation Cyclin-dependent kinase 11B OS=Homo sapiens OX=9606 GN=CDK11B PE=1 SV=4
Q9 UQ 88	CD11 A_H UMA N	75 .5	10	10	1.50E +06	9	9	10	91362	Carbamidomethylation Cyclin-dependent kinase 11A OS=Homo sapiens OX=9606 GN=CDK11A PE=1 SV=4
Q9 UB V2	SE1L 1_HU MAN	75 .2 9	3	3	4.58E +05	3	3	4	88755	Protein sel-1 homolog 1 OS=Homo sapiens OX=9606 GN=SEL1L PE=1 SV=3
Q13 085	ACA CA_ HUM AN	74 .1 6	4	4	8.51E +05	10	10	11	26555 1	Acetyl-CoA carboxylase 1 OS=Homo sapiens OX=9606 GN=ACACA PE=1 SV=2
Q9 Y52 0	PRC2 C_H UMA N	74 . .	2	2	7.61E +05	5	5	6	31691 1	Protein PRRC2C OS=Homo sapiens OX=9606 GN=PRRC2C PE=1 SV=4

Q9 P0 K7	RAI1 4_HU MAN	73 .9 9	8	8	2.16E +05	8	8	8	11004 1	Ankycorbin OS=Homo sapiens OX=9606 GN=RAI14 PE=1 SV=2
P08 670	VIME _HU MAN	73 .5 4	10	10	3.13E +05	5	4	7	53652	Vimentin OS=Homo sapiens OX=9606 GN=VIM PE=1 SV=4
P46 977	STT3 A_H UMA N	73 .5 3	4	4	1.39E +05	3	3	3	80530	Dolichyl- diphosphooligosac- charide--protein glycosyltransferase subunit STT3A OS=Homo sapiens OX=9606 GN=STT3A PE=1 SV=2
Q8 TD D1	DDX 54_H UMA N	72 .5 2	4	4	1.47E +05	4	4	4	98595	ATP-dependent RNA helicase DDX54 OS=Homo sapiens OX=9606 GN=DDX54 PE=1 SV=2
P42 224	STAT 1_HU MAN	70 .8 5	5	5	2.20E +05	4	4	5	87335	Signal transducer and activator of transcription 1- alpha/beta OS=Homo sapiens OX=9606 GN=STAT1 PE=1 SV=2
Q6 PK G0	LARP 1_HU MAN	70 .5	5	5	2.85E +05	6	6	6	12351 0	La-related protein 1 OS=Homo sapiens OX=9606 GN=LARP1 PE=1 SV=2
P61 247	RS3A _HU MAN	70 .4 7	19	19	7.17E +05	6	6	6	29945	40S ribosomal protein S3a OS=Homo sapiens OX=9606 GN=RPS3A PE=1 SV=2
Q5 SSJ 5	HP1B 3_HU MAN	70 .3 6	10	10	4.97E +05	6	6	7	61207	Heterochromatin protein 1-binding protein 3 OS=Homo sapiens OX=9606 GN=HP1BP3 PE=1 SV=1
P46 777	RL5_ HUM AN	67 .2 7	12	12	1.06E +06	6	6	6	34363	60S ribosomal protein L5 OS=Homo sapiens OX=9606 GN=RPL5 PE=1 SV=3

O95490	AGR L2_H UMA N	65.2	5	5	1.29E+05	6	6	6	Carbamidomethylation	163348	Adhesion G protein-coupled receptor L2 OS=Homo sapiens OX=9606 GN=ADGRL2 PE=1 SV=2
Q9NYF8	BCLF1_HU MAN	64.8	6	6	6.34E+05	6	6	6		106122	Bcl-2-associated transcription factor 1 OS=Homo sapiens OX=9606 GN=BCLAF1 PE=1 SV=2
Q9BPX3	CND3_HU MAN	64.7	3	3	7.91E+05	4	4	4	Carbamidomethylation	114334	Condensin complex subunit 3 OS=Homo sapiens OX=9606 GN=NCAPG PE=1 SV=1

Table S2. Proteins specifically bound to biotin-labeled bi-(AID-1-T)

Protein ID	Accession	-10lg P	Coverage (%)	Coverage (%)	Area Sample 1	#Peptides	#Unique	#Spec Sample 1	PTM		Avg. Mass	Description
P08621-2	RU17_HUMAN	146.32	25	25	6.95E+08	9	9	27	Oxidation (M)	Deamidation (NQ)	50618	Isoform 2 of U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens OX=9606 GN=SNRNP 70
P08621	RU17_HUMAN	146.32	24	24	6.95E+08	9	9	27	Oxidation (M)	Deamidation (NQ)	51557	U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens OX=9606 GN=SNRNP 70 PE=1 SV=2
O76021	RL1D1_HUMAN	92.3	11	11	6.86E+07	5	5	6	Carbamidomethylation		54973	Ribosomal L1 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=RSL1D1 PE=1 SV=3

O60 506- 2	HNRPQ _HUMAN	66.8 7	4	4	1.15E+ 07	3	3	3	65682	Isoform 2 of Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens OX=9606 GN=SYNCRIP
O60 506	HNRPQ _HUMAN	66.8 7	4	4	1.15E+ 07	3	3	3	69603	Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens OX=9606 GN=SYNCRIP PE=1 SV=2
O43 390- 4	HNRPR _HUMAN	66.8 7	4	4	1.15E+ 07	3	3	3	59953	Isoform 4 of Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens OX=9606 GN=HNRNPR
O43 390	HNRPR _HUMAN	66.8 7	4	4	1.15E+ 07	3	3	3	70943	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens OX=9606 GN=HNRNPR PE=1 SV=1
O43 390- 2	HNRPR _HUMAN	66.8 7	4	4	1.15E+ 07	3	3	3	71214	Isoform 2 of Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens OX=9606 GN=HNRNPR
P276 94	RFA1_HUMAN	62.9 3	6	6	5.18E+ 06	3	3	5	68138	Replication protein A 70 kDa DNA-binding subunit OS=Homo sapiens

											OX=9606 GN=RPA1 PE=1 SV=2
Q8I YB3- 2	SRRM1_ HUMA N	62.2 7	4	4	6.64E+ 06	3	3	5	Oxidation (M)	102126	Isoform 2 of Serine/argini ne repetitive matrix protein 1 OS=Homo sapiens OX=9606 GN=SRRM1
Q8I YB3	SRRM1_ HUMA N	62.2 7	4	4	6.64E+ 06	3	3	5	Oxidation (M)	102335	Serine/argini ne repetitive matrix protein 1 OS=Homo sapiens OX=9606 GN=SRRM1 PE=1 SV=2
Q9U NF1- 2	MAGD2 _HUMA N	61.4 7	7	7	1.14E+ 06	3	3	4	Deamidation (NQ)	63167	Isoform 2 of Melanoma- associated antigen D2 OS=Homo sapiens OX=9606 GN=MAGE D2
Q9U NF1	MAGD2 _HUMA N	61.4 7	7	7	1.14E+ 06	3	3	4	Deamidation (NQ)	64954	Melanoma- associated antigen D2 OS=Homo sapiens OX=9606 GN=MAGE D2 PE=1 SV=2
P263 68-2	U2AF2_ HUMA N	60.8 1	5	5	1.68E+ 07	3	3	5	Oxidation (M)	53121	Isoform 2 of Splicing factor U2AF 65 kDa subunit OS=Homo sapiens OX=9606 GN=U2AF2
P263 68	U2AF2_ HUMA N	60.8 1	5	5	1.68E+ 07	3	3	5	Oxidation (M)	53501	Splicing factor U2AF 65 kDa subunit OS=Homo sapiens OX=9606

											GN=U2AF2 PE=1 SV=4
Q12 797- 7	ASPH_ HUMA N	54.4 6	12	12	9.26E+ 05	1	1	3	Deamidation (NQ)	21963	Isoform 7 of Aspartyl/asp araginyln beta- hydroxylase OS=Homo sapiens OX=9606 GN=ASPH
Q12 797- 6	ASPH_ HUMA N	54.4 6	9	9	9.26E+ 05	1	1	3	Deamidation (NQ)	29757	Isoform 6 of Aspartyl/asp araginyln beta- hydroxylase OS=Homo sapiens OX=9606 GN=ASPH
Q12 797- 11	ASPH_ HUMA N	54.4 6	9	9	9.26E+ 05	1	1	3	Deamidation (NQ)	32420	Isoform 11 of Aspartyl/asp araginyln beta- hydroxylase OS=Homo sapiens OX=9606 GN=ASPH
Q12 797- 2	ASPH_ HUMA N	54.4 6	8	8	9.26E+ 05	1	1	3	Deamidation (NQ)	34646	Isoform 2 of Aspartyl/asp araginyln beta- hydroxylase OS=Homo sapiens OX=9606 GN=ASPH
Q12 797	ASPH_ HUMA N	54.4 6	3	3	9.26E+ 05	1	1	3	Deamidation (NQ)	85863	Aspartyl/asp araginyln beta- hydroxylase OS=Homo sapiens OX=9606 GN=ASPH PE=1 SV=3
Q9Y 2X3	NOP58_ HUMA N	54.2 4	3	3	4.50E+ 06	1	1	1	Carbamidomethy lation	59578	Nucleolar protein 58 OS=Homo sapiens OX=9606 GN=NOP58 PE=1 SV=1

Q15 428	SF3A2_ HUMAN	47.7 2	3	3	1.68E+ 06	1	1	4	49256	Splicing factor 3A subunit 2 OS=Homo sapiens OX=9606 GN=SF3A2 PE=1 SV=2
Q9U Q35	SRRM2_ HUMAN	46.6 7	1	1	0	2	2	2	299616	Serine/argini ne repetitive matrix protein 2 OS=Homo sapiens OX=9606 GN=SRRM2 PE=1 SV=2
P0C G39	POTEJ_ HUMAN	41.2 5	1	1	4.66E+ 06	1	1	1	117390	POTE ankyrin domain family member J OS=Homo sapiens OX=9606 GN=POTEJ PE=3 SV=1
P632 67-2	ACTH_ HUMAN	41.2 5	3	3	4.66E+ 06	1	1	1	37083	Isoform 2 of Actin gamma- enteric smooth muscle OS=Homo sapiens OX=9606 GN=ACTG2
P632 67	ACTH_ HUMAN	41.2 5	3	3	4.66E+ 06	1	1	1	41877	Actin gamma- enteric smooth muscle OS=Homo sapiens OX=9606 GN=ACTG2 PE=1 SV=1
P627 36	ACTA_ HUMAN	41.2 5	3	3	4.66E+ 06	1	1	1	42009	Actin aortic smooth muscle OS=Homo sapiens OX=9606 GN=ACTA2 PE=1 SV=1

P68032	ACTC_HUMAN	41.25	3	3	4.66E+06	1	1	1	42019	Actin alpha cardiac muscle 1 OS=Homo sapiens OX=9606 GN=ACTC1 PE=1 SV=1
P68133	ACTS_HUMAN	41.25	3	3	4.66E+06	1	1	1	42051	Actin alpha skeletal muscle OS=Homo sapiens OX=9606 GN=ACTA1 PE=1 SV=1
A5A3E0	POTEF_HUMAN	41.25	1	1	4.66E+06	1	1	1	121444	POTE ankyrin domain family member F OS=Homo sapiens OX=9606 GN=POTEF PE=1 SV=2
Q6S8J3	POTEE_HUMAN	41.25	1	1	4.66E+06	1	1	1	121363	POTE ankyrin domain family member E OS=Homo sapiens OX=9606 GN=POTEE PE=2 SV=3
P0CG38	POTEI_HUMAN	41.25	1	1	4.66E+06	1	1	1	121282	POTE ankyrin domain family member I OS=Homo sapiens OX=9606 GN=POTEI PE=3 SV=1
Q08170	SRSF4_HUMAN	39.77	4	4	5.46E+05	2	2	2	56678	Serine/arginine-rich splicing factor 4 OS=Homo sapiens OX=9606 GN=SRSF4 PE=1 SV=2

Q9Y6M1-5	IF2B2_HUMAN	38.34	2	2	0	1	1	3	54722	Isoform 5 of Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens OX=9606 GN=IGF2BP2
Q9Y6M1-6	IF2B2_HUMAN	38.34	2	2	0	1	1	3	58578	Isoform 6 of Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens OX=9606 GN=IGF2BP2
Q9Y6M1-3	IF2B2_HUMAN	38.34	2	2	0	1	1	3	59001	Isoform 3 of Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens OX=9606 GN=IGF2BP2
Q9Y6M1-4	IF2B2_HUMAN	38.34	2	2	0	1	1	3	59666	Isoform 4 of Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens OX=9606 GN=IGF2BP2
Q9Y6M1-1	IF2B2_HUMAN	38.34	2	2	0	1	1	3	61843	Isoform 2 of Insulin-like growth factor 2 mRNA-binding protein 2

											OS=Homo sapiens OX=9606 GN=IGF2BP2
Q9Y6M1	IF2B2_HUMAN	38.34	2	2	0	1	1	3		66121	Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens OX=9606 GN=IGF2BP2 PE=1 SV=2
Q02040	AK17A_HUMAN	37.73	3	3	1.84E+05	2	2	2	Carbamidomethylation	80736	A-kinase anchor protein 17A OS=Homo sapiens OX=9606 GN=AKAP17A PE=1 SV=2
O76094-2	SRP72_HUMAN	34.81	3	3	1.73E+06	2	2	2		67880	Isoform 2 of Signal recognition particle subunit SRP72 OS=Homo sapiens OX=9606 GN=SRP72
O76094	SRP72_HUMAN	34.81	2	2	1.73E+06	2	2	2		74606	Signal recognition particle subunit SRP72 OS=Homo sapiens OX=9606 GN=SRP72 PE=1 SV=3
P05089-3	ARG1_HUMAN	31.36	3	3	2.11E+05	1	1	1		25356	Isoform 3 of Arginase-1 OS=Homo sapiens OX=9606 GN=ARG1
P05089	ARG1_HUMAN	31.36	2	2	2.11E+05	1	1	1		34735	Arginase-1 OS=Homo sapiens OX=9606

												GN=ARG1 PE=1 SV=2
P050 89-2	ARGI1_ HUMAN	31.3 6	2	2	2.11E+ 05	1	1	1		35664	Isoform 2 of Arginase-1 OS=Homo sapiens OX=9606 GN=ARG1	
P277 97	CALR_ HUMAN	30.9 9	2	2	5.69E+ 06	1	1	1		48142	Calreticulin OS=Homo sapiens OX=9606 GN=CALR PE=1 SV=1	
Q96 PZ2	F111A_ HUMAN	30.9 9	1	1	5.92E+ 04	1	1	1		70196	Serine protease FAM111A OS=Homo sapiens OX=9606 GN=FAM111 A PE=1 SV=2	
O00 425- 2	IF2B3_H UMAN	29.5 8	5	5	2.11E+ 05	1	1	2		21630	Isoform 2 of Insulin-like growth factor 2 mRNA- binding protein 3 OS=Homo sapiens OX=9606 GN=IGF2BP 3	
O00 425	IF2B3_H UMAN	29.5 8	2	2	2.11E+ 05	1	1	2		63705	Insulin-like growth factor 2 mRNA- binding protein 3 OS=Homo sapiens OX=9606 GN=IGF2BP 3 PE=1 SV=2	
Q9U HX1 -4	PUF60_ HUMAN	27.4 8	2	2	3.97E+ 06	1	1	1	Oxidation (M)	54025	Isoform 4 of Poly(U)- binding- splicing factor PUF60 OS=Homo sapiens OX=9606 GN=PUF60	

Q9UHX1-6	PUF60_HUMAN	27.48	2	2	3.97E+06	1	1	1	Oxidation (M)	55400	Isoform 6 of Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens OX=9606 GN=PUF60
Q9UHX1-3	PUF60_HUMAN	27.48	2	2	3.97E+06	1	1	1	Oxidation (M)	55729	Isoform 3 of Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens OX=9606 GN=PUF60
Q9UHX1-5	PUF60_HUMAN	27.48	2	2	3.97E+06	1	1	1	Oxidation (M)	57104	Isoform 5 of Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens OX=9606 GN=PUF60
Q9UHX1-2	PUF60_HUMAN	27.48	1	1	3.97E+06	1	1	1	Oxidation (M)	58172	Isoform 2 of Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens OX=9606 GN=PUF60
Q9UHX1	PUF60_HUMAN	27.48	1	1	3.97E+06	1	1	1	Oxidation (M)	59876	Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens OX=9606 GN=PUF60 PE=1 SV=1
Q5VWX1	KHDR2_HUMAN	27.42	2	2	1.98E+05	1	1	1		38927	KH domain-containing RNA-binding signal transduction-associated protein 2 OS=Homo sapiens

										OX=9606 GN=KHDRB S2 PE=1 SV=1
Q07 666- 2	KHDR1 _HUMA N	27.4 2	2	2	1.98E+ 05	1	1	1	45861	Isoform 2 of KH domain- containing RNA- binding signal transduction -associated protein 1 OS=Homo sapiens OX=9606 GN=KHDRB S1
Q07 666	KHDR1 _HUMA N	27.4 2	2	2	1.98E+ 05	1	1	1	48227	KH domain- containing RNA- binding signal transduction -associated protein 1 OS=Homo sapiens OX=9606 GN=KHDRB S1 PE=1 SV=1
Q69 YN2 -3	C19L1_ HUMA N	26.6 5	2	2	6.65E+ 04	1	1	1	45537	Isoform 3 of CWF19-like protein 1 OS=Homo sapiens OX=9606 GN=CWF19 L1
Q69 YN2	C19L1_ HUMA N	26.6 5	2	2	6.65E+ 04	1	1	1	60619	CWF19-like protein 1 OS=Homo sapiens OX=9606 GN=CWF19 L1 PE=1 SV=2
P079 10-4	HNRPC _HUMA N	26.2 4	4	4	5.68E+ 05	1	1	1	27821	Isoform 4 of Heterogeneo us nuclear ribonucleopr oteins C1/C2 OS=Homo sapiens

										OX=9606 GN=HNRNP C
P079 10-2	HNRPC _HUMAN	26.2 4	3	3	5.68E+ 05	1	1	1	32338	Isoform C1 of Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens OX=9606 GN=HNRNP C
P079 10	HNRPC _HUMAN	26.2 4	3	3	5.68E+ 05	1	1	1	33670	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens OX=9606 GN=HNRNP C PE=1 SV=4
P079 10-3	HNRPC _HUMAN	26.2 4	4	4	5.68E+ 05	1	1	1	25230	Isoform 3 of Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens OX=9606 GN=HNRNP C
P129 56-2	XRCC6_ HUMAN	25.6 6	2	2	1.79E+ 05	1	1	1	65149	Isoform 2 of X-ray repair cross-complementing protein 6 OS=Homo sapiens OX=9606 GN=XRCC6
P129 56	XRCC6_ HUMAN	25.6 6	1	1	1.79E+ 05	1	1	1	69843	X-ray repair cross-complementing protein 6 OS=Homo sapiens OX=9606 GN=XRCC6 PE=1 SV=2
Q9N YF8- 3	BCLF1_ HUMAN	24.0 2	1	1	8.03E+ 04	1	1	1	100232	Isoform 3 of Bcl-2- associated transcription

										factor 1 OS=Homo sapiens OX=9606 GN=BCLAF1
Q9N YF8- 2	BCLF1_ HUMA N	24.0 2	1	1	8.03E+ 04	1	1	1	105948	Isoform 2 of Bcl-2- associated transcription factor 1 OS=Homo sapiens OX=9606 GN=BCLAF1
Q9N YF8	BCLF1_ HUMA N	24.0 2	1	1	8.03E+ 04	1	1	1	106122	Bcl-2- associated transcription factor 1 OS=Homo sapiens OX=9606 GN=BCLAF1 PE=1 SV=2
P619 78	HNRPK _HUMA N	23.8 1	2	2	1.03E+ 05	1	1	1	50976	Heterogeneo us nuclear ribonucleopr oteins K OS=Homo sapiens OX=9606 GN=HNRNP K PE=1 SV=1
P619 78-2	HNRPK _HUMA N	23.8 1	2	2	1.03E+ 05	1	1	1	51028	Isoform 2 of Heterogeneo us nuclear ribonucleopr oteins K OS=Homo sapiens OX=9606 GN=HNRNP K
Q96I 24	FUBP3_ HUMA N	23.3 2	2	2	3.53E+ 05	1	1	1	61640	Far upstream element- binding protein 3 OS=Homo sapiens OX=9606 GN=FUBP3 PE=1 SV=2
Q86 YZ3	HORN_ HUMA N	23.2 1	0	0	6.11E+ 05	1	1	1	282389	Hornerin OS=Homo sapiens

										OX=9606 GN=HRNR PE=1 SV=2
										Isoform 3 of
Q9H2U1-3	DHX36_HUMAN	23.15	1	1	1.13E+06	1	1	1	111479	ATP-dependent DNA/RNA helicase DHX36 OS=Homo sapiens OX=9606 GN=DHX36
										Isoform 2 of
Q9H2U1-2	DHX36_HUMAN	23.15	1	1	1.13E+06	1	1	1	113153	ATP-dependent DNA/RNA helicase DHX36 OS=Homo sapiens OX=9606 GN=DHX36
										ATP-dependent DNA/RNA helicase DHX36 OS=Homo sapiens OX=9606 GN=DHX36 PE=1 SV=2
Q9H2U1	DHX36_HUMAN	23.15	1	1	1.13E+06	1	1	1	114760	