Supporting Information for

Original article

Blockade of the deubiquitinating enzyme USP48 degrades oncogenic HMGA2 and inhibits colorectal cancer invasion and metastasis

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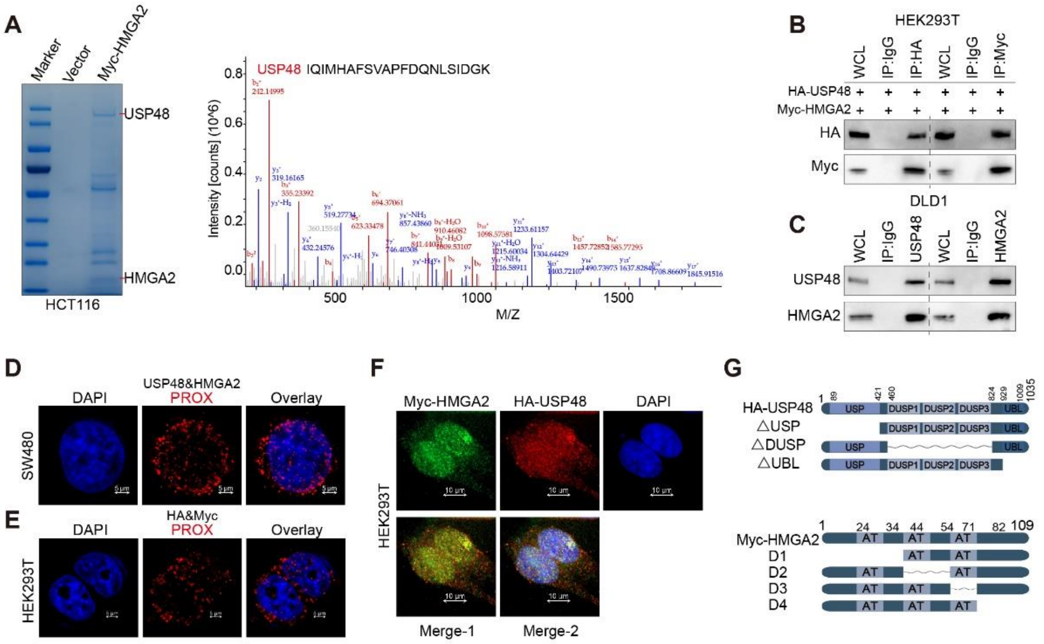


Figure S1. USP48 interacts with HMGA2. (A) Mass spectrometry was employed to analyze a USP48 peptide present in the Myc-HMGA2 precipitate. (B) Co-transfection of HA-USP48 and Myc-HMGA2 was performed in 293T cells, followed by IP with anti-HA or anti-Myc antibodies. (C) IP assays were performed on DLD1 cell lysates using control IgG, anti-USP48, or anti-HMGA2 antibodies and detected with appropriate antibodies. (D) In situ PLA between endogenous USP48 and HMGA2 in SW480 cells. Representative images are shown with merged PLA and DAPI channels from PLA experiments. Scale bar, 10 µm. (E) In situ PLA between exogenous USP48 and HMGA2 in HEK293T cells. Representative images are shown with merged PLA and DAPI channels from PLA experiments. Scale bar, 10 µm. (F) HEK293T cells were co-transfected with HA-USP48 and Myc-HMGA2, followed by Immunofluorescence using antibodies against HA and Myc. Scale bar, 10 µm. (G) A schematic diagram depicting the full-length USP48 and HMGA2 proteins, as well as their respective deletion mutants.

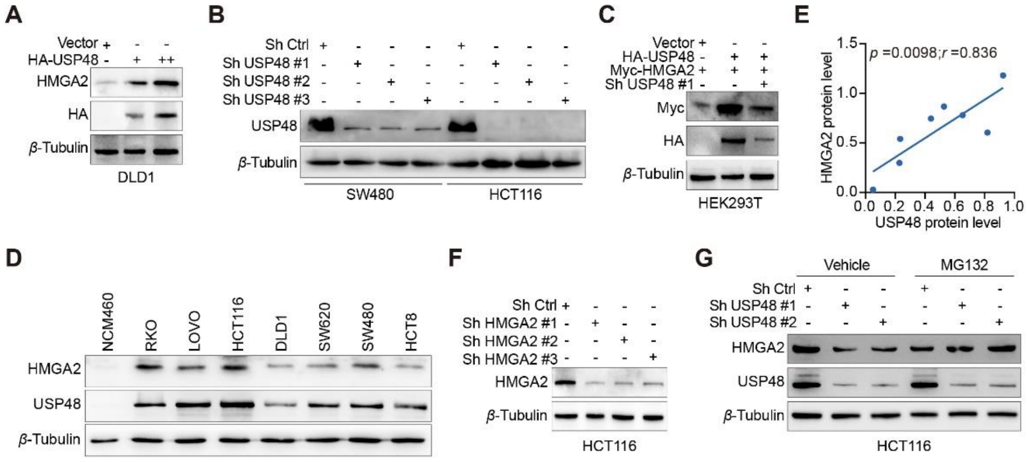


Figure S2. USP48 maintains HMGA2 stability. (A) DLD1 cells were transfected with increasing amounts of HA-tagged USP48, and cell lysates were analyzed by IB using antibodies against HMGA2. (B) SW480 and HCT116 cells were transfected with three distinct USP48 shRNA constructs, followed by subsequent analysis of USP48 protein expression levels. (C) IB analysis of Myc-HMGA2 levels in HEK293T cells transduced with equal amounts of Myc-HMGA2, together with either HA-tagged USP48-WT alone or both HA-tagged USP48-WT and USP48 shRNA. (D) Cell lysates from several CRC cell lines were blotted with USP48 and HMGA2 antibodies. (E) The Pearson correlations of analysis of USP48 and HMGA2 in CRC cell lines. Pearson r indicates the correlation coefficient. (F) SW480 cells were transfected with three independent HMGA2 shRNA, and then HMGA2 protein levels were analyzed. (G) HCT116 cells transfected with two independent USP48 shRNA were treated with DMSO or MG132 (10 μmol/L) for 6 h, and then USP48 and HMGA2 were analyzed. Data are presented as mean ± SD. One-way ANOVA test. All experiments were performed independently at least three times.

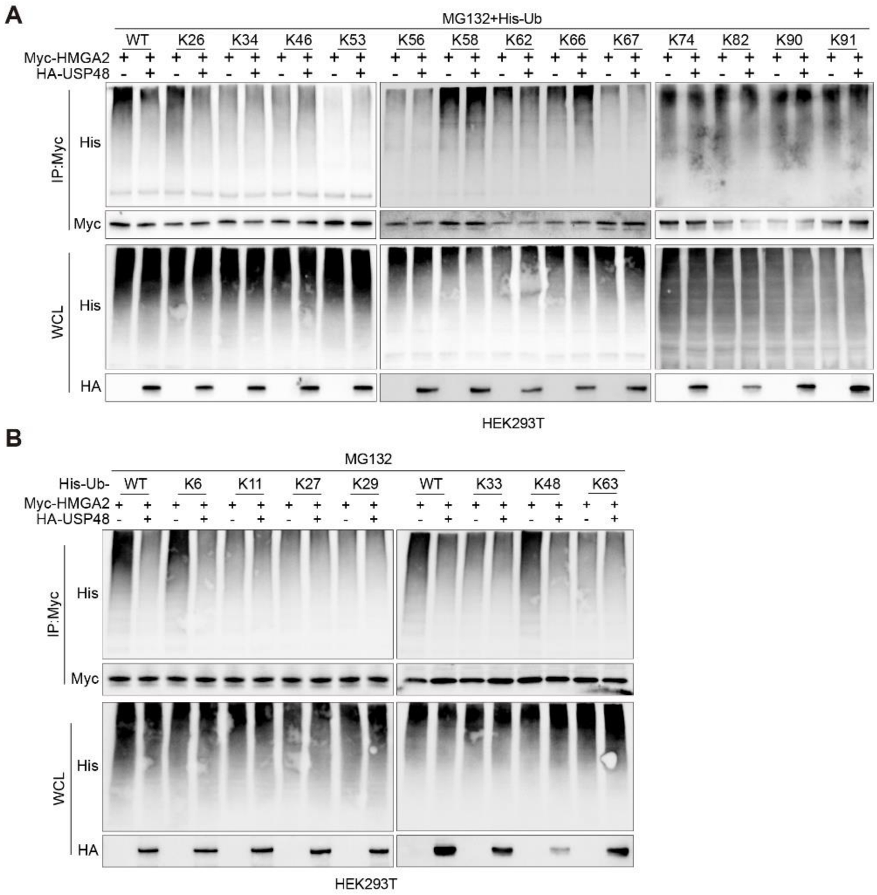


Figure S3. USP48 deubiquitinates HMGA2. (A) USP48 deubiquitinates specific Lys residues on HMGA2. De-ubiquitination assay was performed in HEK293T cells co-transfected with His-Ub, HA-USP48, Myc-HMGA2-WT, and Myc-HMGA2 K26/34/46/53/56/58/62/66/67/74/82/90/91, followed by treatment with 10 µmol/L of MG132 for 6 h. (B) HEK293T cells were co-transfected with indicated plasmids, treated with MG132 for 6 h, and subjected to IP with Myc antibody. IB was performed using anti-His antibodies to detect ubiquitinated HMGA2. For all panels, data are representative results of three independent experiments.

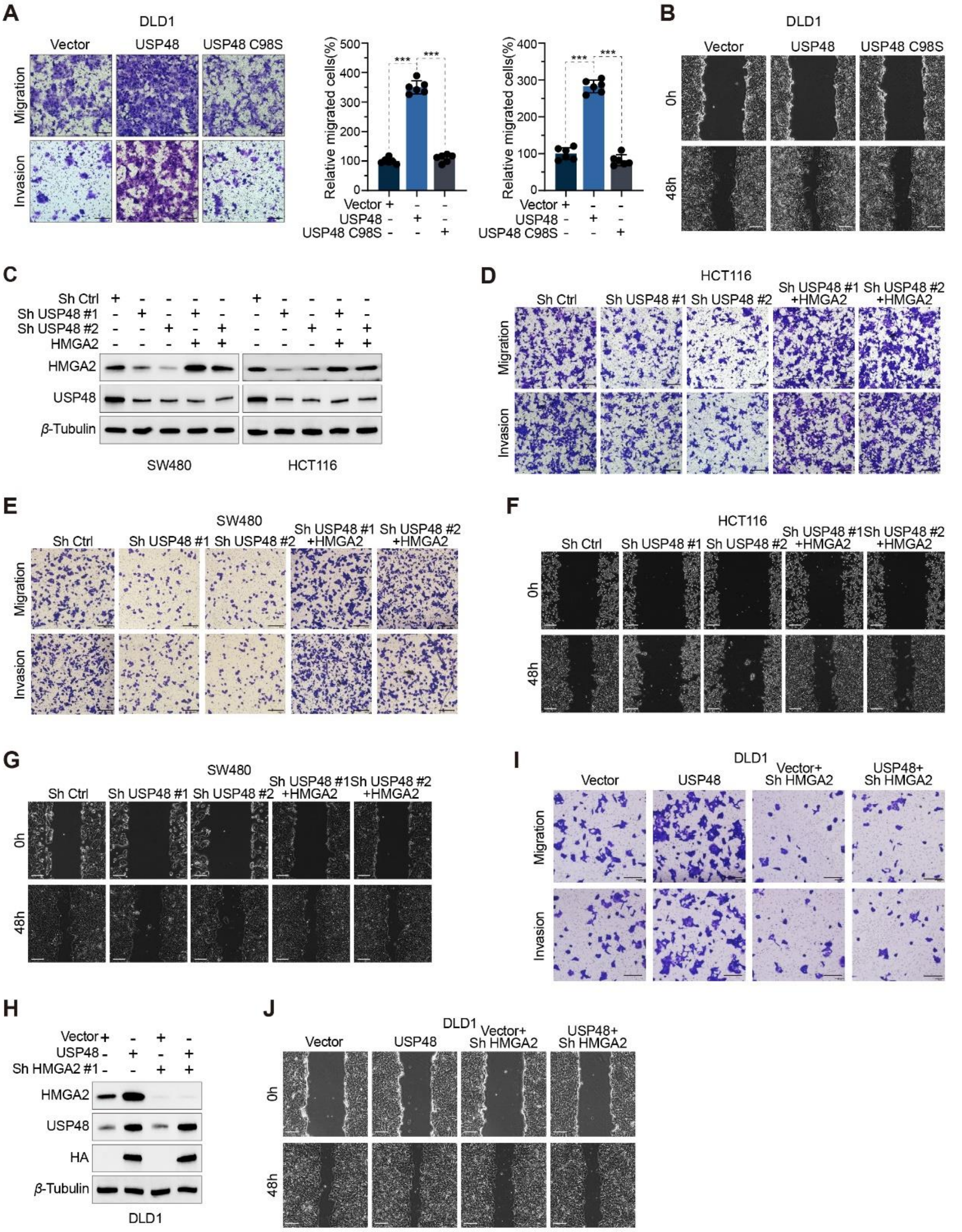


Figure S4. Ablation of USP48 expression impairs the metastatic potential of CRC cells. (A) Transwell migration and invasion assays of DLD1 cells transfected with USP48-WT, USP48-C98S, or vector control. Relative migrated cells in each group were quantified. (B) Wound-healing assay of DLD1 cells transfected with USP48-WT, USP48-C98S, or vector control. Photographs were taken at 0 and 48 h following the initial scratch. (C) IB analysis of USP48 and HMGA2 levels in SW480 and

HCT116 cells expressing Sh-Ctrl or Sh-USP48 #1 orSh-USP48 #2, reconstituted with vector control or HMGA2. (D-G) Knockdown of USP48 was performed in HCT116 and SW480 cells, with or without overexpression of HMGA2. Representative images of migrated cells were captured for each group (D, E), and representative photographs were taken at 0 and 48 h after the initial scratch (F, G). (H) IB analysis of USP48 and HMGA2 levels in DLD1 cells expressing vector control or HMGA2, reconstituted with Sh-Ctrl or Sh-HNGA2 #1. (I-J) USP48 was upregulated in DLD1 cells with or without HMGA2 knockdown. Representative images of migrated cells were captured for each group (I), and representative photographs were taken at 0 and 48 h after the initial scratch (J). Scale bar, 200 μm (A, B, D-G, I and J). Data are presented as mean ± SD. One-way ANOVA test (A). All in vitro experiments were performed independently at least three times. ***P<0.001.

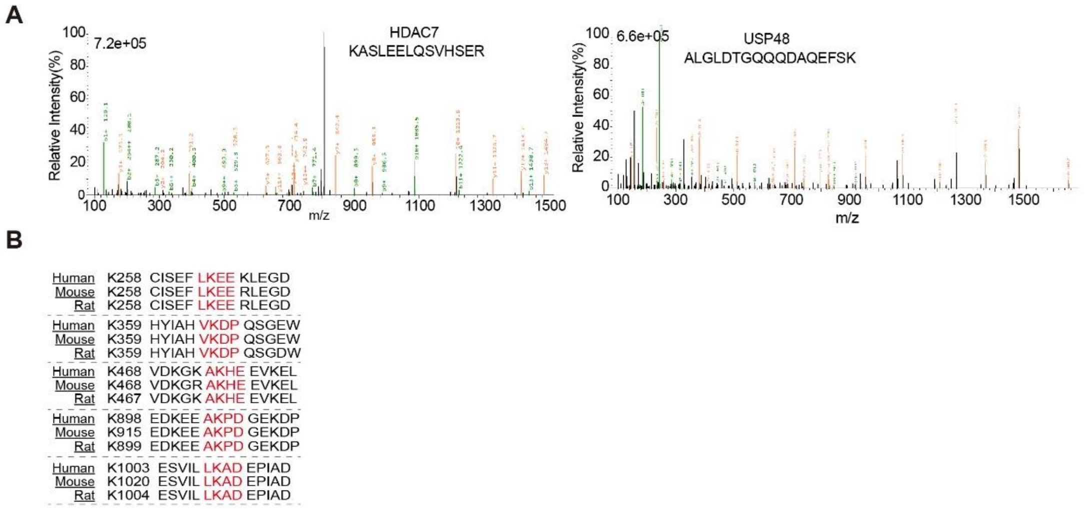


Figure S5. USP48 is SUMOylated by SUMO1 at Lys-258. (A) Mass-spectrometry analysis of HDAC7 and USP48 peptides in HA-USP48 precipitate. (B) Identified five potential SUMO-conjugation consensus motifs are evolutionarily conserved (red) from mouse to man.

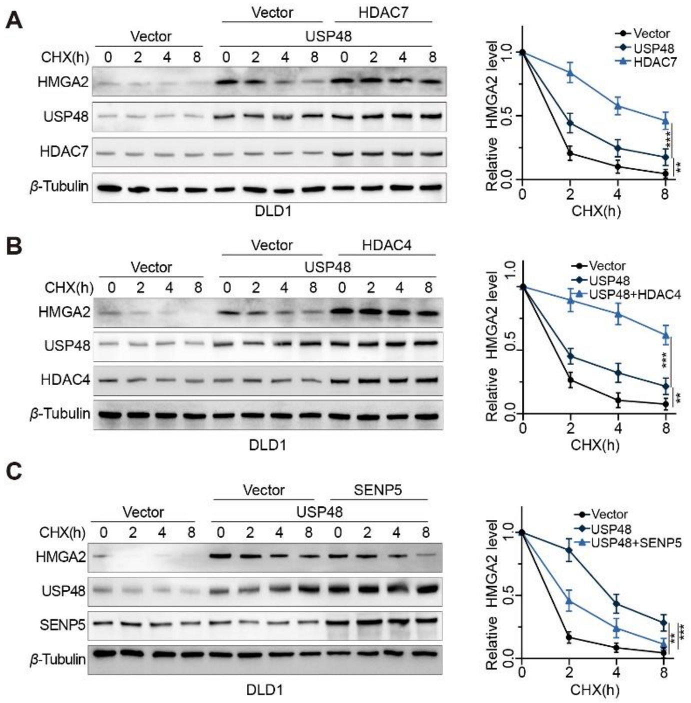
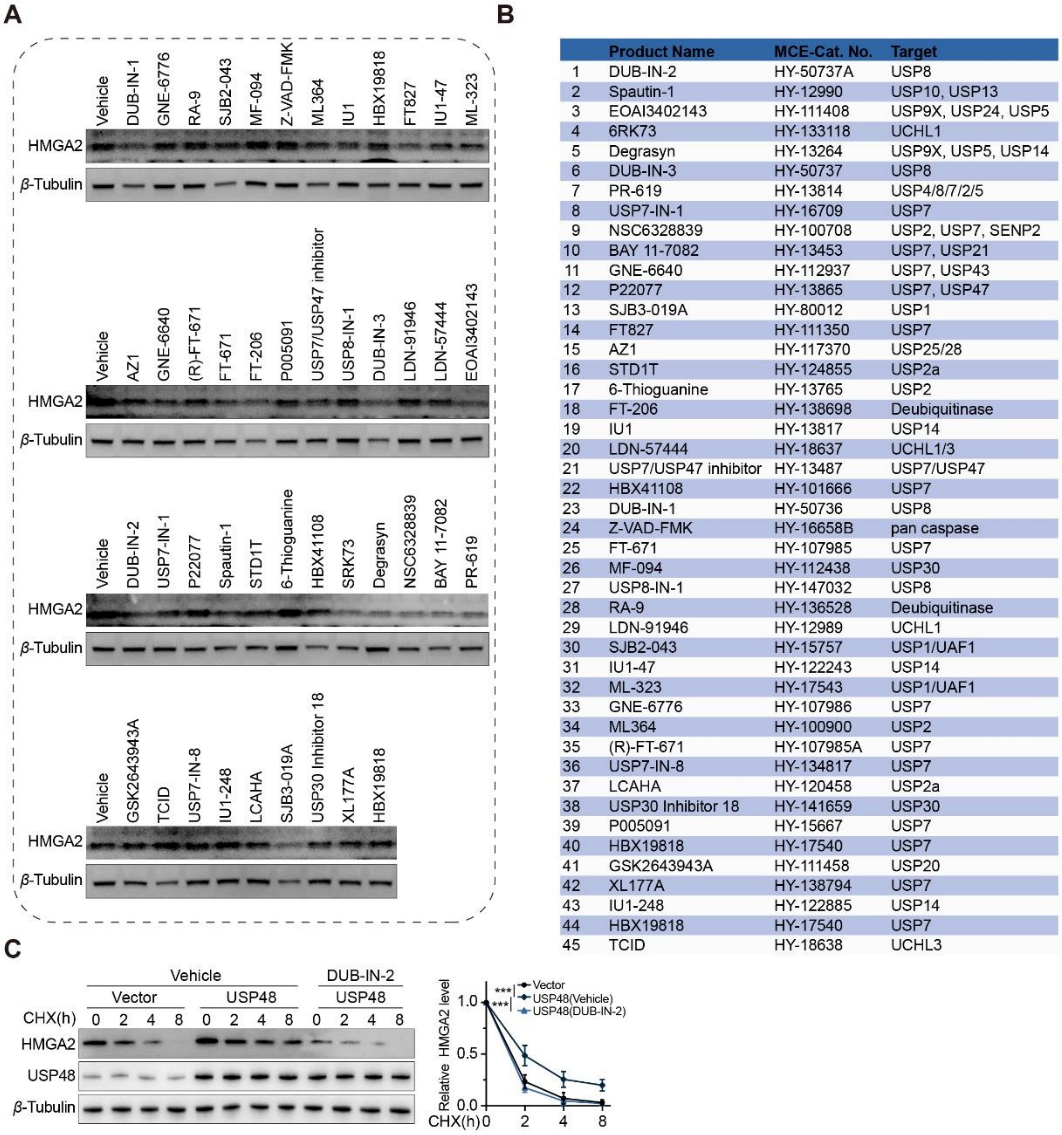


Figure S6. The function of USP48 on HMGA2 is significantly enhanced by SUMOylation at Lys-258.

(A-C) DLD1 cells were transfected with specific plasmids, as indicated and treated with CHX (50 μg/ml) for the indicated time points. Quantification of HMGA2 levels relative to β-Tubulin is shown. Data are presented as mean ± SD. One-way ANOVA test (A-C). All experiments were performed independently at least three times. $^{***}P<0.001$.



	Product Name	MCE-Cat. No.	Target
1	DUB-IN-2	HY-50737A	USP8
2	Spautin-1	HY-12990	USP10, USP13
3	EOAI3402143	HY-111408	USP9X, USP24, USP5
4	6RK73	HY-133118	UCHL1
5	Degrasyn	HY-13264	USP9X, USP5, USP14
6	DUB-IN-3	HY-50737	USP8
7	PR-619	HY-13814	USP4/8/7/2/5
8	USP7-IN-1	HY-16709	USP7
9	NSC6328839	HY-100708	USP2, USP7, SENP2
10	BAY 11-7082	HY-13453	USP7, USP21
11	GNE-6640	HY-112937	USP7, USP43
12	P22077	HY-13865	USP7, USP47
13	SJB3-019A	HY-80012	USP1
14	FT827	HY-111350	USP7
15	AZ1	HY-117370	USP25/28
16	STD1T	HY-124855	USP2a
17	6-Thioguanine	HY-13765	USP2
18	FT-206	HY-138698	Deubiquitinase
19	IU1	HY-13817	USP14
20	LDN-57444	HY-18637	UCHL1/3
21	USP7/USP47 inhibitor	HY-13487	USP7/USP47
22	HBX41108	HY-101666	USP7
23	DUB-IN-1	HY-50736	USP8
24	Z-VAD-FMK	HY-16658B	pan caspase
25	FT-671	HY-107985	USP7
26	MF-094	HY-112438	USP30
27	USP8-IN-1	HY-147032	USP8
28	RA-9	HY-136528	Deubiquitinase
29	LDN-91946	HY-12989	UCHL1
30	SJB2-043	HY-15757	USP1/UAF1
31	IU1-47	HY-122243	USP14
32	ML-323	HY-17543	USP1/UAF1
33	GNE-6776	HY-107986	USP7
34	ML364	HY-100900	USP2
35	(R)-FT-671	HY-107985A	USP7
36	USP7-IN-8	HY-134817	USP7
37	LCAHA	HY-120458	USP2a
38	USP30 Inhibitor 18	HY-141659	USP30
39	P005091	HY-15667	USP7
40	HBX19818	HY-17540	USP7
41	GSK2643943A	HY-111458	USP20
42	XL177A	HY-138794	USP7
43	IU1-248	HY-122885	USP14
44	HBX19818	HY-17540	USP7
45	TCID	HY-18638	UCHL3

Figure S7. DUB-IN-2 hinders the deubiquitinating activity of USP48 and induces the degradation of HMGA2. (A) IB analysis of exogenous HMGA2 expression in SW480 cells. SW480 cells were treated with the library of 45 reported DUB inhibitors at a concentration of 2.5 μmol/L for 12 h and assessed by IB. (B) The information of the library of 45 reported DUB inhibitors. (C) DLD1 cells transfected with control vector or HA-USP48 were treated with DMSO or DUB-IN-2 (2.5 μmol/L) 24 h, then CHX (50 μg/ml) was added at a set time point, and USP48 and HMGA2 were analyzed by IB analysis. ***P<0.001.

Table S1. The primers list

Gene	Forward (5'to3')	Reverse (5'to3')
USP48	CACATCGAGACCGCTTACCG	ACCAACCAAGCAATTCGGATT
HMGA2	ACCCAGGGGAAGACCCAAA	CCTCTTGGCCGTTTTTCTCCA
Slug	CGAACTGGACACACATACAGTG	CTGAGGATCTCTGGTTGTGGT
IGF2BP2	AGCCTGTCACCATCCATGC	CTTCGGCTAGTTTGGTCTCATC
SOX2	GCCGAGTGGAAACTTTTGTCG	GGCAGCGTGTACTTATCCTTCT
GAPDH	GGAGCGAGATCCCTCCAAAAT	GGCTGTTGTCATACTTCTCATGG

Table S2. The sequences of shRNA

Gene		Sense Sequence (5'to3')
shControl	shRNA	TACAAACGCTCTCATCGACAAG
USP48	shRNA1	AAGAAGATTCTAAACTTAT
USP48	shRNA2	GCGAGAACTGTCAAAGCAA
USP48	shRNA3	AGCCCAACACTACTGTTCA
HMGA2	shRNA1	CAACAAGTTGTTCAGAAGA
HMGA2	shRNA2	AGGACTATATTAATCACCT
HMGA2	shRNA3	ACAACAAGTTGTTCAGAAG

Table S3. Related to Figure 1; HMGA2 interacting proteins

Accession	Protein	Description	MW.[kDa]	Protein.score	Sequence.coverage.(%)	#.Unique.Peptides	#.Peptides	#.PSMs	Abundances
Q86UV5	USP48	Ubiquitin carboxyl-terminal hydrolase 48	119	2349	50	39	39	61	5767203050
P14618	PKM	Pyruvate kinase PKM	57.9	1230	47	19	19	29	498628917.3
O60343	TBC1D4	TBC1 domain family member 4	146.5	594	15	15	15	16	122079611.3
P12956	XRCC6	X-ray repair cross-complementing protein 6	69.8	481	28	13	13	14	92465227.81
P00338	LDHA	L-lactate dehydrogenase A chain	36.7	395	32	11	12	15	613604796.5
P53396	ACLY	ATP-citrate synthase	120.8	342	14	11	11	12	73329547
P49327	FASN	Fatty acid synthase	273.3	442	7	11	11	13	35023880.19
P12277	CKB	Creatine kinase B-type	42.6	693	39	10	10	14	212590327.9
P00558	PGK1	Phosphoglycerate kinase 1	44.6	454	29	10	10	12	203919777.1
Q00610	CLTC	Clathrin heavy chain 1	191.5	225	7	9	9	9	44531201.88
P49368	CCT3	T-complex protein 1 subunit gamma	60.5	188	24	8	8	9	109349572.3
P22033	MMUT	Methylmalonyl-CoA mutase, mitochondrial	83.1	274	16	8	8	9	86657579.75
Q96QC0	PPP1R10	Serine/threonine-protein phosphatase 1 regulatory subunit	99	203	13	7	7	9	35973364.63
Q99729	HNRNPAB	Heterogeneous nuclear ribonucleoprotein A/B	36.2	196	22	6	7	8	180104832.5
P49411	TUFM	Elongation factor Tu, mitochondrial	49.5	258	20	6	6	7	231885119
P48643	CCT5	T-complex protein 1 subunit epsilon	59.6	227	19	6	6	6	39817375
P04181	OAT	Ornithine aminotransferase, mitochondrial	48.5	122	15	6	6	6	41321821.75
Q13263	TRIM28	Transcription intermediary factor 1-beta	88.5	321	12	6	6	7	23311911.63
P22314	UBA1	Ubiquitin-like modifier-activating enzyme 1	117.8	166	8	6	6	6	26099544.25

P22102	GART	Trifunctional purine biosynthetic protein adenosine-3	107.7	228	7	6	6	6	27596251.75
P07737	PFN1	Profilin-1	15	233	55	5	5	6	113427829
P00492	HPRT1	Hypoxanthine-guanine phosphoribosyltransferase	24.6	200	28	5	5	5	22595299.5
P62826	RAN	GTP-binding nuclear protein Ran	24.4	157	25	5	5	5	54109130
P04075	ALDOA	Fructose-bisphosphate aldolase A	39.4	180	24	5	5	5	24828406
P07900	HSP90AA1	Heat shock protein HSP 90-alpha	84.6	537	18	5	10	12	63286648
P23526	AHCY	Adenosylhomocysteinase	47.7	257	16	5	5	5	53815497
Q13838	DDX39B	Spliceosome RNA helicase DDX39B	49	163	15	5	5	5	32126999.5
P22234	PAICS	Multifunctional protein ADE2	47	171	13	5	5	5	30025386.13
P40939	HADHA	Trifunctional enzyme subunit alpha, mitochondrial	82.9	264	12	5	5	5	6648115.375
Q96QK1	VPS35	Vacuolar protein sorting-associated protein 35	91.6	181	9	5	5	5	22767036.63
P68371	TUBB4B	Tubulin beta-4B chain	49.8	918	57	4	18	26	1196126405
P35232	PHB	Prohibitin	29.8	173	21	4	4	4	12883002.88
P60891	PRPS1	Ribose-phosphate pyrophosphokinase 1	34.8	189	16	4	4	4	35725547
P62136	PPP1CA	Serine/threonine-protein phosphatase PP1-alpha catalytic	37.5	157	14	4	4	4	9409114.25
P04844	RPN2	Dolichyl-diphosphooligosaccharide--protein glycosyltransf	69.2	188	12	4	4	4	2777882.5
Q09028	RBBP4	Histone-binding protein RBBP4	47.6	187	10	4	4	4	35302922
P27694	RPA1	Replication protein A 70 kDa DNA-binding subunit	68.1	139	9	4	4	4	15018820.25
Q12931	TRAP1	Heat shock protein 75 kDa, mitochondrial	80.1	156	8	4	4	4	98440227.25
P36871	PGM1	Phosphoglucomutase-1	61.4	100	8	4	4	4	12675501.25
Q9NSD9	FARSB	Phenylalanine--tRNA ligase beta subunit	66.1	122	7	4	4	4	11867746.13
P04843	RPN1	Dolichyl-diphosphooligosaccharide--protein glycosyltransf	68.5	89	7	4	4	4	18797843.25

P34932	HSPA4	Heat shock 70 kDa protein 4	94.3	115	6	4	4	4	8528908.25
Q9P2J5	LARS1	Leucine--tRNA ligase, cytoplasmic	134.4	141	5	4	4	4	4478860.75
P53621	COPA	Coatomer subunit alpha	138.3	87	5	4	4	4	8269097.813
P01031	C5	Complement C5	188.2	70	3	4	4	4	24731683.5
P52926	HMGA2	High mobility group protein HMGI-C	11.8	179	33	3	3	5	515931864
P62987	UBA52	Ubiquitin-60S ribosomal protein L40	14.7	83	30	3	3	3	177859651.3
P32119	PRDX2	Peroxiredoxin-2	21.9	128	19	3	4	4	25972879.25
Q07021	C1QBP	Complement component 1 Q subcomponent-binding protei	31.3	97	17	3	3	3	27398328.5
P12004	PCNA	Proliferating cell nuclear antigen	28.8	107	16	3	3	3	25164288.5
Q9HAN9	NMNAT1	Nicotinamide/nicotinic acid mononucleotide adenylyltransf	31.9	85	15	3	3	3	15467312.5
P16152	CBR1	Carbonyl reductase [NADPH] 1	30.4	163	13	3	3	4	28667731
Q16795	NDUFA9	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex s	42.5	66	13	3	3	3	6131614.063
P29692	EEF1D	Elongation factor 1-delta	31.1	62	12	3	3	3	38769531
Q9H9B4	SFXN1	Sideroflexin-1	35.6	126	11	3	3	3	24302534
P22695	UQCRC2	Cytochrome b-c1 complex subunit 2, mitochondrial	48.4	97	11	3	3	3	3261186
P62195	PSMC5	26S proteasome regulatory subunit 8	45.6	186	10	3	3	4	17997023
P43686	PSMC4	26S proteasome regulatory subunit 6B	47.3	149	9	3	3	4	8496432.125
P34897	SHMT2	Serine hydroxymethyltransferase, mitochondrial	56	137	8	3	3	3	23066143.5
P08243	ASNS	Asparagine synthetase [glutamine-hydrolyzing]	64.3	129	8	3	3	3	6561163.75
Q9UQ80	PA2G4	Proliferation-associated protein 2G4	43.8	84	8	3	3	3	15349949.75
P17812	CTPS1	CTP synthase 1	66.6	186	7	3	3	4	15257876.25
P52209	PGD	6-phosphogluconate dehydrogenase, decarboxylating	53.1	139	7	3	3	3	12614580.63

P31939	ATIC	Bifunctional purine biosynthesis protein ATIC	64.6	71	7	3	3	3	5501426
O14744	PRMT5	Protein arginine N-methyltransferase 5	72.6	59	7	3	3	3	20045108.5
Q16658	FSCN1	Fascin	54.5	80	6	3	3	3	26050094
O43776	NARS1	Asparagine--tRNA ligase, cytoplasmic	62.9	68	6	3	3	3	13419340.5
P54886	ALDH18A1	Delta-1-pyrroline-5-carboxylate synthase	87.2	85	5	3	3	3	13036177.75
P49588	AARS1	Alanine--tRNA ligase, cytoplasmic	106.7	120	4	3	3	3	33485952.5
P16615	ATP2A2	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	114.7	68	3	3	3	3	8848696.625
Q13885	TUBB2A	Tubulin beta-2A chain	49.9	864	52	2	17	23	94581273.75
P18085	ARF4	ADP-ribosylation factor 4	20.5	148	26	2	4	4	23049683.25
P63241	EIF5A	Eukaryotic translation initiation factor 5A-1	16.8	155	23	2	2	3	15563643.25
Q9BUF5	TUBB6	Tubulin beta-6 chain	49.8	419	21	2	8	11	4979366.875
Q15185	PTGES3	Prostaglandin E synthase 3	18.7	55	18	2	2	2	9060008.5
P56537	EIF6	Eukaryotic translation initiation factor 6	26.6	66	17	2	2	2	2491518.75
P00491	PNP	Purine nucleoside phosphorylase	32.1	102	14	2	2	2	2861677.25
P00387	CYB5R3	NADH-cytochrome b5 reductase 3	34.2	59	12	2	2	2	8804801.75
Q9NP79	VTA1	Vacuolar protein sorting-associated protein VTA1 homolog	33.9	57	11	2	2	2	6625079
Q15181	PPA1	Inorganic pyrophosphatase	32.6	145	10	2	2	2	1877094.75
P13804	ETFA	Electron transfer flavoprotein subunit alpha, mitochondrial	35.1	61	10	2	2	2	6628321.25
P11177	PDHB	Pyruvate dehydrogenase E1 component subunit beta, mit	39.2	93	9	2	2	2	5662778.5
Q96FW1	OTUB1	Ubiquitin thioesterase OTUB1	31.3	73	9	2	2	2	8612140.75
Q9UBE0	SAE1	SUMO-activating enzyme subunit 1	38.4	66	9	2	2	2	3508511
P10768	ESD	S-formylglutathione hydrolase	31.4	55	9	2	2	2	4940103.5

Q9Y6C9	MTCH2	Mitochondrial carrier homolog 2	33.3	91	8	2	2	2	5482844.5
P23381	WARS1	Tryptophan--tRNA ligase, cytoplasmic	53.1	75	8	2	2	2	6541823
P39748	FEN1	Flap endonuclease 1	42.6	53	8	2	2	2	9707932
P11766	ADH5	Alcohol dehydrogenase class-3	39.7	39	8	2	2	2	10570800
P27695	APEX1	DNA-(apurinic or apyrimidinic site) endonuclease	35.5	112	7	2	2	4	220027073.3
O14929	HAT1	Histone acetyltransferase type B catalytic subunit	49.5	94	7	2	2	2	6233844.5
P62333	PSMC6	26S proteasome regulatory subunit 10B	44.1	79	7	2	2	2	8952334.5
Q99873	PRMT1	Protein arginine N-methyltransferase 1	42.4	78	7	2	2	2	8013396.75
Q9P035	HACD3	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3	43.1	71	7	2	2	2	7590247.75
P06737	PYGL	Glycogen phosphorylase, liver form	97.1	102	6	2	3	3	5217013.25
Q9H0C8	ILKAP	Integrin-linked kinase-associated serine/threonine phosph	42.9	84	6	2	2	2	555246
Q9HAV0	GNB4	Guanine nucleotide-binding protein subunit beta-4	37.5	62	6	2	2	2	12054803
P13489	RNH1	Ribonuclease inhibitor	49.9	60	6	2	2	2	8607313.25
P06493	CDK1	Cyclin-dependent kinase 1	34.1	59	6	2	2	2	26145493
O75874	IDH1	Isocitrate dehydrogenase [NADP] cytoplasmic	46.6	55	6	2	2	2	2614135.25
Q00325	SLC25A3	Phosphate carrier protein, mitochondrial	40.1	54	6	2	2	2	40295813
P48735	IDH2	Isocitrate dehydrogenase [NADP], mitochondrial	50.9	43	6	2	2	2	4364945
P50995	ANXA11	Annexin A11	54.4	42	6	2	2	2	4109689
Q9Y265	RUVBL1	RuvB-like 1	50.2	39	6	2	2	2	12714800
P15121	AKR1B1	Aldo-keto reductase family 1 member B1	35.8	37	6	2	2	2	23139682
Q9BV20	MRI1	Methylthioribose-1-phosphate isomerase	39.1	36	6	2	2	2	10788652.75
P49915	GMPS	GMP synthase [glutamine-hydrolyzing]	76.7	152	5	2	2	3	7820966.75

P61221	ABCE1	ATP-binding cassette sub-family E member 1	67.3	106	5	2	2	2	2253009
Q9UHB9	SRP68	Signal recognition particle subunit SRP68	70.7	91	5	2	2	2	6132342.25
Q15758	SLC1A5	Neutral amino acid transporter B(0)	56.6	81	5	2	2	2	3208796.25
Q15046	KARS1	Lysine--tRNA ligase	68	76	5	2	2	2	5743760.5
P33993	MCM7	DNA replication licensing factor MCM7	81.3	76	5	2	2	2	6351708.75
P00734	F2	Prothrombin	70	71	5	2	2	2	4413048
Q14498	RBM39	RNA-binding protein 39	59.3	65	5	2	2	2	8691258.5
P61160	ACTR2	Actin-related protein 2	44.7	47	5	2	2	2	5991902
P07237	P4HB	Protein disulfide-isomerase	57.1	46	5	2	2	2	2109756
P48444	ARCN1	Coatomer subunit delta	57.2	46	5	2	2	2	8086343.25
P05023	ATP1A1	Sodium/potassium-transporting ATPase subunit alpha-1	112.8	114	3	2	2	2	
P26639	TARS1	Threonine--tRNA ligase 1, cytoplasmic	83.4	97	3	2	2	2	7389461.625
Q13200	PSMD2	26S proteasome non-ATPase regulatory subunit 2	100.1	95	3	2	2	3	4072206.375
P49591	SARS1	Serine--tRNA ligase, cytoplasmic	58.7	84	3	2	2	2	8842737.875
O95373	IPO7	Importin-7	119.4	78	3	2	2	2	759849.6875
P43490	NAMPT	Nicotinamide phosphoribosyltransferase	55.5	62	3	2	2	2	9252771.5
P13797	PLS3	Plastin-3	70.8	57	3	2	2	2	10786233
Q16531	DDB1	DNA damage-binding protein 1	126.9	46	3	2	2	2	3931207.25
P26640	VARS1	Valine--tRNA ligase	140.4	77	2	2	2	2	73267270.75
P55265	ADAR	Double-stranded RNA-specific adenosine deaminase	136	75	2	2	2	2	4694519.25
P12814	ACTN1	Alpha-actinin-1	103	69	2	2	2	2	3366506.5
O75643	SNRNP200	U5 small nuclear ribonucleoprotein 200 kDa helicase	244.4	64	2	2	2	2	1105709.75

Q86VP6	CAND1	Cullin-associated NEDD8-dissociated protein 1	136.3	50	2	2	2	2	9906105
P35579	MYH9	Myosin-9	226.4	57	1	2	2	2	6965459.75
Q71DI3	H3C15	Histone H3.2	15.4	34	24	1	1	2	
P61204	ARF3	ADP-ribosylation factor 3	20.6	135	22	1	3	3	7598234
P31946	YWHAB	14-3-3 protein beta/alpha	28.1	113	15	1	3	3	645343.5625
P13929	ENO3	Beta-enolase	47	389	14	1	4	6	31342040
A0A0C4DH72	IGKV1-6	Immunoglobulin kappa variable 1-6	12.7	35	14	1	1	1	17365038
P61981	YWHAG	14-3-3 protein gamma	28.3	127	13	1	3	3	5445280
P06454	PTMA	Prothymosin alpha	12.2	52	13	1	1	1	4033580.5
P56134	ATP5MF	ATP synthase subunit f, mitochondrial	10.9	37	12	1	1	1	3153842
O00487	PSMD14	26S proteasome non-ATPase regulatory subunit 14	34.6	43	11	1	1	1	
P14406	COX7A2	Cytochrome c oxidase subunit 7A2, mitochondrial	9.4	24	11	1	1	1	1334592
Q06830	PRDX1	Peroxiredoxin-1	22.1	66	10	1	2	2	14150475
P81605	DCD	Dermcidin	11.3	25	10	1	1	1	
O14880	MGST3	Microsomal glutathione S-transferase 3	16.5	88	9	1	1	1	3426874.75
Q9NVQ4	FAIM	Fas apoptotic inhibitory molecule 1	20.2	58	9	1	1	1	
Q13185	CBX3	Chromobox protein homolog 3	20.8	51	9	1	1	1	1695501.875
P52434	POLR2H	DNA-directed RNA polymerases I, II, and III subunit RPA	17.1	38	9	1	1	1	2350833
Q15056	EIF4H	Eukaryotic translation initiation factor 4H	27.4	57	8	1	1	1	2803987
O60762	DPM1	Dolichol-phosphate mannosyltransferase subunit 1	29.6	39	8	1	1	1	1620260.875
P14174	MIF	Macrophage migration inhibitory factor	12.5	31	8	1	1	1	17117540
A6NHL2	TUBAL3	Tubulin alpha chain-like 3	49.9	122	7	1	3	4	5058086.5

Q9UL25	RAB21	Ras-related protein Rab-21	24.3	71	7	1	1	1	5168701
P24534	EEF1B2	Elongation factor 1-beta	24.7	69	7	1	1	1	21787794
Q9NVS2	MRPS18A	39S ribosomal protein S18a, mitochondrial	22.2	66	7	1	1	1	1034303.438
O00299	CLIC1	Chloride intracellular channel protein 1	26.9	62	7	1	1	1	3482020.25
P19623	SRM	Spermidine synthase	33.8	45	7	1	1	1	1288989.5
P08134	RHOC	Rho-related GTP-binding protein RhoC	22	32	7	1	1	1	3005311.75
Q9UKK9	NUDT5	ADP-sugar pyrophosphatase	24.3	29	7	1	1	1	4451319
P48047	ATP5PO	ATP synthase subunit O, mitochondrial	23.3	27	7	1	1	1	8115029
Q9BYZ2	LDHAL6B	L-lactate dehydrogenase A-like 6B	41.9	70	6	1	2	3	
O75396	SEC22B	Vesicle-trafficking protein SEC22b	24.7	69	6	1	1	1	6193561
P21266	GSTM3	Glutathione S-transferase Mu 3	26.5	67	6	1	1	1	3063222.5
P09972	ALDOC	Fructose-bisphosphate aldolase C	39.4	64	6	1	1	1	4484634
P12268	IMPDH2	Inosine-5'-monophosphate dehydrogenase 2	55.8	60	6	1	1	1	
P52907	CAPZA1	F-actin-capping protein subunit alpha-1	32.9	51	6	1	1	1	4515663
P31930	UQCRC1	Cytochrome b-c1 complex subunit 1, mitochondrial	52.6	50	6	1	1	1	
Q16629	SRSF7	Serine/arginine-rich splicing factor 7	27.4	41	6	1	1	1	6294779
P01706	IGLV2-11	Immunoglobulin lambda variable 2-11	12.6	31	6	1	1	1	82753912
Q16637	SMN1	Survival motor neuron protein	31.8	30	6	1	1	1	2255687.75
Q92665	MRPS31	28S ribosomal protein S31, mitochondrial	45.3	24	6	1	1	1	987568.75
Q12849	GRSF1	G-rich sequence factor 1	53.1	76	5	1	1	1	1968221.5
Q96C36	PYCR2	Pyrroline-5-carboxylate reductase 2	33.6	75	5	1	1	1	
O96008	TOMM40	Mitochondrial import receptor subunit TOM40 homolog	37.9	71	5	1	1	1	820417.3125
Q9NQT5	EXOSC3	Exosome complex component RRP40	29.6	66	5	1	1	1	4340486.5

P35250	RFC2	Replication factor C subunit 2	39.1	55	5	1	1	1	
Q9UBQ7	GRHPR	Glyoxylate reductase/hydroxypyruvate reductase	35.6	50	5	1	1	1	2501210.5
Q15050	RRS1	Ribosome biogenesis regulatory protein homolog	41.2	48	5	1	1	1	1085017600
Q14257	RCN2	Reticulocalbin-2	36.9	47	5	1	1	1	3226434.5
P30520	ADSS2	Adenylosuccinate synthetase isozyme 2	50.1	47	5	1	1	1	2043345.125
P43897	TSFM	Elongation factor Ts, mitochondrial	35.4	46	5	1	1	1	1633265.75
P57088	TMEM33	Transmembrane protein 33	28	41	5	1	1	1	3913598
P60900	PSMA6	Proteasome subunit alpha type-6	27.4	40	5	1	1	1	2818280.25
Q96CW1	AP2M1	AP-2 complex subunit mu	49.6	37	5	1	1	1	1711324
P30048	PRDX3	Thioredoxin-dependent peroxide reductase, mitochondrial	27.7	37	5	1	1	1	3517441.25
P62714	PPP2CB	Serine/threonine-protein phosphatase 2A catalytic subunit	35.6	36	5	1	1	1	1705104.125
Q5XKP0	MICOS13	MICOS complex subunit MIC13	13.1	28	5	1	1	1	920486.625
Q9Y4Z0	LSM4	U6 snRNA-associated Sm-like protein LSm4	15.3	26	5	1	1	1	3451556.75
Q13595	TRA2A	Transformer-2 protein homolog alpha	32.7	25	5	1	1	1	3053881.75
Q16186	ADRM1	Proteasomal ubiquitin receptor ADRM1	42.1	65	4	1	1	1	1796114
P40925	MDH1	Malate dehydrogenase, cytoplasmic	36.4	54	4	1	1	1	3681855
Q15102	PAFAH1B3	Platelet-activating factor acetylhydrolase IB subunit alpha	25.7	51	4	1	1	1	4717042.5
P30041	PRDX6	Peroxiredoxin-6	25	43	4	1	1	1	2029202.5
O76003	GLRX3	Glutaredoxin-3	37.4	40	4	1	1	1	3300081.25
P68402	PAFAH1B2	Platelet-activating factor acetylhydrolase IB subunit alpha	25.6	39	4	1	1	1	1692729.75
P17980	PSMC3	26S proteasome regulatory subunit 6A	49.2	38	4	1	1	1	1648111.25
Q9UJZ1	STOML2	Stomatin-like protein 2, mitochondrial	38.5	37	4	1	1	1	

P50395	GDI2	Rab GDP dissociation inhibitor beta	50.6	34	4	1	1	1	
P00403	MT-CO2	Cytochrome c oxidase subunit 2	25.5	30	4	1	1	1	5288784
Q9BQA1	WDR77	Methylosome protein 50	36.7	30	4	1	1	1	5522065
Q12765	SCRN1	Secernin-1	46.4	29	4	1	1	1	
P53007	SLC25A1	Tricarboxylate transport protein, mitochondrial	34	27	4	1	1	1	3009174.75
Q14558	PRPSAP1	Phosphoribosyl pyrophosphate synthase-associated prote	39.4	23	4	1	1	1	1587866.375
Q9H9J2	MRPL44	39S ribosomal protein L44, mitochondrial	37.5	23	4	1	1	1	
P41250	GARS1	Glycine--tRNA ligase	83.1	158	3	1	1	2	1844549.5
O43242	PSMD3	26S proteasome non-ATPase regulatory subunit 3	60.9	108	3	1	1	2	5523251.75
Q9UMR2	DDX19B	ATP-dependent RNA helicase DDX19B	53.9	87	3	1	1	1	1527581.875
P11216	PYGB	Glycogen phosphorylase, brain form	96.6	83	3	1	2	2	2584958
P27169	PON1	Serum paraoxonase/arylesterase 1	39.7	77	3	1	1	2	75924042
O00232	PSMD12	26S proteasome non-ATPase regulatory subunit 12	52.9	71	3	1	1	1	2016867.875
Q3SXM5	HSDL1	Inactive hydroxysteroid dehydrogenase-like protein 1	37	67	3	1	1	1	812361.4375
P27824	CANX	Calnexin	67.5	66	3	1	1	1	
Q14739	LBR	Delta(14)-sterol reductase LBR	70.7	65	3	1	1	1	5269150.5
Q9UJS0	SLC25A13	Calcium-binding mitochondrial carrier protein Aralar2	74.1	64	3	1	1	1	719684.1875
P35998	PSMC2	26S proteasome regulatory subunit 7	48.6	55	3	1	1	1	5291414.5
P78347	GTF2I	General transcription factor II-I	112.3	53	3	1	1	1	1254423.125
Q9Y5K5	UCHL5	Ubiquitin carboxyl-terminal hydrolase isozyme L5	37.6	52	3	1	1	1	966898.0625
O75083	WDR1	WD repeat-containing protein 1	66.2	52	3	1	1	1	3679914.25
O00154	ACOT7	Cytosolic acyl coenzyme A thioester hydrolase	41.8	47	3	1	1	1	4622503

P62191	PSMC1	26S proteasome regulatory subunit 4	49.2	45	3	1	1	1	4269369.5
P55010	EIF5	Eukaryotic translation initiation factor 5	49.2	43	3	1	1	1	1040244.75
P13861	PRKAR2A	cAMP-dependent protein kinase type II-alpha regulatory s	45.5	39	3	1	1	1	1158570.625
P53582	METAP1	Methionine aminopeptidase 1	43.2	38	3	1	1	1	
P48382	RFX5	DNA-binding protein RFX5	65.3	38	3	1	1	1	704025.5
P41240	CSK	Tyrosine-protein kinase CSK	50.7	36	3	1	1	1	1721485.5
O75955	FLOT1	Flotillin-1	47.3	33	3	1	1	1	1182583.625
Q96KP4	CNDP2	Cytosolic non-specific dipeptidase	52.8	33	3	1	1	1	484485.9063
P05198	EIF2S1	Eukaryotic translation initiation factor 2 subunit 1	36.1	32	3	1	1	1	1183472.875
Q6P1J9	CDC73	Parafibromin	60.5	29	3	1	1	1	1197483.5
O00442	RTCA	RNA 3'-terminal phosphate cyclase	39.3	24	3	1	1	1	
Q53GS9	USP39	U4/U6.U5 tri-snRNP-associated protein 2	65.3	22	3	1	1	1	
P31040	SDHA	Succinate dehydrogenase [ubiquinone] flavoprotein subun	72.6	127	2	1	1	1	
Q08945	SSRP1	FACT complex subunit SSRP1	81	55	2	1	1	1	4621388
Q9NRW7	VPS45	Vacuolar protein sorting-associated protein 45	65	53	2	1	1	1	778508.3125
P63010	AP2B1	AP-2 complex subunit beta	104.5	53	2	1	1	1	
Q6P4Q7	CNNM4	Metal transporter CNNM4	86.6	51	2	1	1	1	3983875.5
P18754	RCC1	Regulator of chromosome condensation	44.9	45	2	1	1	1	6983288.5
P10155	RO60	60 kDa SS-A/Ro ribonucleoprotein	60.6	44	2	1	1	1	3421549.75
P56545	CTBP2	C-terminal-binding protein 2	48.9	43	2	1	1	1	7677481
O00505	KPNA3	Importin subunit alpha-4	57.8	42	2	1	1	1	1132129.875
Q96T37	RBM15	RNA-binding protein 15	107.1	42	2	1	1	1	

P14923	JUP	Junction plakoglobin	81.7	41	2	1	1	1	
P36957	DLST	Dihydrolipoyllysine-residue succinyltransferase componen	48.7	41	2	1	1	1	4379225
Q15645	TRIP13	Pachytene checkpoint protein 2 homolog	48.5	40	2	1	1	1	4016814
P33992	MCM5	DNA replication licensing factor MCM5	82.2	40	2	1	1	1	2800414.5
Q15436	SEC23A	Protein transport protein Sec23A	86.1	39	2	1	1	1	3622323.75
P30837	ALDH1B1	Aldehyde dehydrogenase X, mitochondrial	57.2	38	2	1	1	1	
P55060	CSE1L	Exportin-2	110.3	37	2	1	1	1	
P33176	KIF5B	Kinesin-1 heavy chain	109.6	36	2	1	1	1	
P56192	MARS1	Methionine--tRNA ligase, cytoplasmic	101.1	34	2	1	1	1	3237876.75
Q8WVM8	SCFD1	Sec1 family domain-containing protein 1	72.3	34	2	1	1	1	1905743
P33991	MCM4	DNA replication licensing factor MCM4	96.5	33	2	1	1	1	568122.5625
Q9H9T3	ELP3	Elongator complex protein 3	62.2	33	2	1	1	1	
P35611	ADD1	Alpha-adducin	80.9	33	2	1	1	1	
Q15291	RBBP5	Retinoblastoma-binding protein 5	59.1	32	2	1	1	1	
P14868	DARS1	Aspartate--tRNA ligase, cytoplasmic	57.1	31	2	1	1	1	4917642
P35520	CBS	Cystathionine beta-synthase	60.5	30	2	1	1	1	2073406.5
Q9NPQ8	RIC8A	Synembryn-A	59.7	30	2	1	1	1	576408.5
Q14145	KEAP1	Kelch-like ECH-associated protein 1	69.6	29	2	1	1	1	16070964
P49643	PRIM2	DNA primase large subunit	58.8	28	2	1	1	1	1173046.375
Q9UBT2	UBA2	SUMO-activating enzyme subunit 2	71.2	28	2	1	1	1	4652618.5
P54578	USP14	Ubiquitin carboxyl-terminal hydrolase 14	56	28	2	1	1	1	1366149.75
Q9NQW7	XPNPEP1	Xaa-Pro aminopeptidase 1	69.9	27	2	1	1	1	
P46977	STT3A	Dolichyl-diphosphooligosaccharide--protein glycosyltransf	80.5	27	2	1	1	1	

O43929	ORC4	Origin recognition complex subunit 4	50.3	26	2	1	1	1	
O94808	GFPT2	Glutamine--fructose-6-phosphate aminotransferase [isome	76.9	26	2	1	1	1	654845
P08195	SLC3A2	4F2 cell-surface antigen heavy chain	68	25	2	1	1	1	1926039.75
Q6NVY1	HIBCH	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	43.5	24	2	1	1	1	2477920
O75390	CS	Citrate synthase, mitochondrial	51.7	24	2	1	1	1	4235922.5
Q8WTT2	NOC3L	Nucleolar complex protein 3 homolog	92.5	23	2	1	1	1	909306.375
P43246	MSH2	DNA mismatch repair protein Msh2	104.7	80	1	1	1	1	1124893.875
Q99460	PSMD1	26S proteasome non-ATPase regulatory subunit 1	105.8	72	1	1	1	1	2243860.75
P42704	LRPPRC	Leucine-rich PPR motif-containing protein, mitochondrial	157.8	67	1	1	1	1	1173530.125
P00450	CP	Ceruloplasmin	122.1	65	1	1	1	1	2427498.25
Q9Y4L1	HYOU1	Hypoxia up-regulated protein 1	111.3	65	1	1	1	1	1208369
Q9Y2L1	DIS3	Exosome complex exonuclease RRP44	108.9	60	1	1	1	1	3172484.5
Q68EM7	ARHGAP17	Rho GTPase-activating protein 17	95.4	59	1	1	1	1	
Q8WUM4	PDCD6IP	Programmed cell death 6-interacting protein	96	54	1	1	1	1	
P53992	SEC24C	Protein transport protein Sec24C	118.2	51	1	1	1	1	1177476.5
P08133	ANXA6	Annexin A6	75.8	47	1	1	1	1	1612213.375
Q13620	CUL4B	Cullin-4B	103.9	46	1	1	1	1	1019978
Q9BVJ6	UTP14A	U3 small nucleolar RNA-associated protein 14 homolog A	87.9	41	1	1	1	1	1918060.5
Q7L014	DDX46	Probable ATP-dependent RNA helicase DDX46	117.3	40	1	1	1	1	
O43747	AP1G1	AP-1 complex subunit gamma-1	91.3	39	1	1	1	1	1506611
P53618	COPB1	Coatomer subunit beta	107.1	39	1	1	1	1	
O95782	AP2A1	AP-2 complex subunit alpha-1	107.5	39	1	1	1	1	

Q13045	FLII	Protein flightless-1 homolog	144.7	39	1	1	1	1	1046191.5
Q9Y3T9	NOC2L	Nucleolar complex protein 2 homolog	84.9	39	1	1	1	1	1371463.25
Q9NQH7	XPNPEP3	Xaa-Pro aminopeptidase 3	57	38	1	1	1	1	27984678
Q9HAV4	XPO5	Exportin-5	136.2	36	1	1	1	1	
Q14974	KPNB1	Importin subunit beta-1	97.1	36	1	1	1	1	1610898.75
Q9BPX3	NCAPG	Condensin complex subunit 3	114.3	35	1	1	1	1	
O00159	MYO1C	Unconventional myosin-Ic	121.6	35	1	1	1	1	
Q6PI48	DARS2	Aspartate--tRNA ligase, mitochondrial	73.5	35	1	1	1	1	2541134.5
Q8TEX9	IPO4	Importin-4	118.6	35	1	1	1	1	
Q01813	PFKP	ATP-dependent 6-phosphofructokinase, platelet type	85.5	34	1	1	1	1	2369671.25
P52701	MSH6	DNA mismatch repair protein Msh6	152.7	34	1	1	1	1	1696498.25
Q86YS3	RAB11FIP4	Rab11 family-interacting protein 4	71.9	33	1	1	1	1	2897770.75
P28331	NDUFS1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitoch	79.4	32	1	1	1	1	4429126.5
P19367	HK1	Hexokinase-1	102.4	30	1	1	1	1	6765532.5
Q9C0C9	UBE2O	(E3-independent) E2 ubiquitin-conjugating enzyme	141.2	29	1	1	1	1	834833.8125
O95347	SMC2	Structural maintenance of chromosomes protein 2	135.6	29	1	1	1	1	1851995.25
P35606	COPB2	Coatomer subunit beta'	102.4	27	1	1	1	1	5704954
O60299	LZTS3	Leucine zipper putative tumor suppressor 3	71.7	27	1	1	1	1	8168197.5
P49189	ALDH9A1	4-trimethylaminobutyraldehyde dehydrogenase	53.8	26	1	1	1	1	6977843
Q5BKZ1	ZNF326	DBIRD complex subunit ZNF326	65.6	25	1	1	1	1	4168504.25
Q15020	SART3	Squamous cell carcinoma antigen recognized by T-cells 3	109.9	25	1	1	1	1	
O60763	USO1	General vesicular transport factor p115	107.8	23	1	1	1	1	1429639.875

Q9Y4W6	AFG3L2	AFG3-like protein 2	88.5	20	1	1	1	1	3175201.75

Table S4. Related to Figure 5; USP48 interacting proteins

Accession	Description	Gene_names	#PepCount	#UniquePepCount	CoverPercent	MW [kDa]	PI
P35579	sp|P35579|MYH9_HUMAN Myosin-9 OS=Homo sapiens OX=9606 GN=MYH9 PE=1 SV=4	MYH9	75	61	33.320%	226529.66	5.5
Q86UV5	sp|Q86UV5|UBP48_HUMAN Ubiquitin carboxyl-terminal hydrolase 48 OS=Homo sapiens OX=9606 GN=USP48 PE=1 SV=1	USP48	102	58	57.290%	119030.99	5.75
P56524	sp|P56524|HDAC4_HUMAN Histone deacetylase 4 OS=Homo sapiens OX=9606 GN=HDAC4 PE=1 SV=3	HDAC4	121	57	60.240%	119038.31	6.49
B2R9F5	tr|B2R9F5|B2R9F5_HUMAN cDNA, FLJ94365 OS=Homo sapiens OX=9606 PE=2 SV=1		98	57	71.130%	86693.03	9.26
A0A0U4BW16	tr|A0A0U4BW16|A0A0U4BW16_HUMAN Non-muscle myosin heavy chain 9 OS=Homo sapiens OX=9606 GN=MYH9 PE=2 SV=1	MYH9	68	55	29.440%	226514.51	5.43
P09874	sp|P09874|PARP1_HUMAN Poly [ADP-ribose] polymerase 1 OS=Homo sapiens OX=9606 GN=PARP1 PE=1 SV=4	PARP1	71	52	46.550%	113082.48	8.99
Q8WUI4	sp|Q8WUI4|HDAC7_HUMAN Histone deacetylase 7 OS=Homo sapiens OX=9606 GN=HDAC7 PE=1 SV=2	HDAC7	96	43	51.890%	102925.99	7.24
Q00839	sp|Q00839|HNRPU_HUMAN Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens OX=9606 GN=HNRNPU PE=1 SV=6	HNRNPU	60	40	50.300%	90583.42	5.76
A0A7I2V428	tr|A0A7I2V428|A0A7I2V428_HUMAN Nucleolin OS=Homo sapiens OX=9606 GN=NCL PE=1 SV=1	NCL	46	37	43.540%	74739.48	4.55

P07900	sp|P07900|HS90A_HUMAN Heat shock protein HSP 90-alpha OS=Homo sapiens OX=9606 GN=HSP90AA1 PE=1 SV=5	HSP90AA1	45	34	46.170%	84658.73	4.94
P08238	sp|P08238|HS90B_HUMAN Heat shock protein HSP 90-beta OS=Homo sapiens OX=9606 GN=HSP90AB1 PE=1 SV=4	HSP90AB1	40	34	47.790%	83263.22	4.97
Q92499	sp|Q92499|DDX1_HUMAN ATP-dependent RNA helicase DDX1 OS=Homo sapiens OX=9606 GN=DDX1 PE=1 SV=2	DDX1	42	32	47.030%	82431.21	6.8
P49327	sp|P49327|FAS_HUMAN Fatty acid synthase OS=Homo sapiens OX=9606 GN=FASN PE=1 SV=3	FASN	32	31	15.530%	273423.4	6.01
P11142	sp|P11142|HSP7C_HUMAN Heat shock cognate 71 kDa protein OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1	HSPA8	40	29	45.670%	70897.24	5.37
Q9Y2W1	sp|Q9Y2W1|TR150_HUMAN Thyroid hormone receptor-associated protein 3 OS=Homo sapiens OX=9606 GN=THRAP3 PE=1 SV=2	THRAP3	35	28	25.970%	108664.45	10.16
O75643	sp|O75643|U520_HUMAN U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens OX=9606 GN=SNRNP200 PE=1 SV=2	SNRNP200	29	28	14.470%	244504.79	5.73
A0A024R5M9	tr|A0A024R5M9|A0A024R5M9_HUMAN Nuclear mitotic apparatus protein 1, isoform CRA_a OS=Homo sapiens OX=9606 GN=NUMA1 PE=4 SV=1	NUMA1	29	28	15.900%	236512.79	5.64
P23246	sp|P23246|SFPQ_HUMAN Splicing factor, proline- and glutamine-rich OS=Homo sapiens OX=9606 GN=SFPQ PE=1 SV=2	SFPQ	36	25	32.250%	76148.51	9.45
P08670	sp|P08670|VIME_HUMAN Vimentin OS=Homo sapiens OX=9606 GN=VIM PE=1 SV=4	VIM	29	25	47.000%	53651.05	5.06
A0A7I2V5Y7	tr|A0A7I2V5Y7|A0A7I2V5Y7_HUMAN Non-POU domain-containing octamer-binding protein OS=Homo sapiens OX=9606 GN=NONO PE=1 SV=1	NONO	34	24	42.020%	54825.68	8.85
A8K5I0	tr|A8K5I0|A8K5I0_HUMAN Epididymis secretory protein Li 103 OS=Homo sapiens OX=9606 GN=HEL-S-103 PE=2 SV=1	HEL-S-103	33	24	43.680%	70051.38	5.48
Q6P2Q9	sp|Q6P2Q9|PRP8_HUMAN Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens OX=9606 GN=PRPF8 PE=1 SV=2	PRPF8	25	24	9.720%	273597.13	8.95

P39023	sp|P39023|RL3_HUMAN 60S ribosomal protein L3 OS=Homo sapiens OX=9606 GN=RPL3 PE=1 SV=2	RPL3	29	22	50.120%	46108.35	10.19
O76021	sp|O76021|RL1D1_HUMAN Ribosomal L1 domain-containing protein 1 OS=Homo sapiens OX=9606 GN=RSL1D1 PE=1 SV=3	RSL1D1	24	22	41.020%	54971.83	10.13
Q9BQG0	sp|Q9BQG0|MBB1A_HUMAN Myb-binding protein 1A OS=Homo sapiens OX=9606 GN=MYBBP1A PE=1 SV=2	MYBBP1A	24	21	16.340%	148852.77	9.34
A0A024R1N4	tr|A0A024R1N4|A0A024R1N4_HUMAN ATP-dependent DNA helicase 2 subunit 1 OS=Homo sapiens OX=9606 GN=XRCC6 PE=3 SV=1	XRCC6	24	21	30.050%	69842.23	6.23
H7BXY3	tr|H7BXY3|H7BXY3_HUMAN RNA helicase OS=Homo sapiens OX=9606 GN=DHX30 PE=1 SV=1	DHX30	23	21	19.380%	130548.66	8.8
Q53SY7	tr|Q53SY7|Q53SY7_HUMAN Aspartate carbamoyltransferase (Fragment) OS=Homo sapiens OX=9606 GN=CAD PE=3 SV=1	CAD	22	21	10.930%	235175.06	6.15
P53621	sp|P53621|COPA_HUMAN Coatomer subunit alpha OS=Homo sapiens OX=9606 GN=COPA PE=1 SV=2	COPA	21	21	18.060%	138344.15	7.7
Q00610	sp|Q00610|CLH1_HUMAN Clathrin heavy chain 1 OS=Homo sapiens OX=9606 GN=CLTC PE=1 SV=5	CLTC	21	21	14.510%	191612.41	5.48
F4ZW66	tr|F4ZW66|F4ZW66_HUMAN NF110b OS=Homo sapiens OX=9606 PE=2 SV=1		24	20	23.160%	95776.73	8.9
J3KTA4	tr|J3KTA4|J3KTA4_HUMAN DEAD box protein 5 OS=Homo sapiens OX=9606 GN=DDX5 PE=1 SV=1	DDX5	23	20	32.410%	69086.33	9.01
H0YAR2	tr|H0YAR2|H0YAR2_HUMAN Polyadenylate-binding protein OS=Homo sapiens OX=9606 GN=PABPC1 PE=1 SV=2	PABPC1	22	20	33.720%	66649.4	9.31
Q7Z406	sp|Q7Z406|MYH14_HUMAN Myosin-14 OS=Homo sapiens OX=9606 GN=MYH14 PE=1 SV=2	MYH14	21	20	10.230%	227867.88	5.52
Q9H583	sp|Q9H583|HEAT1_HUMAN HEAT repeat-containing protein 1 OS=Homo sapiens OX=9606 GN=HEATR1 PE=1 SV=3	HEATR1	20	20	10.400%	242367.36	6.11

P36578	sp|P36578|RL4_HUMAN 60S ribosomal protein L4 OS=Homo sapiens OX=9606 GN=RPL4 PE=1 SV=5	RPL4	25	19	45.200%	47696.77	11.07
P13010	sp|P13010|XRCC5_HUMAN X-ray repair cross-complementing protein 5 OS=Homo sapiens OX=9606 GN=XRCC5 PE=1 SV=3	XRCC5	22	19	24.180%	82703.57	5.55
P68363	sp|P68363|TBA1B_HUMAN Tubulin alpha-1B chain OS=Homo sapiens OX=9606 GN=TUBA1B PE=1 SV=1	TUBA1B	24	18	44.790%	50151.07	4.94
A0A2R8Y5G6	tr|A0A2R8Y5G6|A0A2R8Y5G6_HUMAN RNA helicase OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=1	DDX3X	24	18	32.960%	69047.05	7.21
Q9H0A0	sp|Q9H0A0|NAT10_HUMAN RNA cytidine acetyltransferase OS=Homo sapiens OX=9606 GN=NAT10 PE=1 SV=2	NAT10	21	18	19.510%	115728.51	8.5
P14625	sp|P14625|ENPL_HUMAN Endoplasmin OS=Homo sapiens OX=9606 GN=HSP90B1 PE=1 SV=1	HSP90B1	19	18	20.800%	92467.76	4.76
P20700	sp|P20700|LMNB1_HUMAN Lamin-B1 OS=Homo sapiens OX=9606 GN=LMNB1 PE=1 SV=2	LMNB1	19	18	26.280%	66407.58	5.11
O43390	sp|O43390|HNRPR_HUMAN Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens OX=9606 GN=HNRNPR PE=1 SV=1	HNRNPR	18	18	28.590%	70942.21	8.23
A0A804HL40	tr|A0A804HL40|A0A804HL40_HUMAN Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens OX=9606 GN=LRPPRC PE=4 SV=1	LRPPRC	18	18	13.570%	157774.1	5.85
A0A024RBK3	tr|A0A024RBK3|A0A024RBK3_HUMAN 60S ribosomal protein L6 OS=Homo sapiens OX=9606 GN=RPL6 PE=3 SV=1	RPL6	25	17	46.530%	32727.51	10.59
A0A7I2V3P1	tr|A0A7I2V3P1|A0A7I2V3P1_HUMAN Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens OX=9606 GN=HNRNPA2B1 PE=1 SV=1	HNRNPA2B1	23	17	46.930%	33270.83	8.41
B7Z475	tr|B7Z475|B7Z475_HUMAN cDNA FLJ55712, highly similar to F-box-like/WD repeat protein TBL1XR1 OS=Homo sapiens OX=9606 PE=2 SV=1		21	17	49.730%	40755.92	6.34
P21333	sp|P21333|FLNA_HUMAN Filamin-A OS=Homo sapiens OX=9606 GN=FLNA PE=1 SV=4	FLNA	18	17	7.250%	280735.67	5.7

Q5SU16	tr|Q5SU16|Q5SU16_HUMAN Tubulin beta chain OS=Homo sapiens OX=9606 GN=TUBB PE=1 SV=1	TUBB	27	16	40.990%	49670.28	4.78
Q1KLZ0	tr|Q1KLZ0|Q1KLZ0_HUMAN HCG15971, isoform CRA_a OS=Homo sapiens OX=9606 GN=PS1TP5BP1 PE=1 SV=1	PS1TP5BP1	19	16	44.530%	41736.29	5.29
Q1KMD3	sp|Q1KMD3|HNRL2_HUMAN Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens OX=9606 GN=HNRNPUL2 PE=1 SV=1	HNRNPUL2	17	16	21.150%	85103.67	4.85
Q92841	sp|Q92841|DDX17_HUMAN Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens OX=9606 GN=DDX17 PE=1 SV=2	DDX17	17	16	23.730%	80271.54	8.53
O60264	sp|O60264|SMCA5_HUMAN SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens OX=9606 GN=SMARCA5 PE=1 SV=1	SMARCA5	16	16	15.300%	121903.95	8.27
E9PGM1	tr|E9PGM1|E9PGM1_HUMAN Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens OX=9606 GN=EIF4G1 PE=1 SV=1	EIF4G1	16	16	11.900%	166745.25	5.15
Q8IWP6	tr|Q8IWP6|Q8IWP6_HUMAN Tubulin beta chain OS=Homo sapiens OX=9606 PE=2 SV=1		25	15	36.400%	49752.41	4.82
P09651	sp|P09651|ROA1_HUMAN Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens OX=9606 GN=HNRNPA1 PE=1 SV=5	HNRNPA1	22	15	38.980%	38746.19	9.17
P14618	sp|P14618|KPYM_HUMAN Pyruvate kinase PKM OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=4	PKM	19	15	36.350%	57936.25	7.96
B4E356	tr|B4E356|B4E356_HUMAN ATP-dependent DNA helicase 2 subunit 1 OS=Homo sapiens OX=9606 PE=2 SV=1		17	15	29.620%	54451.46	8.95
O75376	sp|O75376|NCOR1_HUMAN Nuclear receptor corepressor 1 OS=Homo sapiens OX=9606 GN=NCOR1 PE=1 SV=2	NCOR1	16	15	6.430%	270206.63	6.66
F5H2F4	tr|F5H2F4|F5H2F4_HUMAN C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens OX=9606 GN=MTHFD1 PE=1 SV=2	MTHFD1	16	15	17.530%	104708.74	7.35

Q01804	sp|Q01804|OTUD4_HUMAN OTU domain-containing protein 4 OS=Homo sapiens OX=9606 GN=OTUD4 PE=1 SV=4	OTUD4	15	15	14.720%	124043.03	6.25
A8K8U1	tr|A8K8U1|A8K8U1_HUMAN cDNA FLJ77762, highly similar to Homo sapiens cullin-associated and neddylation-dissociated 1 (CAND1), mRNA OS=Homo sapiens OX=9606 PE=2 SV=1		15	15	14.390%	136316.18	5.55
A0A384MEE3	tr|A0A384MEE3|A0A384MEE3_HUMAN Tubulin beta chain OS=Homo sapiens OX=9606 PE=2 SV=1		23	14	35.060%	49952.54	4.78
A0A024RDE5	tr|A0A024RDE5|A0A024RDE5_HUMAN Ras-GTPase activating protein SH3 domain-binding protein 2, isoform CRA_a OS=Homo sapiens OX=9606 GN=G3BP2 PE=4 SV=1	G3BP2	19	14	28.420%	54120.49	5.41
B7Z597	tr|B7Z597|B7Z597_HUMAN 60 kDa chaperonin OS=Homo sapiens OX=9606 PE=2 SV=1		16	14	26.950%	60046.79	5.59
B9EG90	tr|B9EG90|B9EG90_HUMAN DNA topoisomerase I OS=Homo sapiens OX=9606 GN=TOP1 PE=2 SV=1	TOP1	16	14	17.390%	90698.62	9.34
P04843	sp|P04843|RPN1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens OX=9606 GN=RPN1 PE=1 SV=1	RPN1	15	14	22.240%	68568.55	5.96
P11388	sp|P11388|TOP2A_HUMAN DNA topoisomerase 2-alpha OS=Homo sapiens OX=9606 GN=TOP2A PE=1 SV=3	TOP2A	15	14	10.120%	174383.05	8.82
D2CFK9	tr|D2CFK9|D2CFK9_HUMAN Nucleolar GTP-binding protein 1 OS=Homo sapiens OX=9606 GN=GTPBP4 PE=3 SV=1	GTPBP4	15	14	21.920%	73963.66	9.52
O60841	sp|O60841|IF2P_HUMAN Eukaryotic translation initiation factor 5B OS=Homo sapiens OX=9606 GN=EIF5B PE=1 SV=4	EIF5B	14	14	15.160%	138825.19	5.39
Q14690	sp|Q14690|RRP5_HUMAN Protein RRP5 homolog OS=Homo sapiens OX=9606 GN=PDCD11 PE=1 SV=3	PDCD11	14	14	8.390%	208698.27	8.99
A0A7I2V659	tr|A0A7I2V659|A0A7I2V659_HUMAN Elongation factor 1-alpha OS=Homo sapiens OX=9606 GN=EEF1A1 PE=1 SV=1	EEF1A1	18	13	32.900%	49823.86	9.05
A8K6V7	tr|A8K6V7|A8K6V7_HUMAN cDNA FLJ76053, highly similar to Homo sapiens Ras-GTPase activating protein SH3 domain-binding protein 2 (G3BP2), transcript variant 3, mRNA OS=Homo		18	13	31.180%	50815.83	5.27

	sapiens OX=9606 PE=2 SV=1						
P26599	sp|P26599|PTBP1_HUMAN Polypyrimidine tract-binding protein 1 OS=Homo sapiens OX=9606 GN=PTBP1 PE=1 SV=1	PTBP1	17	13	29.000%	57220.64	9.22
Q9NYF8	sp|Q9NYF8|BCLF1_HUMAN Bcl-2-associated transcription factor 1 OS=Homo sapiens OX=9606 GN=BCLAF1 PE=1 SV=2	BCLAF1	16	13	13.480%	106120.82	9.99
Q05CW7	tr|Q05CW7|Q05CW7_HUMAN NAT10 protein (Fragment) OS=Homo sapiens OX=9606 GN=NAT10 PE=2 SV=1	NAT10	16	13	29.060%	62383.72	9.35
O00567	sp|O00567|NOP56_HUMAN Nucleolar protein 56 OS=Homo sapiens OX=9606 GN=NOP56 PE=1 SV=4	NOP56	15	13	22.050%	66049.12	9.24
B4DUQ1	tr|B4DUQ1|B4DUQ1_HUMAN Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens OX=9606 PE=2 SV=1		15	13	36.220%	48509.93	5.69
P22314	sp|P22314|UBA1_HUMAN Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens OX=9606 GN=UBA1 PE=1 SV=3	UBA1	14	13	13.520%	117847.64	5.49
A0A024R4F1	tr|A0A024R4F1|A0A024R4F1_HUMAN 2-phospho-D-glycerate hydro-lyase OS=Homo sapiens OX=9606 GN=HEL-S-17 PE=2 SV=1	HEL-S-17	14	13	33.410%	47168.41	7.01
A0A1U9X7W7	tr|A0A1U9X7W7|A0A1U9X7W7_HUMAN Epididymis secretory sperm binding protein OS=Homo sapiens OX=9606 PE=2 SV=1		19	12	18.560%	70374.21	5.76
A8MXP9	tr|A8MXP9|A8MXP9_HUMAN Matrin-3 OS=Homo sapiens OX=9606 GN=MATR3 PE=1 SV=1	MATR3	16	12	19.110%	99966.01	5.71
V9HW26	tr|V9HW26|V9HW26_HUMAN ATP synthase subunit alpha OS=Homo sapiens OX=9606 GN=HEL-S-123m PE=1 SV=1	HEL-S-123m	16	12	27.310%	59749.91	9.16
O43143	sp|O43143|DHX15_HUMAN Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens OX=9606 GN=DHX15 PE=1 SV=2	DHX15	14	12	15.720%	90931.82	7.12
D3DTW3	tr|D3DTW3|D3DTW3_HUMAN Insulin-like growth factor 2 mRNA binding protein 1 deltaN CRDBP OS=Homo sapiens OX=9606 GN=IGF2BP1 PE=2 SV=1	IGF2BP1	14	12	29.480%	47912.39	9.52

Q53YD7	tr|Q53YD7|Q53YD7_HUMAN Elongation factor 1-gamma OS=Homo sapiens OX=9606 GN=EEF1G PE=2 SV=1	EEF1G	14	12	26.770%	50118.19	6.25
X5DR09	tr|X5DR09|X5DR09_HUMAN General transcription factor IIi isoform A (Fragment) OS=Homo sapiens OX=9606 GN=GTF2I PE=2 SV=1	GTF2I	14	12	11.820%	112415.01	6.09
O14654	sp|O14654|IRS4_HUMAN Insulin receptor substrate 4 OS=Homo sapiens OX=9606 GN=IRS4 PE=1 SV=1	IRS4	13	12	9.390%	133766.06	8.72
P34932	sp|P34932|HSP74_HUMAN Heat shock 70 kDa protein 4 OS=Homo sapiens OX=9606 GN=HSPA4 PE=1 SV=4	HSPA4	13	12	17.140%	94329.87	5.11
M0QYS1	tr|M0QYS1|M0QYS1_HUMAN 60S ribosomal protein L13a (Fragment) OS=Homo sapiens OX=9606 GN=RPL13A PE=1 SV=2	RPL13A	13	12	37.140%	24104.41	10.85
P17987	sp|P17987|TCPA_HUMAN T-complex protein 1 subunit alpha OS=Homo sapiens OX=9606 GN=TCP1 PE=1 SV=1	TCP1	12	12	23.560%	60342.9	5.8
A0A024R4Z6	tr|A0A024R4Z6|A0A024R4Z6_HUMAN FACT complex subunit SSRP1 OS=Homo sapiens OX=9606 GN=SSRP1 PE=3 SV=1	SSRP1	12	12	16.930%	81073.88	6.45
A8K329	tr|A8K329|A8K329_HUMAN cDNA FLJ76656, highly similar to Homo sapiens scaffold attachment factor B (SAFB), mRNA OS=Homo sapiens OX=9606 PE=2 SV=1		12	12	14.520%	102752.57	5.3
V9HW84	tr|V9HW84|V9HW84_HUMAN 75 kDa glucose-regulated protein OS=Homo sapiens OX=9606 GN=HEL-S-124m PE=2 SV=1	HEL-S-124m	12	12	20.320%	73778.79	5.97
B3KSM6	tr|B3KSM6|B3KSM6_HUMAN cDNA FLJ36606 fis, clone TRACH2015654, highly similar to HEAT SHOCK 70 kDa PROTEIN 6 OS=Homo sapiens OX=9606 PE=2 SV=1		17	11	15.710%	70971.2	5.81
E9PCY7	tr|E9PCY7|E9PCY7_HUMAN Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens OX=9606 GN=HNRNPH1 PE=1 SV=1	HNRNPH1	15	11	30.770%	47086.62	5.93
P62258	sp|P62258|1433E_HUMAN 14-3-3 protein epsilon OS=Homo sapiens OX=9606 GN=YWHAE PE=1 SV=1	YWHAE	14	11	35.290%	29173.58	4.63
P68133	sp|P68133|ACTS_HUMAN Actin, alpha skeletal muscle OS=Homo sapiens OX=9606 GN=ACTA1 PE=1 SV=1	ACTA1	14	11	25.990%	42050.59	5.23

Q9BZZ5	sp|Q9BZZ5|API5_HUMAN Apoptosis inhibitor 5 OS=Homo sapiens OX=9606 GN=API5 PE=1 SV=3	API5	14	11	22.140%	59003.87	6.99
A8K088	tr|A8K088|A8K088_HUMAN RNA helicase OS=Homo sapiens OX=9606 PE=2 SV=1		13	11	26.850%	46125.37	5.32
Q5U077	tr|Q5U077|Q5U077_HUMAN L-lactate dehydrogenase OS=Homo sapiens OX=9606 GN=LDHB PE=2 SV=1	LDHB	13	11	31.140%	36638.07	5.71
P00338	sp|P00338|LDHA_HUMAN L-lactate dehydrogenase A chain OS=Homo sapiens OX=9606 GN=LDHA PE=1 SV=2	LDHA	12	11	34.640%	36688.3	8.44
P10412	sp|P10412|H14_HUMAN Histone H1.4 OS=Homo sapiens OX=9606 GN=H1-4 PE=1 SV=2	H1-4	12	11	34.250%	21864.98	11.03
P16403	sp|P16403|H12_HUMAN Histone H1.2 OS=Homo sapiens OX=9606 GN=H1-2 PE=1 SV=2	H1-2	12	11	37.090%	21364.47	10.94
P63104	sp|P63104|1433Z_HUMAN 14-3-3 protein zeta/delta OS=Homo sapiens OX=9606 GN=YWHAZ PE=1 SV=1	YWHAZ	12	11	46.940%	27744.79	4.73
Q92598	sp|Q92598|HS105_HUMAN Heat shock protein 105 kDa OS=Homo sapiens OX=9606 GN=HSPH1 PE=1 SV=1	HSPH1	12	11	15.270%	96863.87	5.28
H3BUF6	tr|H3BUF6|H3BUF6_HUMAN Ataxin-2-like protein OS=Homo sapiens OX=9606 GN=ATXN2L PE=1 SV=1	ATXN2L	12	11	9.270%	112712.57	8.79
P41252	sp|P41252|SYIC_HUMAN Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=IARS1 PE=1 SV=2	IARS1	11	11	8.240%	144496.4	5.82
A0A6Q8PFY2	tr|A0A6Q8PFY2|A0A6Q8PFY2_HUMAN Alanine--tRNA ligase OS=Homo sapiens OX=9606 GN=AARS1 PE=1 SV=1	AARS1	11	11	12.380%	107929.55	5.34
I6TRR8	tr|I6TRR8|I6TRR8_HUMAN SND1-BRAF fusion OS=Homo sapiens OX=9606 PE=2 SV=1		11	11	10.010%	109145.65	9.36
Q4ZG57	tr|Q4ZG57|Q4ZG57_HUMAN DNA replication licensing factor MCM6 (Fragment) OS=Homo sapiens OX=9606 GN=MCM6 PE=3 SV=1	MCM6	11	11	14.780%	88944.82	5.44

Q53HV2	tr|Q53HV2|Q53HV2_HUMAN T-complex protein 1 subunit eta (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		11	11	20.440%	59339.88	7.55
Q6IQ30	tr|Q6IQ30|Q6IQ30_HUMAN Polyadenylate-binding protein OS=Homo sapiens OX=9606 GN=PABPC4 PE=2 SV=1	PABPC4	11	11	19.390%	72359.8	9.38
Q96BS4	tr|Q96BS4|Q96BS4_HUMAN FBL protein (Fragment) OS=Homo sapiens OX=9606 GN=FBL PE=2 SV=2	FBL	12	10	44.620%	28449.14	9.45
V9HW80	tr|V9HW80|V9HW80_HUMAN 15S Mg(2+)-ATPase p97 subunit OS=Homo sapiens OX=9606 GN=HEL-S-70 PE=1 SV=1	HEL-S-70	12	10	16.500%	89320.79	5.14
P16402	sp|P16402|H13_HUMAN Histone H1.3 OS=Homo sapiens OX=9606 GN=H1-3 PE=1 SV=2	H1-3	11	10	31.670%	22349.61	11.02
A0A024RCM3	tr|A0A024RCM3|A0A024RCM3_HUMAN RNA helicase OS=Homo sapiens OX=9606 GN=hCG_2005638 PE=4 SV=1	hCG_20056	11	10	21.260%	48990.79	5.44
Q6FI03	tr|Q6FI03|Q6FI03_HUMAN G3BP protein OS=Homo sapiens OX=9606 GN=G3BP PE=2 SV=1	G3BP	11	10	24.250%	52163.66	5.42
P13797	sp|P13797|PLST_HUMAN Plastin-3 OS=Homo sapiens OX=9606 GN=PLS3 PE=1 SV=4	PLS3	10	10	19.840%	70810.21	5.41
P46013	sp|P46013|KI67_HUMAN Proliferation marker protein Ki-67 OS=Homo sapiens OX=9606 GN=MKI67 PE=1 SV=2	MKI67	10	10	3.560%	358689.46	9.49
Q04917	sp|Q04917|1433F_HUMAN 14-3-3 protein eta OS=Homo sapiens OX=9606 GN=YWHAH PE=1 SV=4	YWHAH	10	10	36.590%	28218.4	4.76
Q12788	sp|Q12788|TBL3_HUMAN Transducin beta-like protein 3 OS=Homo sapiens OX=9606 GN=TBL3 PE=1 SV=2	TBL3	10	10	14.600%	89033.66	6.44
Q13263	sp|Q13263|TIF1B_HUMAN Transcription intermediary factor 1-beta OS=Homo sapiens OX=9606 GN=TRIM28 PE=1 SV=5	TRIM28	10	10	12.340%	88548.76	5.52
Q15029	sp|Q15029|U5S1_HUMAN 116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens OX=9606 GN=EFTUD2 PE=1 SV=1	EFTUD2	10	10	10.910%	109434.5	4.84

A0A0S2Z3G9	tr|A0A0S2Z3G9|A0A0S2Z3G9_HUMAN Actinin alpha 4 isoform 1 (Fragment) OS=Homo sapiens OX=9606 GN=ACTN4 PE=2 SV=1	ACTN4	10	10	13.940%	104852.81	5.27
A0A384N6C7	tr|A0A384N6C7|A0A384N6C7_HUMAN Epididymis secretory sperm binding protein OS=Homo sapiens OX=9606 PE=2 SV=1		10	10	15.620%	64085.97	8.49
A0A3B3IRQ9	tr|A0A3B3IRQ9|A0A3B3IRQ9_HUMAN Double-stranded RNA-specific adenosine deaminase (Fragment) OS=Homo sapiens OX=9606 GN=ADAR PE=1 SV=1	ADAR	10	10	10.100%	128269.05	8.84
A8K3W4	tr|A8K3W4|A8K3W4_HUMAN cDNA FLJ75163, highly similar to Homo sapiens heterogeneous nuclear ribonucleoprotein U-like 1 (HNRPUL1), transcript variant 4, mRNA OS=Homo sapiens OX=9606 PE=2 SV=1		10	10	16.010%	84820.78	8.99
B3KMR5	tr|B3KMR5|B3KMR5_HUMAN cDNA FLJ12434 fis, clone NT2RM1000037, highly similar to Homo sapiens KIAA0690 protein OS=Homo sapiens OX=9606 PE=2 SV=1		10	10	8.940%	143670.44	8.97
B9A067	tr|B9A067|B9A067_HUMAN MICOS complex subunit MIC60 OS=Homo sapiens OX=9606 GN=IMMT PE=1 SV=2	IMMT	10	10	15.050%	78972.79	6.62
H0YEN5	tr|H0YEN5|H0YEN5_HUMAN 40S ribosomal protein S2 (Fragment) OS=Homo sapiens OX=9606 GN=RPS2 PE=1 SV=1	RPS2	10	10	53.850%	21153.69	9.86
B0QYK0	tr|B0QYK0|B0QYK0_HUMAN RNA-binding protein EWS OS=Homo sapiens OX=9606 GN=EWSR1 PE=1 SV=1	EWSR1	16	9	16.990%	64928.66	9.42
B2R4R0	tr|B2R4R0|B2R4R0_HUMAN Histone H4 OS=Homo sapiens OX=9606 GN=HIST1H4J PE=2 SV=1	HIST1H4J	14	9	62.140%	11367.2	11.36
P62987	sp|P62987|RL40_HUMAN Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens OX=9606 GN=UBA52 PE=1 SV=2	UBA52	13	9	54.690%	14728.16	9.87
P11021	sp|P11021|BIP_HUMAN Endoplasmic reticulum chaperone BiP OS=Homo sapiens OX=9606 GN=HSPA5 PE=1 SV=2	HSPA5	12	9	13.910%	72332.07	5.07
O60907	sp|O60907|TBL1X_HUMAN F-box-like/WD repeat-containing protein TBL1X OS=Homo sapiens OX=9606 GN=TBL1X PE=1 SV=3	TBL1X	11	9	22.880%	62494.98	6.08

P05141	sp|P05141|ADT2_HUMAN ADP/ATP translocase 2 OS=Homo sapiens OX=9606 GN=SLC25A5 PE=1 SV=7	SLC25A5	11	9	29.870%	32851.84	9.71
O00148	sp|O00148|DX39A_HUMAN ATP-dependent RNA helicase DDX39A OS=Homo sapiens OX=9606 GN=DDX39A PE=1 SV=2	DDX39A	10	9	19.910%	49128.98	5.46
P40227	sp|P40227|TCPZ_HUMAN T-complex protein 1 subunit zeta OS=Homo sapiens OX=9606 GN=CCT6A PE=1 SV=3	CCT6A	10	9	18.640%	58023.51	6.24
Q9NVI7	sp|Q9NVI7|ATD3A_HUMAN ATPase family AAA domain-containing protein 3A OS=Homo sapiens OX=9606 GN=ATAD3A PE=1 SV=2	ATAD3A	10	9	15.140%	71368.33	9.08
A1A5C4	tr|A1A5C4|A1A5C4_HUMAN RRBP1 protein OS=Homo sapiens OX=9606 GN=RRBP1 PE=2 SV=1	RRBP1	10	9	10.600%	102823.45	5.32
E9PFK5	tr|E9PFK5|E9PFK5_HUMAN Nucleolar protein 14 OS=Homo sapiens OX=9606 GN=NOP14 PE=1 SV=1	NOP14	10	9	9.770%	88865	5.85
Q6NXR8	tr|Q6NXR8|Q6NXR8_HUMAN 40S ribosomal protein S3a OS=Homo sapiens OX=9606 GN=RPS3A PE=1 SV=1	RPS3A	10	9	33.330%	29974.62	9.75
P27694	sp|P27694|RFA1_HUMAN Replication protein A 70 kDa DNA-binding subunit OS=Homo sapiens OX=9606 GN=RPA1 PE=1 SV=2	RPA1	9	9	13.960%	68137.42	6.92
Q06787	sp|Q06787|FMR1_HUMAN Synaptic functional regulator FMR1 OS=Homo sapiens OX=9606 GN=FMR1 PE=1 SV=1	FMR1	9	9	15.350%	71173.63	7
Q14692	sp|Q14692|BMS1_HUMAN Ribosome biogenesis protein BMS1 homolog OS=Homo sapiens OX=9606 GN=BMS1 PE=1 SV=1	BMS1	9	9	7.330%	145805.51	6.04
A0A0S2Z4T1	tr|A0A0S2Z4T1|A0A0S2Z4T1_HUMAN DNA replication licensing factor MCM3 (Fragment) OS=Homo sapiens OX=9606 GN=MCM3 PE=2 SV=1	MCM3	9	9	11.880%	90979.76	5.53
A0A384NKW7	tr|A0A384NKW7|A0A384NKW7_HUMAN Chromosome segregation 1-like protein OS=Homo sapiens OX=9606 PE=2 SV=1		9	9	9.990%	110415.28	5.51
A0A6Q8PGG9	tr|A0A6Q8PGG9|A0A6Q8PGG9_HUMAN E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens OX=9606 GN=TRIP12 PE=1 SV=1	TRIP12	9	9	6.000%	228581.02	8.85

A8K6V3	tr|A8K6V3|A8K6V3_HUMAN cDNA FLJ78677, highly similar to Homo sapiens splicing factor 3b, subunit 3, 130kDa (SF3B3), mRNA OS=Homo sapiens OX=9606 PE=2 SV=1		9	9	7.230%	135576.72	5.09
B3KNB4	tr|B3KNB4|B3KNB4_HUMAN cDNA FLJ14168 fis, clone NT2RP2001440, highly similar to 14-3-3 protein gamma OS=Homo sapiens OX=9606 PE=2 SV=1		9	9	31.170%	28242.24	4.8
B3KXX5	tr|B3KXX5|B3KXX5_HUMAN Structural maintenance of chromosomes protein OS=Homo sapiens OX=9606 PE=2 SV=1		9	9	6.810%	144454.3	6.62
B7ZAR1	tr|B7ZAR1|B7ZAR1_HUMAN CCT-epsilon OS=Homo sapiens OX=9606 GN=CCT5 PE=1 SV=1	CCT5	9	9	18.090%	55348.35	5.33
H3BLX5	tr|H3BLX5|H3BLX5_HUMAN Ubiquitin carboxyl-terminal hydrolase 48 (Fragment) OS=Homo sapiens OX=9606 GN=USP48 PE=1 SV=1	USP48	16	8	77.390%	13251.99	6.57
A0A2U3TZH3	tr|A0A2U3TZH3|A0A2U3TZH3_HUMAN Elongation factor 1-alpha OS=Homo sapiens OX=9606 GN=EEF1A2 PE=1 SV=1	EEF1A2	11	8	16.940%	54339.92	9.13
B3KN82	tr|B3KN82|B3KN82_HUMAN cDNA FLJ13913 fis, clone Y79AA1000231, highly similar to Nucleolar protein NOP5 OS=Homo sapiens OX=9606 PE=2 SV=1		11	8	21.890%	52288.04	9.12
Q5JR94	tr|Q5JR94|Q5JR94_HUMAN 40S ribosomal protein S8 OS=Homo sapiens OX=9606 GN=RPS8 PE=2 SV=1	RPS8	10	8	37.980%	24204.9	10.32
Q8NCA5	sp|Q8NCA5|FA98A_HUMAN Protein FAM98A OS=Homo sapiens OX=9606 GN=FAM98A PE=1 SV=2	FAM98A	9	8	14.860%	55271.88	9.1
Q59EG8	tr|Q59EG8|Q59EG8_HUMAN 26S proteasome non-ATPase regulatory subunit 2 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		9	8	10.730%	100587.03	5.04
Q5SWX3	tr|Q5SWX3|Q5SWX3_HUMAN Calcium/calmodulin-dependent protein kinase OS=Homo sapiens OX=9606 GN=CAMK2G PE=1 SV=1	CAMK2G	9	8	16.090%	57796.03	6.87
V9HWD6	tr|V9HWD6|V9HWD6_HUMAN Epididymis secretory protein Li 1 OS=Homo sapiens OX=9606 GN=HEL-S-1 PE=2 SV=1	HEL-S-1	9	8	33.330%	28082.08	4.76
O00541	sp|O00541|PESC_HUMAN Pescadillo homolog OS=Homo sapiens OX=9606 GN=PES1 PE=1 SV=1	PES1	8	8	13.950%	68001.82	6.93

P00558	sp|P00558|PGK1_HUMAN Phosphoglycerate kinase 1 OS=Homo sapiens OX=9606 GN=PGK1 PE=1 SV=3	PGK1	8	8	25.900%	44614.2	8.3
P05023	sp|P05023|AT1A1_HUMAN Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens OX=9606 GN=ATP1A1 PE=1 SV=1	ATP1A1	8	8	6.550%	112894.82	5.33
P19525	sp|P19525|E2AK2_HUMAN Interferon-induced, double-stranded RNA-activated protein kinase OS=Homo sapiens OX=9606 GN=EIF2AK2 PE=1 SV=2	EIF2AK2	8	8	13.430%	62093.53	8.58
P26038	sp|P26038|MOES_HUMAN Moesin OS=Homo sapiens OX=9606 GN=MSN PE=1 SV=3	MSN	8	8	10.570%	67819.26	6.08
Q5T5X7	sp|Q5T5X7|BEND3_HUMAN BEN domain-containing protein 3 OS=Homo sapiens OX=9606 GN=BEND3 PE=1 SV=1	BEND3	8	8	13.040%	94473.51	5.29
Q9Y2L1	sp|Q9Y2L1|RRP44_HUMAN Exosome complex exonuclease RRP44 OS=Homo sapiens OX=9606 GN=DIS3 PE=1 SV=2	DIS3	8	8	9.810%	109001.5	6.69
A0A024R158	tr|A0A024R158|A0A024R158_HUMAN Structural maintenance of chromosomes protein OS=Homo sapiens OX=9606 GN=SMC2L1 PE=3 SV=1	SMC2L1	8	8	7.940%	135654.48	8.54
A0A024R592	tr|A0A024R592|A0A024R592_HUMAN Glucosidase, alpha neutral AB, isoform CRA_b OS=Homo sapiens OX=9606 GN=GANAB PE=3 SV=1	GANAB	8	8	11.100%	96188.28	5.5
A0A0S2Z471	tr|A0A0S2Z471|A0A0S2Z471_HUMAN Creatine kinase (Fragment) OS=Homo sapiens OX=9606 GN=CKB PE=2 SV=1	CKB	8	8	24.200%	44921.28	5.72
A0A1U9X609	tr|A0A1U9X609|A0A1U9X609_HUMAN ABCF1 OS=Homo sapiens OX=9606 PE=4 SV=1		8	8	10.060%	95924.6	6.4
A0A223PQH6	tr|A0A223PQH6|A0A223PQH6_HUMAN HCFC1 OS=Homo sapiens OX=9606 PE=4 SV=1		8	8	4.130%	208756.22	7.32
A0A2R8Y212	tr|A0A2R8Y212|A0A2R8Y212_HUMAN DNA helicase OS=Homo sapiens OX=9606 GN=CHD4 PE=1 SV=1	CHD4	8	8	3.970%	218187.33	5.64
B4DED6	tr|B4DED6|B4DED6_HUMAN RNA helicase OS=Homo sapiens OX=9606 PE=2 SV=1		8	8	15.090%	72157.15	8.73

C9JIJ5	tr|C9JIJ5|C9JIJ5_HUMAN 60S ribosomal protein L7 (Fragment) OS=Homo sapiens OX=9606 GN=RPL7 PE=1 SV=1	RPL7	8	8	45.450%	11892.22	11.38
D3DP78	tr|D3DP78|D3DP78_HUMAN Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=DARS PE=3 SV=1	DARS	8	8	17.740%	53463.55	6.1
Q53FG5	tr|Q53FG5|Q53FG5_HUMAN DNA replication licensing factor MCM5 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		8	8	11.440%	82235.59	8.56
Q53HW2	tr|Q53HW2|Q53HW2_HUMAN 60S acidic ribosomal protein P0 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		8	8	29.020%	34301.12	5.72
V9HWK0	tr|V9HWK0|V9HWK0_HUMAN Signal recognition particle subunit SRP72 OS=Homo sapiens OX=9606 GN=HEL103 PE=2 SV=1	HEL103	8	8	15.650%	74605.31	9.31
F4ZW62	tr|F4ZW62|F4ZW62_HUMAN NF45 OS=Homo sapiens OX=9606 PE=1 SV=1		9	7	18.970%	43061.62	5.19
P33778	sp|P33778|H2B1B_HUMAN Histone H2B type 1-B OS=Homo sapiens OX=9606 GN=H2BC3 PE=1 SV=2	H2BC3	8	7	46.830%	13950.02	10.31
Q07020	sp|Q07020|RL18_HUMAN 60S ribosomal protein L18 OS=Homo sapiens OX=9606 GN=RPL18 PE=1 SV=2	RPL18	8	7	34.570%	21634.23	11.73
A0A024RAC5	tr|A0A024RAC5|A0A024RAC5_HUMAN Epididymis secretory sperm binding protein OS=Homo sapiens OX=9606 GN=RCC2 PE=2 SV=1	RCC2	8	7	15.520%	56083.89	9.02
A0A140VJE8	tr|A0A140VJE8|A0A140VJE8_HUMAN AP complex subunit beta OS=Homo sapiens OX=9606 GN=AP2B1 PE=2 SV=1	AP2B1	8	7	6.730%	105690.58	5.19
H0YEU2	tr|H0YEU2|H0YEU2_HUMAN 40S ribosomal protein S3 (Fragment) OS=Homo sapiens OX=9606 GN=RPS3 PE=1 SV=1	RPS3	8	7	42.690%	18560.5	8.54
J3KPS3	tr|J3KPS3|J3KPS3_HUMAN Fructose-bisphosphate aldolase OS=Homo sapiens OX=9606 GN=ALDOA PE=1 SV=1	ALDOA	8	7	18.750%	39817.02	8.3
Q6PJV4	tr|Q6PJV4|Q6PJV4_HUMAN THRAP3 protein (Fragment) OS=Homo sapiens OX=9606 GN=THRAP3 PE=2 SV=1	THRAP3	8	7	20.000%	41857.06	11.51

O75694	sp|O75694|NU155_HUMAN Nuclear pore complex protein Nup155 OS=Homo sapiens OX=9606 GN=NUP155 PE=1 SV=1	NUP155	7	7	4.820%	155197.41	5.78
Q02880	sp|Q02880|TOP2B_HUMAN DNA topoisomerase 2-beta OS=Homo sapiens OX=9606 GN=TOP2B PE=1 SV=3	TOP2B	7	7	4.000%	183264.98	8.14
Q14008	sp|Q14008|CKAP5_HUMAN Cytoskeleton-associated protein 5 OS=Homo sapiens OX=9606 GN=CKAP5 PE=1 SV=3	CKAP5	7	7	3.590%	225492	7.95
Q5UIP0	sp|Q5UIP0|RIF1_HUMAN Telomere-associated protein RIF1 OS=Homo sapiens OX=9606 GN=RIF1 PE=1 SV=2	RIF1	7	7	3.400%	274462.51	5.39
Q9BVJ6	sp|Q9BVJ6|UT14A_HUMAN U3 small nucleolar RNA-associated protein 14 homolog A OS=Homo sapiens OX=9606 GN=UTP14A PE=1 SV=1	UTP14A	7	7	11.800%	87976.78	7.67
Q9NSD9	sp|Q9NSD9|SYFB_HUMAN Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens OX=9606 GN=FARSB PE=1 SV=3	FARSB	7	7	12.390%	66114.83	6.39
Q9UIG0	sp|Q9UIG0|BAZ1B_HUMAN Tyrosine-protein kinase BAZ1B OS=Homo sapiens OX=9606 GN=BAZ1B PE=1 SV=2	BAZ1B	7	7	5.120%	170900.87	8.7
A0A0A0MTB8	tr|A0A0A0MTB8|A0A0A0MTB8_HUMAN WD repeat-containing protein 36 OS=Homo sapiens OX=9606 GN=WDR36 PE=1 SV=1	WDR36	7	7	7.600%	99365.03	6.96
A0A7P0Z4B9	tr|A0A7P0Z4B9|A0A7P0Z4B9_HUMAN DNA damage-binding protein 1 OS=Homo sapiens OX=9606 GN=DDB1 PE=1 SV=1	DDB1	7	7	6.230%	123277.26	5.1
A4QPB0	tr|A4QPB0|A4QPB0_HUMAN IQ motif containing GTPase activating protein 1 OS=Homo sapiens OX=9606 GN=IQGAP1 PE=1 SV=1	IQGAP1	7	7	4.530%	189277.77	6.08
B3GQE6	tr|B3GQE6|B3GQE6_HUMAN RNA helicase OS=Homo sapiens OX=9606 GN=DDX27 PE=2 SV=1	DDX27	7	7	9.410%	86633.54	9.29
B3KQH1	tr|B3KQH1|B3KQH1_HUMAN cDNA FLJ90452 fis, clone NT2RP3001475, highly similar to Splicing factor 3B subunit 3 OS=Homo sapiens OX=9606 PE=2 SV=1		7	7	7.020%	99920.53	5.02
B4DZC3	tr|B4DZC3|B4DZC3_HUMAN 5'-3' exoribonuclease OS=Homo sapiens OX=9606 PE=2 SV=1		7	7	9.040%	102415.18	7.55

C6EMX8	tr|C6EMX8|C6EMX8_HUMAN DNA replication licensing factor MCM7 OS=Homo sapiens OX=9606 GN=MCM7 PE=2 SV=1	MCM7	7	7	11.270%	81278.95	5.98
E7EQR4	tr|E7EQR4|E7EQR4_HUMAN Ezrin OS=Homo sapiens OX=9606 GN=EZR PE=1 SV=3	EZR	7	7	9.040%	69370.88	5.87
J9R021	tr|J9R021|J9R021_HUMAN Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens OX=9606 GN=eIF3a PE=2 SV=1	eIF3a	7	7	5.570%	166480.35	6.38
P61313	sp|P61313|RL15_HUMAN 60S ribosomal protein L15 OS=Homo sapiens OX=9606 GN=RPL15 PE=1 SV=2	RPL15	8	6	30.390%	24145.77	11.62
F6KPG5	tr|F6KPG5|F6KPG5_HUMAN Albumin (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		8	6	10.940%	66530.6	5.73
O00410	sp|O00410|IPO5_HUMAN Importin-5 OS=Homo sapiens OX=9606 GN=IPO5 PE=1 SV=4	IPO5	7	6	9.210%	123628.63	4.83
O60832	sp|O60832|DKC1_HUMAN H/ACA ribonucleoprotein complex subunit DKC1 OS=Homo sapiens OX=9606 GN=DKC1 PE=1 SV=3	DKC1	7	6	12.260%	57673.43	9.46
P63151	sp|P63151|2ABA_HUMAN Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Homo sapiens OX=9606 GN=PPP2R2A PE=1 SV=1	PPP2R2A	7	6	17.450%	51691.5	5.82
Q10567	sp|Q10567|AP1B1_HUMAN AP-1 complex subunit beta-1 OS=Homo sapiens OX=9606 GN=AP1B1 PE=1 SV=2	AP1B1	7	6	7.380%	104635.47	4.94
Q93079	sp|Q93079|H2B1H_HUMAN Histone H2B type 1-H OS=Homo sapiens OX=9606 GN=H2BC9 PE=1 SV=3	H2BC9	7	6	46.030%	13891.94	10.31
A0A024R7T3	tr|A0A024R7T3|A0A024R7T3_HUMAN Heterogeneous nuclear ribonucleoprotein F, isoform CRA_a OS=Homo sapiens OX=9606 GN=HNRPF PE=4 SV=1	HNRPF	7	6	17.110%	45671.36	5.38
A0A024RBS3	tr|A0A024RBS3|A0A024RBS3_HUMAN Nuclear receptor co-repressor 2, isoform CRA_c OS=Homo sapiens OX=9606 GN=NCOR2 PE=1 SV=1	NCOR2	7	6	1.710%	273884.72	7.21
A0A024RDB5	tr|A0A024RDB5|A0A024RDB5_HUMAN Heterogeneous nuclear ribonucleoprotein D-like, isoform CRA_a OS=Homo sapiens OX=9606 GN=HNRPDL PE=4 SV=1	HNRPDL	7	6	16.670%	46436.97	9.59

A0A384MTQ3	tr|A0A384MTQ3|A0A384MTQ3_HUMAN Adenosylhomocysteinase OS=Homo sapiens OX=9606 PE=2 SV=1		7	6	14.580%	47715.57	5.92
A8KAQ5	tr|A8KAQ5|A8KAQ5_HUMAN U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens OX=9606 PE=2 SV=1		7	6	11.900%	51495.03	10.01
B4DKP9	tr|B4DKP9|B4DKP9_HUMAN cDNA FLJ58012, moderately similar to Eukaryotic initiation factor 4A-I OS=Homo sapiens OX=9606 PE=2 SV=1		7	6	25.500%	23258.87	5.49
B5BU25	tr|B5BU25|B5BU25_HUMAN U2 snRNP auxiliary factor large subunit OS=Homo sapiens OX=9606 GN=U2AF2 PE=2 SV=1	U2AF2	7	6	16.770%	53135.99	9.19
G3V529	tr|G3V529|G3V529_HUMAN RNA helicase OS=Homo sapiens OX=9606 GN=DDX24 PE=1 SV=1	DDX24	7	6	8.700%	91479.97	8.95
Q53HU0	tr|Q53HU0|Q53HU0_HUMAN CCT-theta (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		7	6	12.040%	59649.96	5.42
Q53Z07	tr|Q53Z07|Q53Z07_HUMAN 60S ribosomal protein L9 OS=Homo sapiens OX=9606 GN=RPL9 PE=2 SV=1	RPL9	7	6	29.690%	21863.15	9.96
Q6I9V5	tr|Q6I9V5|Q6I9V5_HUMAN ADP/ATP translocase OS=Homo sapiens OX=9606 GN=SLC25A6 PE=2 SV=1	SLC25A6	7	6	19.130%	32865.87	9.76
O14617	sp|O14617|AP3D1_HUMAN AP-3 complex subunit delta-1 OS=Homo sapiens OX=9606 GN=AP3D1 PE=1 SV=1	AP3D1	6	6	7.030%	130156.52	8.69
O43175	sp|O43175|SERA_HUMAN D-3-phosphoglycerate dehydrogenase OS=Homo sapiens OX=9606 GN=PHGDH PE=1 SV=4	PHGDH	6	6	10.510%	56649.88	6.29
O43290	sp|O43290|SNUT1_HUMAN U4/U6.U5 tri-snRNP-associated protein 1 OS=Homo sapiens OX=9606 GN=SART1 PE=1 SV=1	SART1	6	6	9.630%	90253.73	5.89
O94776	sp|O94776|MTA2_HUMAN Metastasis-associated protein MTA2 OS=Homo sapiens OX=9606 GN=MTA2 PE=1 SV=1	MTA2	6	6	10.480%	75022.25	9.7
O95782	sp|O95782|AP2A1_HUMAN AP-2 complex subunit alpha-1 OS=Homo sapiens OX=9606 GN=AP2A1 PE=1 SV=3	AP2A1	6	6	5.730%	107544.64	6.63

P26639	sp|P26639|SYTC_HUMAN Threonine--tRNA ligase 1, cytoplasmic OS=Homo sapiens OX=9606 GN=TARS1 PE=1 SV=3	TARS1	6	6	7.610%	83434.14	6.23
P35241	sp|P35241|RADI_HUMAN Radixin OS=Homo sapiens OX=9606 GN=RDX PE=1 SV=1	RDX	6	6	6.690%	68563.08	6.03
Q00341	sp|Q00341|VIGLN_HUMAN Vigilin OS=Homo sapiens OX=9606 GN=HDLBP PE=1 SV=2	HDLBP	6	6	6.070%	141453.95	6.43
Q03701	sp|Q03701|CEBPZ_HUMAN CCAAT/enhancer-binding protein zeta OS=Homo sapiens OX=9606 GN=CEBPZ PE=1 SV=3	CEBPZ	6	6	5.500%	120972.52	5.65
Q07666	sp|Q07666|KHDR1_HUMAN KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens OX=9606 GN=KHDRBS1 PE=1 SV=1	KHDRBS1	6	6	9.480%	48226.78	8.73
Q08J23	sp|Q08J23|NSUN2_HUMAN RNA cytosine C(5)-methyltransferase NSUN2 OS=Homo sapiens OX=9606 GN=NSUN2 PE=1 SV=2	NSUN2	6	6	5.740%	86469.73	6.33
Q14151	sp|Q14151|SAFB2_HUMAN Scaffold attachment factor B2 OS=Homo sapiens OX=9606 GN=SAFB2 PE=1 SV=1	SAFB2	6	6	7.240%	107472.21	5.84
Q15020	sp|Q15020|SART3_HUMAN Squamous cell carcinoma antigen recognized by T-cells 3 OS=Homo sapiens OX=9606 GN=SART3 PE=1 SV=1	SART3	6	6	6.130%	109933.26	5.45
Q15459	sp|Q15459|SF3A1_HUMAN Splicing factor 3A subunit 1 OS=Homo sapiens OX=9606 GN=SF3A1 PE=1 SV=1	SF3A1	6	6	6.810%	88885.11	5.15
Q92616	sp|Q92616|GCN1_HUMAN eIF-2-alpha kinase activator GCN1 OS=Homo sapiens OX=9606 GN=GCN1 PE=1 SV=6	GCN1	6	6	3.440%	292754.88	7.29
Q92621	sp|Q92621|NU205_HUMAN Nuclear pore complex protein Nup205 OS=Homo sapiens OX=9606 GN=NUP205 PE=1 SV=3	NUP205	6	6	3.230%	227918.89	5.81
Q92900	sp|Q92900|RENT1_HUMAN Regulator of nonsense transcripts 1 OS=Homo sapiens OX=9606 GN=UPF1 PE=1 SV=2	UPF1	6	6	5.850%	124343.85	6.18
Q9P2B4	sp|Q9P2B4|CT2NL_HUMAN CTTNBP2 N-terminal-like protein OS=Homo sapiens OX=9606 GN=CTTNBP2NL PE=1 SV=2	CTTNBP2NL	6	6	9.550%	70157.18	8.22

Q9Y230	sp|Q9Y230|RUVB2_HUMAN RuvB-like 2 OS=Homo sapiens OX=9606 GN=RUVBL2 PE=1 SV=3	RUVBL2	6	6	13.820%	51155.99	5.49
A0A087WX41	tr|A0A087WX41|A0A087WX41_HUMAN Clathrin heavy chain 2 OS=Homo sapiens OX=9606 GN=CLTCL1 PE=1 SV=1	CLTCL1	6	6	5.710%	142456.25	6.01
A0A140VJY2	tr|A0A140VJY2|A0A140VJY2_HUMAN Testicular tissue protein Li 209 OS=Homo sapiens OX=9606 PE=2 SV=1		6	6	10.090%	80109.04	8.3
A0A669KBC2	tr|A0A669KBC2|A0A669KBC2_HUMAN Cyclin-dependent kinase-like 5 OS=Homo sapiens OX=9606 GN=CDKL5 PE=1 SV=1	CDKL5	6	6	7.290%	112020.29	9.61
A0A6Q8PFA6	tr|A0A6Q8PFA6|A0A6Q8PFA6_HUMAN Kinesin-like protein OS=Homo sapiens OX=9606 GN=KIF2A PE=1 SV=1	KIF2A	6	6	6.700%	78041.54	6.28
A0A6Q8PFM5	tr|A0A6Q8PFM5|A0A6Q8PFM5_HUMAN Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens OX=9606 GN=AIFM1 PE=1 SV=1	AIFM1	6	6	12.420%	66800.67	9.04
A0A7I2V5S2	tr|A0A7I2V5S2|A0A7I2V5S2_HUMAN Nucleophosmin OS=Homo sapiens OX=9606 GN=NPM1 PE=1 SV=1	NPM1	6	6	16.390%	33875.25	4.68
A0A7P0T8C6	tr|A0A7P0T8C6|A0A7P0T8C6_HUMAN Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens OX=9606 GN=ZC3HAV1 PE=1 SV=1	ZC3HAV1	6	6	11.490%	85194.55	8.95
A3F768	tr|A3F768|A3F768_HUMAN NF-kappaB repressing factor OS=Homo sapiens OX=9606 GN=NRF PE=2 SV=1	NRF	6	6	7.540%	77572.87	8.9
A8K3H8	tr|A8K3H8|A8K3H8_HUMAN cDNA FLJ77680, highly similar to Homo sapiens protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform (PPP2R1A), mRNA OS=Homo sapiens OX=9606 PE=2 SV=1		6	6	12.050%	65291.81	5
A8K586	tr|A8K586|A8K586_HUMAN AP-3 complex subunit beta OS=Homo sapiens OX=9606 PE=2 SV=1		6	6	6.030%	121288.68	5.71
B0AZQ4	tr|B0AZQ4|B0AZQ4_HUMAN Structural maintenance of chromosomes protein OS=Homo sapiens OX=9606 PE=2 SV=1		6	6	6.160%	141527.96	6.77

J3KTE4	tr|J3KTE4|J3KTE4_HUMAN Ribosomal protein L19 OS=Homo sapiens OX=9606 GN=RPL19 PE=1 SV=1	RPL19	6	6	24.230%	23247.44	11.48
Q53G55	tr|Q53G55|Q53G55_HUMAN TNF receptor-associated protein 1 variant (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		6	6	8.380%	80037.92	8.05
V5YQL4	tr|V5YQL4|V5YQL4_HUMAN Adenosylhomocysteinase OS=Homo sapiens OX=9606 GN=FGFR2-AHCYL1 PE=2 SV=1	FGFR2-AHC	6	6	4.360%	130895.34	6.34
W8QEH3	tr|W8QEH3|W8QEH3_HUMAN Lamin A/C OS=Homo sapiens OX=9606 GN=LMNA PE=3 SV=1	LMNA	6	6	10.490%	65115.95	6.4
Q68D71	tr|Q68D71|Q68D71_HUMAN Histone deacetylase OS=Homo sapiens OX=9606 GN=DKFZp779K1053 PE=2 SV=1	DKFZp779K	8	5	5.730%	66302.33	9.07
P21796	sp|P21796|VDAC1_HUMAN Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens OX=9606 GN=VDAC1 PE=1 SV=2	VDAC1	6	5	16.610%	30772.21	8.62
P30050	sp|P30050|RL12_HUMAN 60S ribosomal protein L12 OS=Homo sapiens OX=9606 GN=RPL12 PE=1 SV=1	RPL12	6	5	36.970%	17818.38	9.48
P62910	sp|P62910|RL32_HUMAN 60S ribosomal protein L32 OS=Homo sapiens OX=9606 GN=RPL32 PE=1 SV=2	RPL32	6	5	32.590%	15859.62	11.32
Q58FF6	sp|Q58FF6|H90B4_HUMAN Putative heat shock protein HSP 90-beta 4 OS=Homo sapiens OX=9606 GN=HSP90AB4P PE=5 SV=1	HSP90AB4P	6	5	9.900%	58263.73	4.65
A0A024R1T9	tr|A0A024R1T9|A0A024R1T9_HUMAN ATP-citrate synthase OS=Homo sapiens OX=9606 GN=ACLY PE=3 SV=1	ACLY	6	5	4.180%	120837.85	6.95
A0A384NPH0	tr|A0A384NPH0|A0A384NPH0_HUMAN Epididymis secretory sperm binding protein OS=Homo sapiens OX=9606 PE=2 SV=1		6	5	7.830%	67688.02	5.29
B4DR36	tr|B4DR36|B4DR36_HUMAN cDNA FLJ56414, highly similar to Homo sapiens proline-, glutamic acid-, leucine-rich protein 1 (PELP1), mRNA OS=Homo sapiens OX=9606 PE=2 SV=1		6	5	5.680%	124866.11	4.38
B5MDF5	tr|B5MDF5|B5MDF5_HUMAN GTP-binding nuclear protein Ran OS=Homo sapiens OX=9606 GN=RAN PE=1 SV=1	RAN	6	5	24.030%	26223.86	6.5

E9PF82	tr|E9PF82|E9PF82_HUMAN Calcium/calmodulin-dependent protein kinase OS=Homo sapiens OX=9606 GN=CAMK2D PE=1 SV=1	CAMK2D	6	5	9.940%	60003.88	6.84
Q99529	tr|Q99529|Q99529_HUMAN Non-muscle myosin heavy chain (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		6	5	35.100%	24440.28	4.87
Q9BTQ7	tr|Q9BTQ7|Q9BTQ7_HUMAN 60S ribosomal protein L23 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		6	5	41.040%	14149.41	10.26
O00178	sp|O00178|GTPB1_HUMAN GTP-binding protein 1 OS=Homo sapiens OX=9606 GN=GTPBP1 PE=1 SV=3	GTPBP1	5	5	10.010%	72453.03	8.6
P06737	sp|P06737|PYGL_HUMAN Glycogen phosphorylase, liver form OS=Homo sapiens OX=9606 GN=PYGL PE=1 SV=4	PYGL	5	5	5.080%	97147.43	6.71
P07197	sp|P07197|NFM_HUMAN Neurofilament medium polypeptide OS=Homo sapiens OX=9606 GN=NEFM PE=1 SV=3	NEFM	5	5	5.680%	102470.79	4.9
P0CG39	sp|P0CG39|POTEJ_HUMAN POTE ankyrin domain family member J OS=Homo sapiens OX=9606 GN=POTEJ PE=3 SV=1	POTEJ	5	5	4.720%	117388.73	5.66
P27348	sp|P27348|1433T_HUMAN 14-3-3 protein theta OS=Homo sapiens OX=9606 GN=YWHAQ PE=1 SV=1	YWHAQ	5	5	20.820%	27763.94	4.68
P28331	sp|P28331|NDUS1_HUMAN NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Homo sapiens OX=9606 GN=NDUFS1 PE=1 SV=3	NDUFS1	5	5	7.980%	79466.66	5.89
P46777	sp|P46777|RL5_HUMAN 60S ribosomal protein L5 OS=Homo sapiens OX=9606 GN=RPL5 PE=1 SV=3	RPL5	5	5	14.810%	34362.24	9.73
P50991	sp|P50991|TCPD_HUMAN T-complex protein 1 subunit delta OS=Homo sapiens OX=9606 GN=CCT4 PE=1 SV=4	CCT4	5	5	9.280%	57923.6	7.96
P56192	sp|P56192|SYMC_HUMAN Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=MARS1 PE=1 SV=2	MARS1	5	5	6.670%	101114.58	5.82
P62899	sp|P62899|RL31_HUMAN 60S ribosomal protein L31 OS=Homo sapiens OX=9606 GN=RPL31 PE=1 SV=1	RPL31	5	5	35.200%	14462.69	10.54

P78371	sp|P78371|TCPB_HUMAN T-complex protein 1 subunit beta OS=Homo sapiens OX=9606 GN=CCT2 PE=1 SV=4	CCT2	5	5	12.340%	57487.56	6.01
P83881	sp|P83881|RL36A_HUMAN 60S ribosomal protein L36a OS=Homo sapiens OX=9606 GN=RPL36A PE=1 SV=2	RPL36A	5	5	32.080%	12440.69	10.59
Q13435	sp|Q13435|SF3B2_HUMAN Splicing factor 3B subunit 2 OS=Homo sapiens OX=9606 GN=SF3B2 PE=1 SV=2	SF3B2	5	5	4.920%	100226.38	5.52
Q8TDN6	sp|Q8TDN6|BRX1_HUMAN Ribosome biogenesis protein BRX1 homolog OS=Homo sapiens OX=9606 GN=BRIX1 PE=1 SV=2	BRIX1	5	5	12.460%	41400.87	9.92
Q8WXF1	sp|Q8WXF1|PSPC1_HUMAN Paraspeckle component 1 OS=Homo sapiens OX=9606 GN=PSPC1 PE=1 SV=1	PSPC1	5	5	8.410%	58742.95	6.26
Q93009	sp|Q93009|UBP7_HUMAN Ubiquitin carboxyl-terminal hydrolase 7 OS=Homo sapiens OX=9606 GN=USP7 PE=1 SV=2	USP7	5	5	4.360%	128300.67	5.33
Q99613	sp|Q99613|EIF3C_HUMAN Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens OX=9606 GN=EIF3C PE=1 SV=1	EIF3C	5	5	4.710%	105342.62	5.48
Q9UQ80	sp|Q9UQ80|PA2G4_HUMAN Proliferation-associated protein 2G4 OS=Homo sapiens OX=9606 GN=PA2G4 PE=1 SV=3	PA2G4	5	5	12.440%	43786.38	6.13
A0A024QZN9	tr|A0A024QZN9|A0A024QZN9_HUMAN Outer mitochondrial membrane protein porin 2 OS=Homo sapiens OX=9606 GN=VDAC2 PE=3 SV=1	VDAC2	5	5	14.110%	34480.45	8.25
A0A024R2Z6	tr|A0A024R2Z6|A0A024R2Z6_HUMAN Guanine nucleotide-binding protein-like 3 OS=Homo sapiens OX=9606 GN=GNL3 PE=4 SV=1	GNL3	5	5	8.940%	60571.67	8.94
A0A0S2Z2Z6	tr|A0A0S2Z2Z6|A0A0S2Z2Z6_HUMAN Annexin (Fragment) OS=Homo sapiens OX=9606 GN=ANXA6 PE=2 SV=1	ANXA6	5	5	7.880%	75872.41	5.42
A0A494C0M1	tr|A0A494C0M1|A0A494C0M1_HUMAN DNA mismatch repair protein OS=Homo sapiens OX=9606 GN=MSH6 PE=1 SV=1	MSH6	5	5	3.330%	142852.92	6.11
A0A5K1VW56	tr|A0A5K1VW56|A0A5K1VW56_HUMAN ATPase family AAA domain-containing protein 3B OS=Homo sapiens OX=9606 GN=ATAD3B PE=1 SV=1	ATAD3B	5	5	14.770%	32548.81	9.95

A0A6Q8PGW4	tr|A0A6Q8PGW4|A0A6Q8PGW4_HUMAN Diadenosine tetraphosphate synthetase OS=Homo sapiens OX=9606 GN=GARS1 PE=1 SV=1	GARS1	5	5	8.600%	69931.08	5.79
A0A7G6J4N4	tr|A0A7G6J4N4|A0A7G6J4N4_HUMAN Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens OX=9606 PE=2 SV=1		5	5	7.980%	87532.22	5.16
A0A7I2V3W6	tr|A0A7I2V3W6|A0A7I2V3W6_HUMAN Exportin-1 OS=Homo sapiens OX=9606 GN=XPO1 PE=1 SV=1	XPO1	5	5	5.110%	115155.2	5.79
B0ZBD0	tr|B0ZBD0|B0ZBD0_HUMAN 40S ribosomal protein S19 OS=Homo sapiens OX=9606 GN=RPS19 PE=2 SV=1	RPS19	5	5	31.720%	16060.31	10.31
B2R4V2	tr|B2R4V2|B2R4V2_HUMAN cDNA, FLJ92227, highly similar to Homo sapiens ribosomal protein L36a-like (RPL36AL), mRNA OS=Homo sapiens OX=9606 PE=2 SV=1		5	5	32.080%	12526.83	10.67
B2ZZ89	tr|B2ZZ89|B2ZZ89_HUMAN Spectrin beta chain OS=Homo sapiens OX=9606 GN=SPTBN1 PE=2 SV=1	SPTBN1	5	5	2.750%	274606.02	5.39
B4DLG2	tr|B4DLG2|B4DLG2_HUMAN cDNA FLJ58196, highly similar to Zinc finger CCCH domain-containing protein 11A OS=Homo sapiens OX=9606 PE=2 SV=1		5	5	7.010%	82770.96	8.79
G8JLG1	tr|G8JLG1|G8JLG1_HUMAN Structural maintenance of chromosomes protein OS=Homo sapiens OX=9606 GN=SMC1A PE=1 SV=2	SMC1A	5	5	3.720%	140857.48	7.08
H3BRG4	tr|H3BRG4|H3BRG4_HUMAN Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens OX=9606 GN=UQCRC2 PE=1 SV=1	UQCRC2	5	5	13.350%	44634.14	9.08
I6L9H2	tr|I6L9H2|I6L9H2_HUMAN DNA (cytosine-5)-methyltransferase OS=Homo sapiens OX=9606 GN=DNMT1 PE=2 SV=1	DNMT1	5	5	3.900%	171071.49	8.09
J3QRC4	tr|J3QRC4|J3QRC4_HUMAN 60S ribosomal protein L26 (Fragment) OS=Homo sapiens OX=9606 GN=RPL26 PE=3 SV=1	RPL26	5	5	24.440%	15639.78	11.22
Q4G0D9	tr|Q4G0D9|Q4G0D9_HUMAN BOP1 protein (Fragment) OS=Homo sapiens OX=9606 GN=BOP1 PE=2 SV=1	BOP1	5	5	8.640%	64080.1	9.38
Q53EM5	tr|Q53EM5|Q53EM5_HUMAN Transketolase variant (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		5	5	11.720%	67904.91	7.89

Q53GR7	tr|Q53GR7|Q53GR7_HUMAN Solute carrier family 25, member 13 (Citrin) variant (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		5	5	7.410%	74115.51	8.58
Q59HH3	tr|Q59HH3|Q59HH3_HUMAN Trifunctional purine biosynthetic protein adenosine-3 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		5	5	4.490%	112136.98	7.14
Q5TDG3	tr|Q5TDG3|Q5TDG3_HUMAN WD repeat domain 3, isoform CRA_b OS=Homo sapiens OX=9606 GN=WDR3 PE=2 SV=1	WDR3	5	5	5.200%	106097.69	6.2
Q6NZ52	tr|Q6NZ52|Q6NZ52_HUMAN 60S ribosomal protein L27a OS=Homo sapiens OX=9606 GN=RPL27A PE=2 SV=1	RPL27A	5	5	34.460%	16478.09	11
V9HW31	tr|V9HW31|V9HW31_HUMAN ATP synthase subunit beta OS=Homo sapiens OX=9606 GN=HEL-S-271 PE=1 SV=1	HEL-S-271	5	5	8.320%	56559.22	5.26
V9HW88	tr|V9HW88|V9HW88_HUMAN Calreticulin OS=Homo sapiens OX=9606 GN=HEL-S-99n PE=2 SV=1	HEL-S-99n	5	5	11.270%	48140.96	4.29
Q14974	sp|Q14974|IMB1_HUMAN Importin subunit beta-1 OS=Homo sapiens OX=9606 GN=KPNB1 PE=1 SV=2	KPNB1	6	4	6.740%	97169.13	4.68
P46782	sp|P46782|RS5_HUMAN 40S ribosomal protein S5 OS=Homo sapiens OX=9606 GN=RPS5 PE=1 SV=4	RPS5	5	4	24.510%	22876.13	9.73
P62266	sp|P62266|RS23_HUMAN 40S ribosomal protein S23 OS=Homo sapiens OX=9606 GN=RPS23 PE=1 SV=3	RPS23	5	4	27.270%	15807.36	10.5
Q9H2U1	sp|Q9H2U1|DHX36_HUMAN ATP-dependent DNA/RNA helicase DHX36 OS=Homo sapiens OX=9606 GN=DHX36 PE=1 SV=2	DHX36	5	4	5.360%	114758.8	7.58
A4FTV9	tr|A4FTV9|A4FTV9_HUMAN Histone H2A OS=Homo sapiens OX=9606 GN=HIST1H2AK PE=1 SV=1	HIST1H2AK	5	4	32.310%	14091.3	10.9
B4DMK9	tr|B4DMK9|B4DMK9_HUMAN Dihydrolipoyl dehydrogenase OS=Homo sapiens OX=9606 PE=2 SV=1		5	4	9.470%	51787.86	8.04
B4E312	tr|B4E312|B4E312_HUMAN cDNA FLJ53422, highly similar to TATA-binding protein-associated factor 2N OS=Homo sapiens OX=9606 PE=2 SV=1		5	4	10.130%	40077.8	9.5

D6RD18	tr|D6RD18|D6RD18_HUMAN Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens OX=9606 GN=HNRNPAB PE=1 SV=1	HNRNPAB	5	4	16.610%	30473.57	7.69
Q2TU64	tr|Q2TU64|Q2TU64_HUMAN T-complex protein 1 subunit gamma OS=Homo sapiens OX=9606 PE=2 SV=1		5	4	8.260%	60578.26	5.99
U5UA77	tr|U5UA77|U5UA77_HUMAN Dyskeratosis congenita 1 isoform 6 OS=Homo sapiens OX=9606 PE=2 SV=1		5	4	11.180%	35113.04	9.51
A6NHR9	sp|A6NHR9|SMHD1_HUMAN Structural maintenance of chromosomes flexible hinge domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SMCHD1 PE=1 SV=2	SMCHD1	4	4	2.740%	226370.88	6.95
O14646	sp|O14646|CHD1_HUMAN Chromodomain-helicase-DNA-binding protein 1 OS=Homo sapiens OX=9606 GN=CHD1 PE=1 SV=2	CHD1	4	4	1.580%	196685.2	6.68
O15381	sp|O15381|NVL_HUMAN Nuclear valosin-containing protein-like OS=Homo sapiens OX=9606 GN=NVL PE=1 SV=1	NVL	4	4	5.840%	95049.81	6.11
O75367	sp|O75367|H2AY_HUMAN Core histone macro-H2A.1 OS=Homo sapiens OX=9606 GN=MACROH2A1 PE=1 SV=4	MACROH2A	4	4	15.590%	39616.57	9.8
O95757	sp|O95757|HS74L_HUMAN Heat shock 70 kDa protein 4L OS=Homo sapiens OX=9606 GN=HSPA4L PE=1 SV=3	HSPA4L	4	4	4.770%	94511.45	5.63
P05455	sp|P05455|LA_HUMAN Lupus La protein OS=Homo sapiens OX=9606 GN=SSB PE=1 SV=2	SSB	4	4	8.580%	46836.48	6.68
P17812	sp|P17812|PYRG1_HUMAN CTP synthase 1 OS=Homo sapiens OX=9606 GN=CTPS1 PE=1 SV=2	CTPS1	4	4	9.480%	66689.59	6.02
P19367	sp|P19367|HXK1_HUMAN Hexokinase-1 OS=Homo sapiens OX=9606 GN=HK1 PE=1 SV=3	HK1	4	4	4.580%	102484.82	6.36
P31689	sp|P31689|DNJA1_HUMAN DnaJ homolog subfamily A member 1 OS=Homo sapiens OX=9606 GN=DNAJA1 PE=1 SV=2	DNAJA1	4	4	9.570%	44867.72	6.65
P39656	sp|P39656|OST48_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens OX=9606 GN=DDOST PE=1 SV=4	DDOST	4	4	8.330%	50800.18	6.09

P54136	sp|P54136|SYRC_HUMAN Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=RARS1 PE=1 SV=2	RARS1	4	4	6.820%	75378.13	6.26
P67809	sp|P67809|YBOX1_HUMAN Y-box-binding protein 1 OS=Homo sapiens OX=9606 GN=YBX1 PE=1 SV=3	YBX1	4	4	16.360%	35923.75	9.87
Q15046	sp|Q15046|SYK_HUMAN Lysine--tRNA ligase OS=Homo sapiens OX=9606 GN=KARS1 PE=1 SV=3	KARS1	4	4	5.360%	68047.3	5.94
Q5QJE6	sp|Q5QJE6|TDIF2_HUMAN Deoxynucleotidyltransferase terminal-interacting protein 2 OS=Homo sapiens OX=9606 GN=DNTTIP2 PE=1 SV=2	DNTTIP2	4	4	6.080%	84468.05	5.86
Q8TED0	sp|Q8TED0|UTP15_HUMAN U3 small nucleolar RNA-associated protein 15 homolog OS=Homo sapiens OX=9606 GN=UTP15 PE=1 SV=3	UTP15	4	4	8.300%	58414.5	9.18
Q8WTT2	sp|Q8WTT2|NOC3L_HUMAN Nucleolar complex protein 3 homolog OS=Homo sapiens OX=9606 GN=NOC3L PE=1 SV=1	NOC3L	4	4	7.380%	92546.66	9.22
Q92974	sp|Q92974|ARHG2_HUMAN Rho guanine nucleotide exchange factor 2 OS=Homo sapiens OX=9606 GN=ARHGEF2 PE=1 SV=4	ARHGEF2	4	4	3.750%	111541.29	6.89
Q99661	sp|Q99661|KIF2C_HUMAN Kinesin-like protein KIF2C OS=Homo sapiens OX=9606 GN=KIF2C PE=1 SV=2	KIF2C	4	4	5.100%	81312.04	8.03
Q9H0U4	sp|Q9H0U4|RAB1B_HUMAN Ras-related protein Rab-1B OS=Homo sapiens OX=9606 GN=RAB1B PE=1 SV=1	RAB1B	4	4	18.410%	22170.9	5.55
Q9H8H0	sp|Q9H8H0|NOL11_HUMAN Nucleolar protein 11 OS=Homo sapiens OX=9606 GN=NOL11 PE=1 SV=1	NOL11	4	4	4.730%	81122.66	5.74
Q9NYU2	sp|Q9NYU2|UGGG1_HUMAN UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens OX=9606 GN=UGGT1 PE=1 SV=3	UGGT1	4	4	2.570%	177187.43	5.42
Q9Y262	sp|Q9Y262|EIF3L_HUMAN Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens OX=9606 GN=EIF3L PE=1 SV=1	EIF3L	4	4	6.030%	66726.18	5.93
A0A024R3R5	tr|A0A024R3R5|A0A024R3R5_HUMAN 3-beta-hydroxysterol Delta (14)-reductase OS=Homo sapiens OX=9606 GN=LBR PE=3 SV=1	LBR	4	4	7.800%	70729.36	9.41

A0A024RAV2	tr|A0A024RAV2|A0A024RAV2_HUMAN ATP-dependent DNA helicase OS=Homo sapiens OX=9606 GN=RECQL PE=3 SV=1	RECQL	4	4	5.390%	73456.57	8.13
A0A087WT20	tr|A0A087WT20|A0A087WT20_HUMAN DDB1- and CUL4-associated factor 13 OS=Homo sapiens OX=9606 GN=DCAF13 PE=1 SV=1	DCAF13	4	4	7.370%	67550.43	9.4
A0A087WYN9	tr|A0A087WYN9|A0A087WYN9_HUMAN ATP-dependent RNA helicase DHX29 OS=Homo sapiens OX=9606 GN=DHX29 PE=1 SV=1	DHX29	4	4	2.850%	155289.85	8.37
A0A0B4J2E5	tr|A0A0B4J2E5|A0A0B4J2E5_HUMAN Utp12 domain-containing protein OS=Homo sapiens OX=9606 GN=LOC102724159 PE=1 SV=1	LOC102724	4	4	3.810%	102449.89	5.81
A0A140VJQ4	tr|A0A140VJQ4|A0A140VJQ4_HUMAN Ornithine--oxo-acid aminotransferase OS=Homo sapiens OX=9606 PE=2 SV=1		4	4	8.660%	48534.24	6.57
A0A2R8YE38	tr|A0A2R8YE38|A0A2R8YE38_HUMAN Chromodomain-helicase-DNA-binding protein 4 (Fragment) OS=Homo sapiens OX=9606 GN=CHD4 PE=1 SV=1	CHD4	4	4	9.170%	52145.03	4.68
A0A3B3IU45	tr|A0A3B3IU45|A0A3B3IU45_HUMAN DNA replication licensing factor MCM4 OS=Homo sapiens OX=9606 GN=MCM4 PE=1 SV=1	MCM4	4	4	6.270%	91190.12	5.96
A0A494C001	tr|A0A494C001|A0A494C001_HUMAN RNA-binding protein 15 OS=Homo sapiens OX=9606 GN=RBM15 PE=1 SV=2	RBM15	4	4	6.700%	98012.88	10.06
A0A590UK80	tr|A0A590UK80|A0A590UK80_HUMAN Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=3 SV=1		4	4	3.940%	120933.43	6.38
A0A7I2YQE1	tr|A0A7I2YQE1|A0A7I2YQE1_HUMAN Importin subunit alpha OS=Homo sapiens OX=9606 GN=KPNA2 PE=1 SV=1	KPNA2	4	4	11.910%	57830.3	5.46
A0A804CDA6	tr|A0A804CDA6|A0A804CDA6_HUMAN Dynactin subunit 1 OS=Homo sapiens OX=9606 GN=DCTN1 PE=4 SV=1	DCTN1	4	4	3.060%	141022.55	5.63
A8K3Y5	tr|A8K3Y5|A8K3Y5_HUMAN cDNA FLJ78186 OS=Homo sapiens OX=9606 PE=2 SV=1		4	4	12.930%	43622.3	9.59
A8K6I4	tr|A8K6I4|A8K6I4_HUMAN cDNA FLJ76877, highly similar to Homo sapiens superkiller viralicidic activity 2-like 2 (SKIV2L2), mRNA OS=Homo sapiens OX=9606 PE=2 SV=1		4	4	4.990%	117897.47	6.12

B2R4D8	tr|B2R4D8|B2R4D8_HUMAN 60S ribosomal protein L27 OS=Homo sapiens OX=9606 PE=2 SV=1		4	4	34.560%	15769.47	10.56
B2R9U2	tr|B2R9U2|B2R9U2_HUMAN Peptidylprolyl isomerase OS=Homo sapiens OX=9606 PE=2 SV=1		4	4	10.890%	51833.98	5.35
B2RMQ4	tr|B2RMQ4|B2RMQ4_HUMAN Cytoskeleton associated protein 2 OS=Homo sapiens OX=9606 GN=CKAP2 PE=2 SV=1	CKAP2	4	4	6.450%	76884.7	9.45
B4DV79	tr|B4DV79|B4DV79_HUMAN Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens OX=9606 GN=EIF3B PE=2 SV=1	EIF3B	4	4	5.420%	85133.81	5.13
D3DS96	tr|D3DS96|D3DS96_HUMAN Bromodomain adjacent to zinc finger domain, 1A, isoform CRA_c OS=Homo sapiens OX=9606 GN=BAZ1A PE=4 SV=1	BAZ1A	4	4	3.340%	178571.25	6.24
E9PBS1	tr|E9PBS1|E9PBS1_HUMAN AIR carboxylase (Fragment) OS=Homo sapiens OX=9606 GN=PAICS PE=1 SV=1	PAICS	4	4	9.930%	45651.02	6.29
F5GY37	tr|F5GY37|F5GY37_HUMAN Prohibitin OS=Homo sapiens OX=9606 GN=PHB2 PE=1 SV=1	PHB2	4	4	15.360%	29722.95	9.87
H0YFD6	tr|H0YFD6|H0YFD6_HUMAN Enoyl-CoA hydratase OS=Homo sapiens OX=9606 GN=HADHA PE=1 SV=2	HADHA	4	4	5.050%	86370.63	9.21
H3BN98	tr|H3BN98|H3BN98_HUMAN 40S ribosomal protein S15a (Fragment) OS=Homo sapiens OX=9606 PE=3 SV=2		4	4	14.350%	27167.94	9.6
I3L1P8	tr|I3L1P8|I3L1P8_HUMAN Mitochondrial 2-oxoglutarate/malate carrier protein (Fragment) OS=Homo sapiens OX=9606 GN=SLC25A11 PE=1 SV=1	SLC25A11	4	4	15.880%	32182.07	9.79
J3QS96	tr|J3QS96|J3QS96_HUMAN 60S ribosomal protein L17 (Fragment) OS=Homo sapiens OX=9606 GN=RPL17 PE=1 SV=1	RPL17	4	4	30.430%	15959.33	10.53
M0R210	tr|M0R210|M0R210_HUMAN 40S ribosomal protein S16 OS=Homo sapiens OX=9606 GN=RPS16 PE=1 SV=1	RPS16	4	4	28.680%	14418.75	10.24
Q14222	tr|Q14222|Q14222_HUMAN EEF1A protein (Fragment) OS=Homo sapiens OX=9606 GN=EEF1A PE=2 SV=1	EEF1A	4	4	22.030%	24195.99	9.61

Q59GS8	tr|Q59GS8|Q59GS8_HUMAN Complement component 5 variant (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		4	4	3.620%	123349.87	8.43
Q6N037	tr|Q6N037|Q6N037_HUMAN RNA-binding region (RNP1, RRM) containing 2, isoform CRA_d OS=Homo sapiens OX=9606 GN=DKFZp686A11192 PE=2 SV=1	DKFZp686A	4	4	10.630%	39817.91	6.12
H0YI15	tr|H0YI15|H0YI15_HUMAN Histone deacetylase 7 (Fragment) OS=Homo sapiens OX=9606 GN=HDAC7 PE=1 SV=1	HDAC7	8	3	85.250%	5997.6	9.45
Q9HAV0	sp|Q9HAV0|GBB4_HUMAN Guanine nucleotide-binding protein subunit beta-4 OS=Homo sapiens OX=9606 GN=GNB4 PE=1 SV=3	GNB4	5	3	6.180%	37566.81	5.59
S6B291	tr|S6B291|S6B291_HUMAN IgG H chain OS=Homo sapiens OX=9606 PE=1 SV=1		5	3	4.290%	50869.92	7.89
P43246	sp|P43246|MSH2_HUMAN DNA mismatch repair protein Msh2 OS=Homo sapiens OX=9606 GN=MSH2 PE=1 SV=1	MSH2	4	3	3.640%	104741.87	5.58
Q9Y277	sp|Q9Y277|VDAC3_HUMAN Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens OX=9606 GN=VDAC3 PE=1 SV=1	VDAC3	4	3	9.540%	30658.3	8.84
A0A5C2GKL4	tr|A0A5C2GKL4|A0A5C2GKL4_HUMAN IG c1658_heavy_IGHV3-7_IGHD2-2_IGHJ6 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		4	3	28.350%	14157.8	9.14
K7ERI7	tr|K7ERI7|K7ERI7_HUMAN 60S ribosomal protein L22 OS=Homo sapiens OX=9606 GN=RPL22 PE=1 SV=1	RPL22	4	3	31.580%	11168.4	6.35
Q65ZC9	tr|Q65ZC9|Q65ZC9_HUMAN Single-chain Fv (Fragment) OS=Homo sapiens OX=9606 GN=scFv PE=2 SV=1	scFv	4	3	12.080%	25569.19	9.21
O15379	sp|O15379|HDAC3_HUMAN Histone deacetylase 3 OS=Homo sapiens OX=9606 GN=HDAC3 PE=1 SV=2	HDAC3	3	3	8.180%	48847.19	4.98
O43491	sp|O43491|E41L2_HUMAN Band 4.1-like protein 2 OS=Homo sapiens OX=9606 GN=EPB41L2 PE=1 SV=1	EPB41L2	3	3	2.890%	112586.72	5.34
O43663	sp|O43663|PRC1_HUMAN Protein regulator of cytokinesis 1 OS=Homo sapiens OX=9606 GN=PRC1 PE=1 SV=2	PRC1	3	3	3.390%	71605.79	6.29

O75534	sp|O75534|CSDE1_HUMAN Cold shock domain-containing protein E1 OS=Homo sapiens OX=9606 GN=CSDE1 PE=1 SV=2	CSDE1	3	3	4.010%	88883.64	5.88
O94905	sp|O94905|ERLN2_HUMAN Erlin-2 OS=Homo sapiens OX=9606 GN=ERLIN2 PE=1 SV=1	ERLIN2	3	3	10.320%	37839.1	5.47
O96008	sp|O96008|TOM40_HUMAN Mitochondrial import receptor subunit TOM40 homolog OS=Homo sapiens OX=9606 GN=TOMM40 PE=1 SV=1	TOMM40	3	3	10.530%	37892.66	6.79
P06744	sp|P06744|G6PI_HUMAN Glucose-6-phosphate isomerase OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=4	GPI	3	3	5.910%	63146.37	8.42
P12270	sp|P12270|TPR_HUMAN Nucleoprotein TPR OS=Homo sapiens OX=9606 GN=TPR PE=1 SV=3	TPR	3	3	1.610%	267289.6	4.97
P24928	sp|P24928|RPB1_HUMAN DNA-directed RNA polymerase II subunit RPB1 OS=Homo sapiens OX=9606 GN=POLR2A PE=1 SV=2	POLR2A	3	3	1.370%	217173.69	7.02
P27824	sp|P27824|CALX_HUMAN Calnexin OS=Homo sapiens OX=9606 GN=CANX PE=1 SV=2	CANX	3	3	6.420%	67567.5	4.47
P28288	sp|P28288|ABCD3_HUMAN ATP-binding cassette sub-family D member 3 OS=Homo sapiens OX=9606 GN=ABCD3 PE=1 SV=1	ABCD3	3	3	4.400%	75475.04	9.41
P31939	sp|P31939|PUR9_HUMAN Bifunctional purine biosynthesis protein ATIC OS=Homo sapiens OX=9606 GN=ATIC PE=1 SV=3	ATIC	3	3	3.720%	64615.11	6.27
P45974	sp|P45974|UBP5_HUMAN Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens OX=9606 GN=USP5 PE=1 SV=2	USP5	3	3	4.550%	95785.21	4.91
P49916	sp|P49916|DNLI3_HUMAN DNA ligase 3 OS=Homo sapiens OX=9606 GN=LIG3 PE=1 SV=2	LIG3	3	3	3.170%	112905.67	9.17
P50570	sp|P50570|DYN2_HUMAN Dynamin-2 OS=Homo sapiens OX=9606 GN=DNM2 PE=1 SV=2	DNM2	3	3	2.070%	98063.13	7.04
P51114	sp|P51114|FXR1_HUMAN Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens OX=9606 GN=FXR1 PE=1 SV=3	FXR1	3	3	7.090%	69719.99	5.84

P51532	sp|P51532|SMCA4_HUMAN Transcription activator BRG1 OS=Homo sapiens OX=9606 GN=SMARCA4 PE=1 SV=2	SMARCA4	3	3	1.700%	184643.49	7.83
P52209	sp|P52209|6PGD_HUMAN 6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens OX=9606 GN=PGD PE=1 SV=3	PGD	3	3	7.870%	53139.39	6.8
P56545	sp|P56545|CTBP2_HUMAN C-terminal-binding protein 2 OS=Homo sapiens OX=9606 GN=CTBP2 PE=1 SV=1	CTBP2	3	3	7.640%	48944.3	6.47
Q09028	sp|Q09028|RBBP4_HUMAN Histone-binding protein RBBP4 OS=Homo sapiens OX=9606 GN=RBBP4 PE=1 SV=3	RBBP4	3	3	8.240%	47655.13	4.74
Q13409	sp|Q13409|DC1I2_HUMAN Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens OX=9606 GN=DYNC1I2 PE=1 SV=3	DYNC1I2	3	3	5.170%	71455.75	5.08
Q14978	sp|Q14978|NOLC1_HUMAN Nucleolar and coiled-body phosphoprotein 1 OS=Homo sapiens OX=9606 GN=NOLC1 PE=1 SV=2	NOLC1	3	3	5.010%	73602.31	9.46
Q15717	sp|Q15717|ELAV1_HUMAN ELAV-like protein 1 OS=Homo sapiens OX=9606 GN=ELAVL1 PE=1 SV=2	ELAVL1	3	3	11.660%	36091.47	9.23
Q52LJ0	sp|Q52LJ0|FA98B_HUMAN Protein FAM98B OS=Homo sapiens OX=9606 GN=FAM98B PE=1 SV=2	FAM98B	3	3	8.550%	45546.7	8.88
Q5T8P6	sp|Q5T8P6|RBM26_HUMAN RNA-binding protein 26 OS=Homo sapiens OX=9606 GN=RBM26 PE=1 SV=3	RBM26	3	3	2.580%	113595.92	9.21
Q6DKI1	sp|Q6DKI1|RL7L_HUMAN 60S ribosomal protein L7-like 1 OS=Homo sapiens OX=9606 GN=RPL7L1 PE=1 SV=2	RPL7L1	3	3	13.330%	29668.85	10.52
Q6P1J9	sp|Q6P1J9|CDC73_HUMAN Parafibromin OS=Homo sapiens OX=9606 GN=CDC73 PE=1 SV=1	CDC73	3	3	5.840%	60575.83	9.63
Q86WJ1	sp|Q86WJ1|CHD1L_HUMAN Chromodomain-helicase-DNA-binding protein 1-like OS=Homo sapiens OX=9606 GN=CHD1L PE=1 SV=3	CHD1L	3	3	3.340%	100998.8	6.45
Q8IWA0	sp|Q8IWA0|WDR75_HUMAN WD repeat-containing protein 75 OS=Homo sapiens OX=9606 GN=WDR75 PE=1 SV=1	WDR75	3	3	4.820%	94497.7	5.65

Q8IXT5	sp|Q8IXT5|RB12B_HUMAN RNA-binding protein 12B OS=Homo sapiens OX=9606 GN=RBM12B PE=1 SV=2	RBM12B	3	3	3.600%	118101.34	6.34
Q92734	sp|Q92734|TFG_HUMAN Protein TFG OS=Homo sapiens OX=9606 GN=TFG PE=1 SV=2	TFG	3	3	6.000%	43447.42	4.94
Q93008	sp|Q93008|USP9X_HUMAN Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens OX=9606 GN=USP9X PE=1 SV=4	USP9X	3	3	0.940%	290459.42	5.52
Q96AG4	sp|Q96AG4|LRC59_HUMAN Leucine-rich repeat-containing protein 59 OS=Homo sapiens OX=9606 GN=LRRC59 PE=1 SV=1	LRRC59	3	3	12.700%	34930.05	9.61
Q96S55	sp|Q96S55|WRIP1_HUMAN ATPase WRNIP1 OS=Homo sapiens OX=9606 GN=WRNIP1 PE=1 SV=2	WRNIP1	3	3	4.960%	72132.16	5.73
Q9HCG8	sp|Q9HCG8|CWC22_HUMAN Pre-mRNA-splicing factor CWC22 homolog OS=Homo sapiens OX=9606 GN=CWC22 PE=1 SV=3	CWC22	3	3	3.080%	105465.01	6.6
Q9NQS7	sp|Q9NQS7|INCE_HUMAN Inner centromere protein OS=Homo sapiens OX=9606 GN=INCENP PE=1 SV=3	INCENP	3	3	3.810%	105427.57	9.46
Q9UK59	sp|Q9UK59|DBR1_HUMAN Lariat debranching enzyme OS=Homo sapiens OX=9606 GN=DBR1 PE=1 SV=2	DBR1	3	3	6.070%	61554.23	5.25
Q9UKM9	sp|Q9UKM9|RALY_HUMAN RNA-binding protein Raly OS=Homo sapiens OX=9606 GN=RALY PE=1 SV=1	RALY	3	3	9.800%	32462.76	9.2
Q9Y5J1	sp|Q9Y5J1|UTP18_HUMAN U3 small nucleolar RNA-associated protein 18 homolog OS=Homo sapiens OX=9606 GN=UTP18 PE=1 SV=3	UTP18	3	3	4.860%	62002.9	8.93
Q9Y5Q9	sp|Q9Y5Q9|TF3C3_HUMAN General transcription factor 3C polypeptide 3 OS=Homo sapiens OX=9606 GN=GTF3C3 PE=1 SV=1	GTF3C3	3	3	2.930%	101271.12	4.98
A0A024QZN4	tr|A0A024QZN4|A0A024QZN4_HUMAN Metavinculin OS=Homo sapiens OX=9606 GN=VCL PE=3 SV=1	VCL	3	3	4.130%	116721.09	5.83
A0A024R0Y5	tr|A0A024R0Y5|A0A024R0Y5_HUMAN ATP-dependent 6-phosphofructokinase OS=Homo sapiens OX=9606 GN=PFKM PE=2 SV=1	PFKM	3	3	3.460%	85181.59	8.23

A0A024R254	tr|A0A024R254|A0A024R254_HUMAN Melanoma antigen family D, 1, isoform CRA_a OS=Homo sapiens OX=9606 GN=MAGED1 PE=4 SV=1	MAGED1	3	3	3.080%	86177.88	5.64
A0A024R363	tr|A0A024R363|A0A024R363_HUMAN Chromosome 3 open reading frame 63, isoform CRA_b OS=Homo sapiens OX=9606 GN=C3orf63 PE=4 SV=1	C3orf63	3	3	2.840%	140051.67	5.44
A0A024R9D2	tr|A0A024R9D2|A0A024R9D2_HUMAN Metadherin, isoform CRA_a OS=Homo sapiens OX=9606 GN=MTDH PE=4 SV=1	MTDH	3	3	6.870%	63836.17	9.33
A0A024R9D3	tr|A0A024R9D3|A0A024R9D3_HUMAN 60S ribosomal protein L30 OS=Homo sapiens OX=9606 GN=RPL30 PE=3 SV=1	RPL30	3	3	31.300%	12783.92	9.65
A0A068L529	tr|A0A068L529|A0A068L529_HUMAN TBLR1-RARA fusion protein OS=Homo sapiens OX=9606 GN=TBLR1-RARA fusion PE=2 SV=1	TBLR1-RAR	3	3	5.500%	59796.45	6.07
A0A090N8Y2	tr|A0A090N8Y2|A0A090N8Y2_HUMAN Protein disulfide-isomerase A4 OS=Homo sapiens OX=9606 GN=ERP70 PE=2 SV=1	ERP70	3	3	4.340%	72931.58	4.96
A0A0A0MRW6	tr|A0A0A0MRW6|A0A0A0MRW6_HUMAN Nucleolar protein 6 OS=Homo sapiens OX=9606 GN=NOL6 PE=1 SV=1	NOL6	3	3	3.570%	112155.9	7.4
A0A0C4DG17	tr|A0A0C4DG17|A0A0C4DG17_HUMAN 40S ribosomal protein SA OS=Homo sapiens OX=9606 GN=RPSA PE=1 SV=1	RPSA	3	3	12.670%	33313.24	4.79
A0A0C4DG98	tr|A0A0C4DG98|A0A0C4DG98_HUMAN THO complex subunit 2 OS=Homo sapiens OX=9606 GN=THOC2 PE=1 SV=1	THOC2	3	3	1.960%	169579.72	8.85
A0A0S2Z404	tr|A0A0S2Z404|A0A0S2Z404_HUMAN Regulator of chromosome condensation 1 isoform 2 (Fragment) OS=Homo sapiens OX=9606 GN=RCC1 PE=2 SV=1	RCC1	3	3	6.640%	48145.04	8.44
A0A0S2Z4R1	tr|A0A0S2Z4R1|A0A0S2Z4R1_HUMAN Tyrosine--tRNA ligase (Fragment) OS=Homo sapiens OX=9606 GN=YARS PE=2 SV=1	YARS	3	3	5.680%	59142.76	6.61
A0A140VJF3	tr|A0A140VJF3|A0A140VJF3_HUMAN Testicular tissue protein Li 27 OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	8.590%	36954.1	6.37
A0A140VJS9	tr|A0A140VJS9|A0A140VJS9_HUMAN Serine/threonine-protein phosphatase OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	10.850%	38630.97	6.2

A0A140VK53	tr|A0A140VK53|A0A140VK53_HUMAN Testicular secretory protein Li 53 OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	1.340%	299611.6	12.05
A0A1U9X7X5	tr|A0A1U9X7X5|A0A1U9X7X5_HUMAN Kinesin-like protein OS=Homo sapiens OX=9606 PE=3 SV=1		3	3	5.790%	73774.8	9.15
A0A1Y0BRN3	tr|A0A1Y0BRN3|A0A1Y0BRN3_HUMAN Unconventional myosin-6 OS=Homo sapiens OX=9606 GN=MYO6 PE=1 SV=1	MYO6	3	3	2.880%	148602.19	8.74
A0A2R8Y849	tr|A0A2R8Y849|A0A2R8Y849_HUMAN 40S ribosomal protein S24 OS=Homo sapiens OX=9606 GN=RPS24 PE=1 SV=1	RPS24	3	3	19.850%	15196.79	10.91
A0A3Q8B022	tr|A0A3Q8B022|A0A3Q8B022_HUMAN Protein arginine N-methyltransferase 1 transcript variant 6 OS=Homo sapiens OX=9606 GN=PRMT1 PE=2 SV=1	PRMT1	3	3	10.600%	39967.25	5.04
A0A494C189	tr|A0A494C189|A0A494C189_HUMAN Histone H2A OS=Homo sapiens OX=9606 GN=H2AZ1 PE=1 SV=1	H2AZ1	3	3	20.470%	13495.51	10.58
A0A5F9ZHL1	tr|A0A5F9ZHL1|A0A5F9ZHL1_HUMAN Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens OX=9606 GN=ACAT1 PE=1 SV=1	ACAT1	3	3	8.760%	46108.17	9.1
A0A7I2YQI6	tr|A0A7I2YQI6|A0A7I2YQI6_HUMAN Eukaryotic translation initiation factor 3 subunit I OS=Homo sapiens OX=9606 GN=EIF3I PE=1 SV=1	EIF3I	3	3	6.140%	44900.18	9.04
A0A7P0T9C0	tr|A0A7P0T9C0|A0A7P0T9C0_HUMAN Transportin-1 OS=Homo sapiens OX=9606 GN=TNPO1 PE=1 SV=1	TNPO1	3	3	3.140%	90651.54	4.78
A0A804HK61	tr|A0A804HK61|A0A804HK61_HUMAN Alpha-actinin-1 OS=Homo sapiens OX=9606 GN=ACTN1 PE=4 SV=1	ACTN1	3	3	3.500%	102580.07	5.3
A1L4G8	tr|A1L4G8|A1L4G8_HUMAN C18orf34 protein OS=Homo sapiens OX=9606 GN=C18orf34 PE=2 SV=1	C18orf34	3	3	2.540%	102038.93	6.34
A8K946	tr|A8K946|A8K946_HUMAN mRNA cap guanine-N7 methyltransferase OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	8.130%	57749.96	7.82
B0UZZ8	tr|B0UZZ8|B0UZZ8_HUMAN Chromosome 6 open reading frame 11 OS=Homo sapiens OX=9606 GN=C6orf11 PE=2 SV=1	C6orf11	3	3	5.570%	68040.25	9.69

B2R6D0	tr|B2R6D0|B2R6D0_HUMAN 26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	3.880%	105837.06	5.25
B2R858	tr|B2R858|B2R858_HUMAN RNA helicase OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	7.420%	53215.83	8.85
B2RAM6	tr|B2RAM6|B2RAM6_HUMAN cDNA, FLJ95005, highly similar to Homo sapiens kinesin family member 11 (KIF11), mRNA OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	2.750%	119130.59	5.52
B2RNR6	tr|B2RNR6|B2RNR6_HUMAN Zinc finger RNA binding protein OS=Homo sapiens OX=9606 GN=ZFR PE=2 SV=1	ZFR	3	3	3.540%	117012.74	9.17
B3KM65	tr|B3KM65|B3KM65_HUMAN RNA helicase OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	8.230%	46138.32	9.69
B3KRR1	tr|B3KRR1|B3KRR1_HUMAN cDNA FLJ34725 fis, clone MESAN2005958, highly similar to RNA-binding protein Luc7-like 2 OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	7.080%	40490.59	10.15
B3KXZ4	tr|B3KXZ4|B3KXZ4_HUMAN DNA replication licensing factor MCM2 OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	4.210%	91270.8	6.05
B3KY60	tr|B3KY60|B3KY60_HUMAN cDNA FLJ16777 fis, clone BRHIP2029567, highly similar to Cell division cycle 5-like protein OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	3.870%	92275.64	8.22
B4DES6	tr|B4DES6|B4DES6_HUMAN cDNA FLJ52441, highly similar to Zinc finger protein 512 OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	9.090%	53120.64	9.66
B4DHJ3	tr|B4DHJ3|B4DHJ3_HUMAN DNA-directed RNA polymerase subunit beta OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	3.260%	133025.28	6.86
B4DI38	tr|B4DI38|B4DI38_HUMAN Adenylyl cyclase-associated protein 1 OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	10.840%	49079.53	8.34
B4DI57	tr|B4DI57|B4DI57_HUMAN cDNA FLJ54111, highly similar to Serotransferrin OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	3.330%	63436.49	6.95
B4DLV7	tr|B4DLV7|B4DLV7_HUMAN Rab GDP dissociation inhibitor OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	7.130%	51153.36	8.37

B4DX55	tr|B4DX55|B4DX55_HUMAN cDNA FLJ58171, moderately similar to Melanoma-associated antigen D2 OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	5.190%	55499.7	5.75
B7Z5C1	tr|B7Z5C1|B7Z5C1_HUMAN cDNA FLJ56126, highly similar to Programmed cell death 6-interacting protein OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	4.310%	71818.63	6.04
B7Z766	tr|B7Z766|B7Z766_HUMAN cDNA FLJ54564, highly similar to 150 kDa oxygen-regulated protein (Orp150) OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	2.830%	94198.34	4.96
D6R9I9	tr|D6R9I9|D6R9I9_HUMAN ATP-binding cassette sub-family E member 1 OS=Homo sapiens OX=9606 GN=ABCE1 PE=1 SV=1	ABCE1	3	3	5.940%	47036.5	8.63
E7ERM3	tr|E7ERM3|E7ERM3_HUMAN Angiomotin OS=Homo sapiens OX=9606 GN=AMOT PE=1 SV=1	AMOT	3	3	2.700%	92502.99	7
E9PFW3	tr|E9PFW3|E9PFW3_HUMAN AP-2 complex subunit mu OS=Homo sapiens OX=9606 GN=AP2M1 PE=1 SV=1	AP2M1	3	3	4.780%	52302.9	9.53
E9PKF6	tr|E9PKF6|E9PKF6_HUMAN Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens OX=9606 GN=PPP6R3 PE=1 SV=1	PPP6R3	3	3	3.700%	93731.97	4.52
G1UI21	tr|G1UI21|G1UI21_HUMAN Talin-2 OS=Homo sapiens OX=9606 GN=TLN2 PE=2 SV=1	TLN2	3	3	1.200%	166575.87	5.18
G3V3B0	tr|G3V3B0|G3V3B0_HUMAN Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens OX=9606 GN=ACIN1 PE=1 SV=1	ACIN1	3	3	5.840%	67493.93	7.22
G3V5Z7	tr|G3V5Z7|G3V5Z7_HUMAN Proteasome subunit alpha type OS=Homo sapiens OX=9606 GN=PSMA6 PE=1 SV=1	PSMA6	3	3	13.890%	28147.01	6.35
H3BPZ1	tr|H3BPZ1|H3BPZ1_HUMAN Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase OS=Homo sapiens OX=9606 GN=HACD3 PE=1 SV=1	HACD3	3	3	9.790%	40068.53	9.06
H7C2L4	tr|H7C2L4|H7C2L4_HUMAN Transformer-2 protein homolog beta (Fragment) OS=Homo sapiens OX=9606 GN=TRA2B PE=1 SV=1	TRA2B	3	3	25.230%	12547.53	10.51
Q53F90	tr|Q53F90|Q53F90_HUMAN Glutamine amidotransferase (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	4.180%	76695.47	6.24

Q53GG0	tr|Q53GG0|Q53GG0_HUMAN Epithelial protein lost in neoplasm beta variant (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	5.010%	85252.61	6.41
Q53HC3	tr|Q53HC3|Q53HC3_HUMAN Phosphate carrier protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	6.930%	39928.23	9.43
Q562Z4	tr|Q562Z4|Q562Z4_HUMAN Actin-like protein (Fragment) OS=Homo sapiens OX=9606 GN=ACT PE=4 SV=1	ACT	3	3	52.430%	11555.22	7.1
Q59G73	tr|Q59G73|Q59G73_HUMAN Exosome component 10 isoform 2 variant (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	11.140%	49221.36	5.79
Q59GE4	tr|Q59GE4|Q59GE4_HUMAN Ribosomal protein S10 variant (Fragment) OS=Homo sapiens OX=9606 PE=3 SV=1		3	3	13.790%	19859.65	9.92
Q5JR04	tr|Q5JR04|Q5JR04_HUMAN RNA helicase OS=Homo sapiens OX=9606 GN=MOV10 PE=1 SV=1	MOV10	3	3	2.850%	107208.6	8.97
Q5T5C7	tr|Q5T5C7|Q5T5C7_HUMAN Seryl-tRNA synthetase OS=Homo sapiens OX=9606 GN=SARS1 PE=1 SV=1	SARS1	3	3	6.340%	61312.49	6.64
Q5TCT4	tr|Q5TCT4|Q5TCT4_HUMAN RNA-binding protein 34 (Fragment) OS=Homo sapiens OX=9606 GN=RBM34 PE=1 SV=1	RBM34	3	3	16.590%	24079.02	9.55
Q5TFJ7	tr|Q5TFJ7|Q5TFJ7_HUMAN Importin subunit alpha-7 (Fragment) OS=Homo sapiens OX=9606 GN=KPNA6 PE=1 SV=1	KPNA6	3	3	8.720%	35457.42	5.3
Q5VU21	tr|Q5VU21|Q5VU21_HUMAN PAI-1 mRNA-binding protein variant OS=Homo sapiens OX=9606 PE=2 SV=1		3	3	9.300%	42426.12	8.43
Q5VVD0	tr|Q5VVD0|Q5VVD0_HUMAN 60S ribosomal protein L11 OS=Homo sapiens OX=9606 GN=RPL11 PE=2 SV=1	RPL11	3	3	16.850%	20252.15	9.64
Q6AHZ7	tr|Q6AHZ7|Q6AHZ7_HUMAN Uncharacterized protein DKFZp686A111 OS=Homo sapiens OX=9606 GN=DKFZp686A111 PE=2 SV=1	DKFZp686A	3	3	1.280%	238798.05	7.11
Q6IPI1	tr|Q6IPI1|Q6IPI1_HUMAN 60S ribosomal protein L29 OS=Homo sapiens OX=9606 GN=RPL29 PE=2 SV=1	RPL29	3	3	18.010%	17951.11	11.67

Q86Y65	tr|Q86Y65|Q86Y65_HUMAN KIAA1529 protein (Fragment) OS=Homo sapiens OX=9606 GN=KIAA1529 PE=2 SV=2	KIAA1529	3	3	1.890%	104486.04	5.19
Q9BSP4	tr|Q9BSP4|Q9BSP4_HUMAN PFKL protein (Fragment) OS=Homo sapiens OX=9606 GN=PFKL PE=2 SV=2	PFKL	3	3	5.970%	53646.16	8.58
R4GMQ1	tr|R4GMQ1|R4GMQ1_HUMAN Lysine-specific histone demethylase OS=Homo sapiens OX=9606 GN=KDM1A PE=1 SV=2	KDM1A	3	3	3.730%	93596.36	6.11
R4GMU7	tr|R4GMU7|R4GMU7_HUMAN 60S ribosomal protein L7-like 1 (Fragment) OS=Homo sapiens OX=9606 GN=RPL7L1 PE=1 SV=2	RPL7L1	3	3	12.120%	22873.98	10.64
V9HW21	tr|V9HW21|V9HW21_HUMAN Carbonic anhydrase OS=Homo sapiens OX=9606 GN=HEL-76 PE=2 SV=1	HEL-76	3	3	18.080%	29245.67	6.87
V9HWF5	tr|V9HWF5|V9HWF5_HUMAN Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens OX=9606 GN=HEL-S-69p PE=1 SV=1	HEL-S-69p	3	3	15.150%	18012.3	7.68
P52926	sp|P52926|ZC3HF_HUMAN High mobility group protein HMGI-C OS=Homo sapiens OX=9606 GN=HMGA2 PE=1 SV=1	HMGA2	3	3	37.610%	11831.91	10.63
Q53T94	sp|Q53T94|TAF1B_HUMAN TATA box-binding protein-associated factor RNA polymerase I subunit B OS=Homo sapiens OX=9606 GN=TAF1B PE=1 SV=1	TAF1B	4	2	1.700%	68831.01	8.27
A0A2U8J8D6	tr|A0A2U8J8D6|A0A2U8J8D6_HUMAN Ig heavy chain variable region (Fragment) OS=Homo sapiens OX=9606 GN=IgH PE=2 SV=1	IgH	4	2	22.640%	11840.06	6.75
A0A5C2GAS0	tr|A0A5C2GAS0|A0A5C2GAS0_HUMAN IGH + IGL c356_heavy_IGHV3-20_IGHD3-22_IGHJ5 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		4	2	16.670%	13133.48	8.06
B2R9I9	tr|B2R9I9|B2R9I9_HUMAN cDNA, FLJ94417, highly similar to Homo sapiens WD repeat domain 57 (U5 snRNP specific) (WDR57), mRNA OS=Homo sapiens OX=9606 PE=2 SV=1		4	2	2.800%	39266.08	8.69
P63173	sp|P63173|RL38_HUMAN 60S ribosomal protein L38 OS=Homo sapiens OX=9606 GN=RPL38 PE=1 SV=2	RPL38	3	2	35.710%	8217.79	10.1
Q9H4L4	sp|Q9H4L4|SENP3_HUMAN Sentrin-specific protease 3 OS=Homo sapiens OX=9606 GN=SENP3 PE=1 SV=2	SENP3	3	2	1.220%	65009.07	8.82

A0A0A0MRJ3	tr|A0A0A0MRJ3|A0A0A0MRJ3_HUMAN Neuron navigator 1 OS=Homo sapiens OX=9606 GN=NAV1 PE=1 SV=1	NAV1	3	2	0.550%	197403	8.37
A0A0A0MTQ8	tr|A0A0A0MTQ8|A0A0A0MTQ8_HUMAN Coiled-coil domain-containing protein 175 OS=Homo sapiens OX=9606 GN=CCDC175 PE=1 SV=1	CCDC175	3	2	2.290%	97412.64	5.79
A0A5C2G5V9	tr|A0A5C2G5V9|A0A5C2G5V9_HUMAN IGH c356_heavy__IGHV3-43_IGHD3-9_IGHJ3 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		3	2	20.170%	12806.2	5.14
A0A5C2G9S1	tr|A0A5C2G9S1|A0A5C2G9S1_HUMAN IGH + IGL c463_heavy_IGHV3-11_IGHD3-3_IGHJ5 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		3	2	12.800%	13767.2	6.34
A0A5C2GFE8	tr|A0A5C2GFE8|A0A5C2GFE8_HUMAN IG c282_heavy_IGHV3-23_IGHD3-22_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		3	2	12.700%	13614.16	5.54
A0A5C2GH44	tr|A0A5C2GH44|A0A5C2GH44_HUMAN IG c518_heavy_IGHV3-30_IGHD3-10_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		3	2	20.770%	14354.88	7.95
A0A5C2GQU8	tr|A0A5C2GQU8|A0A5C2GQU8_HUMAN IG c1712_heavy_IGHV3-23_IGHD4-11_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		3	2	20.170%	12645.83	6.46
A0A5C2GXJ3	tr|A0A5C2GXJ3|A0A5C2GXJ3_HUMAN IG c1327_heavy_IGHV3-9_IGHD2-2_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		3	2	16.530%	13191.59	5.73
A0A7I2V497	tr|A0A7I2V497|A0A7I2V497_HUMAN Heterogeneous nuclear ribonucleoprotein A1 (Fragment) OS=Homo sapiens OX=9606 GN=HNRNPA1 PE=1 SV=1	HNRNPA1	3	2	78.130%	3135.28	11
A8MV53	tr|A8MV53|A8MV53_HUMAN HCG2033702, isoform CRA_a OS=Homo sapiens OX=9606 GN=PPAN PE=1 SV=1	PPAN	3	2	5.710%	47144.48	9.86
B4DYY5	tr|B4DYY5|B4DYY5_HUMAN cDNA FLJ55671, highly similar to Ubiquitin-associated protein 2-like OS=Homo sapiens OX=9606 PE=2 SV=1		3	2	2.230%	113558.36	6.2
M0R2N5	tr|M0R2N5|M0R2N5_HUMAN Very-long-chain enoyl-CoA reductase OS=Homo sapiens OX=9606 GN=TECR PE=1 SV=1	TECR	3	2	4.910%	39966.69	9.65
Q68DJ3	tr|Q68DJ3|Q68DJ3_HUMAN Uncharacterized protein DKFZp781A0653 OS=Homo sapiens OX=9606 GN=DKFZp781A0653 PE=2 SV=1	DKFZp781A	3	2	2.120%	54206.48	7.01

Q8IWY7	tr|Q8IWY7|Q8IWY7_HUMAN Tau-tubulin kinase OS=Homo sapiens OX=9606 GN=TTBK2 PE=1 SV=1	TTBK2	3	2	0.790%	182464.91	6.58
A0A075B6R9	sp|A0A075B6R9|KVD24_HUMAN Probable non-functional immunoglobulin kappa variable 2D-24 OS=Homo sapiens OX=9606 GN=IGKV2D-24 PE=1 SV=1	IGKV2D-24	2	2	10.000%	13078.78	8.98
O00411	sp|O00411|RPOM_HUMAN DNA-directed RNA polymerase, mitochondrial OS=Homo sapiens OX=9606 GN=POLRMT PE=1 SV=2	POLRMT	2	2	1.300%	138618.81	9.19
O43660	sp|O43660|PLRG1_HUMAN Pleiotropic regulator 1 OS=Homo sapiens OX=9606 GN=PLRG1 PE=1 SV=1	PLRG1	2	2	3.700%	57193.17	9.24
O43719	sp|O43719|HTSF1_HUMAN HIV Tat-specific factor 1 OS=Homo sapiens OX=9606 GN=HTATSF1 PE=1 SV=1	HTATSF1	2	2	1.850%	85851.81	4.29
O60524	sp|O60524|NEMF_HUMAN Nuclear export mediator factor NEMF OS=Homo sapiens OX=9606 GN=NEMF PE=1 SV=4	NEMF	2	2	1.580%	122952.96	5.97
O75037	sp|O75037|KI21B_HUMAN Kinesin-like protein KIF21B OS=Homo sapiens OX=9606 GN=KIF21B PE=1 SV=2	KIF21B	2	2	0.670%	182659.61	6.7
O75179	sp|O75179|ANR17_HUMAN Ankyrin repeat domain-containing protein 17 OS=Homo sapiens OX=9606 GN=ANKRD17 PE=1 SV=3	ANKRD17	2	2	0.650%	274254.81	6.07
O75475	sp|O75475|PSIP1_HUMAN PC4 and SFRS1-interacting protein OS=Homo sapiens OX=9606 GN=PSIP1 PE=1 SV=1	PSIP1	2	2	3.580%	60102.54	9.15
O95602	sp|O95602|RPA1_HUMAN DNA-directed RNA polymerase I subunit RPA1 OS=Homo sapiens OX=9606 GN=POLR1A PE=1 SV=2	POLR1A	2	2	1.340%	194809.02	6.61
O95793	sp|O95793|STAU1_HUMAN Double-stranded RNA-binding protein Staufen homolog 1 OS=Homo sapiens OX=9606 GN=STAU1 PE=1 SV=2	STAU1	2	2	3.470%	63181.55	9.46
P04844	sp|P04844|RPN2_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens OX=9606 GN=RPN2 PE=1 SV=3	RPN2	2	2	5.710%	69283.12	5.44
P09972	sp|P09972|ALDOC_HUMAN Fructose-bisphosphate aldolase C OS=Homo sapiens OX=9606 GN=ALDOC PE=1 SV=2	ALDOC	2	2	8.240%	39455.4	6.41

P10155	sp|P10155|RO60_HUMAN 60 kDa SS-A/Ro ribonucleoprotein OS=Homo sapiens OX=9606 GN=RO60 PE=1 SV=2	RO60	2	2	3.350%	60669.98	8.27
P15121	sp|P15121|ALDR_HUMAN Aldo-keto reductase family 1 member B1 OS=Homo sapiens OX=9606 GN=AKR1B1 PE=1 SV=3	AKR1B1	2	2	4.750%	35852.98	6.52
P15170	sp|P15170|ERF3A_HUMAN Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens OX=9606 GN=GSPT1 PE=1 SV=1	GSPT1	2	2	4.010%	55755.3	5.45
P21108	sp|P21108|PRPS3_HUMAN Ribose-phosphate pyrophosphokinase 3 OS=Homo sapiens OX=9606 GN=PRPS1L1 PE=1 SV=2	PRPS1L1	2	2	7.550%	34838.95	5.92
P28074	sp|P28074|PSB5_HUMAN Proteasome subunit beta type-5 OS=Homo sapiens OX=9606 GN=PSMB5 PE=1 SV=3	PSMB5	2	2	7.980%	28479.95	6.44
P30101	sp|P30101|PDIA3_HUMAN Protein disulfide-isomerase A3 OS=Homo sapiens OX=9606 GN=PDIA3 PE=1 SV=4	PDIA3	2	2	4.360%	56781.7	5.98
P35251	sp|P35251|RFC1_HUMAN Replication factor C subunit 1 OS=Homo sapiens OX=9606 GN=RFC1 PE=1 SV=4	RFC1	2	2	1.740%	128253.08	9.38
P35520	sp|P35520|CBS_HUMAN Cystathionine beta-synthase OS=Homo sapiens OX=9606 GN=CBS PE=1 SV=2	CBS	2	2	2.180%	60585.85	6.2
P46459	sp|P46459|NSF_HUMAN Vesicle-fusing ATPase OS=Homo sapiens OX=9606 GN=NSF PE=1 SV=3	NSF	2	2	2.280%	82593.4	6.52
P49454	sp|P49454|CENPF_HUMAN Centromere protein F OS=Homo sapiens OX=9606 GN=CENPF PE=1 SV=3	CENPF	2	2	0.420%	357523.05	5.06
P52434	sp|P52434|RPAB3_HUMAN DNA-directed RNA polymerases I, II, and III subunit RPABC3 OS=Homo sapiens OX=9606 GN=POLR2H PE=1 SV=4	POLR2H	2	2	16.670%	17143.1	4.5
P53618	sp|P53618|COPB_HUMAN Coatomer subunit beta OS=Homo sapiens OX=9606 GN=COPB1 PE=1 SV=3	COPB1	2	2	1.780%	107141.04	5.72
P58107	sp|P58107|EPIPL_HUMAN Epiplakin OS=Homo sapiens OX=9606 GN=EPPK1 PE=1 SV=3	EPPK1	2	2	0.690%	555651.44	5.45

P61160	sp|P61160|ARP2_HUMAN Actin-related protein 2 OS=Homo sapiens OX=9606 GN=ACTR2 PE=1 SV=1	ACTR2	2	2	3.050%	44760.27	6.29
P62854	sp|P62854|RS26_HUMAN 40S ribosomal protein S26 OS=Homo sapiens OX=9606 GN=RPS26 PE=1 SV=3	RPS26	2	2	18.260%	13015.29	11.01
Q06265	sp|Q06265|EXOS9_HUMAN Exosome complex component RRP45 OS=Homo sapiens OX=9606 GN=EXOSC9 PE=1 SV=3	EXOSC9	2	2	5.010%	48948.49	5.19
Q09161	sp|Q09161|NCBP1_HUMAN Nuclear cap-binding protein subunit 1 OS=Homo sapiens OX=9606 GN=NCBP1 PE=1 SV=1	NCBP1	2	2	2.780%	91838.39	5.99
Q13045	sp|Q13045|FLII_HUMAN Protein flightless-1 homolog OS=Homo sapiens OX=9606 GN=FLII PE=1 SV=2	FLII	2	2	1.340%	144749.47	5.75
Q13162	sp|Q13162|PRDX4_HUMAN Peroxiredoxin-4 OS=Homo sapiens OX=9606 GN=PRDX4 PE=1 SV=1	PRDX4	2	2	8.860%	30539.52	5.86
Q13257	sp|Q13257|MD2L1_HUMAN Mitotic spindle assembly checkpoint protein MAD2A OS=Homo sapiens OX=9606 GN=MAD2L1 PE=1 SV=1	MAD2L1	2	2	6.340%	23509.66	5.02
Q13415	sp|Q13415|ORC1_HUMAN Origin recognition complex subunit 1 OS=Homo sapiens OX=9606 GN=ORC1 PE=1 SV=2	ORC1	2	2	1.280%	97348.59	9.34
Q13523	sp|Q13523|PRP4B_HUMAN Serine/threonine-protein kinase PRP4 homolog OS=Homo sapiens OX=9606 GN=PRPF4B PE=1 SV=3	PRPF4B	2	2	2.380%	116985.48	10.26
Q13601	sp|Q13601|KRR1_HUMAN KRR1 small subunit processome component homolog OS=Homo sapiens OX=9606 GN=KRR1 PE=1 SV=4	KRR1	2	2	4.200%	43664.43	9.78
Q14004	sp|Q14004|CDK13_HUMAN Cyclin-dependent kinase 13 OS=Homo sapiens OX=9606 GN=CDK13 PE=1 SV=2	CDK13	2	2	1.190%	164921.24	9.71
Q14244	sp|Q14244|MAP7_HUMAN Ensconsin OS=Homo sapiens OX=9606 GN=MAP7 PE=1 SV=1	MAP7	2	2	2.670%	84050.76	9.62
Q14571	sp|Q14571|ITPR2_HUMAN Inositol 1,4,5-trisphosphate receptor type 2 OS=Homo sapiens OX=9606 GN=ITPR2 PE=1 SV=2	ITPR2	2	2	0.480%	308060.24	6.01

Q15084	sp|Q15084|PDIA6_HUMAN Protein disulfide-isomerase A6 OS=Homo sapiens OX=9606 GN=PDIA6 PE=1 SV=1	PDIA6	2	2	5.680%	48120.74	4.95
Q15349	sp|Q15349|KS6A2_HUMAN Ribosomal protein S6 kinase alpha-2 OS=Homo sapiens OX=9606 GN=RPS6KA2 PE=1 SV=2	RPS6KA2	2	2	1.770%	83237.79	8.82
Q15365	sp|Q15365|PCBP1_HUMAN Poly(rC)-binding protein 1 OS=Homo sapiens OX=9606 GN=PCBP1 PE=1 SV=2	PCBP1	2	2	7.580%	37497.43	6.66
Q15746	sp|Q15746|MYLK_HUMAN Myosin light chain kinase, smooth muscle OS=Homo sapiens OX=9606 GN=MYLK PE=1 SV=4	MYLK	2	2	0.680%	210712.65	5.85
Q16181	sp|Q16181|SEPT7_HUMAN Septin-7 OS=Homo sapiens OX=9606 GN=SEPTIN7 PE=1 SV=2	SEPTIN7	2	2	4.120%	50679.38	8.76
Q16513	sp|Q16513|PKN2_HUMAN Serine/threonine-protein kinase N2 OS=Homo sapiens OX=9606 GN=PKN2 PE=1 SV=1	PKN2	2	2	1.520%	112033.31	5.95
Q32MK0	sp|Q32MK0|MYLK3_HUMAN Myosin light chain kinase 3 OS=Homo sapiens OX=9606 GN=MYLK3 PE=1 SV=3	MYLK3	2	2	1.830%	88391.85	5.76
Q4G0J3	sp|Q4G0J3|LARP7_HUMAN La-related protein 7 OS=Homo sapiens OX=9606 GN=LARP7 PE=1 SV=1	LARP7	2	2	2.580%	66897.85	9.57
Q53GS9	sp|Q53GS9|SNUT2_HUMAN U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens OX=9606 GN=USP39 PE=1 SV=2	USP39	2	2	2.480%	65379.72	9.02
Q5CZC0	sp|Q5CZC0|FSIP2_HUMAN Fibrous sheath-interacting protein 2 OS=Homo sapiens OX=9606 GN=FSIP2 PE=2 SV=4	FSIP2	2	2	0.190%	780598.32	6.27
Q5JQF8	sp|Q5JQF8|PAP1M_HUMAN Polyadenylate-binding protein 1-like 2 OS=Homo sapiens OX=9606 GN=PABPC1L2A PE=2 SV=1	PABPC1L2A	2	2	10.000%	22798.78	9.18
Q5SRE5	sp|Q5SRE5|NU188_HUMAN Nucleoporin NUP188 OS=Homo sapiens OX=9606 GN=NUP188 PE=1 SV=1	NUP188	2	2	1.600%	196040.82	6.27
Q69YN4	sp|Q69YN4|VIR_HUMAN Protein virilizer homolog OS=Homo sapiens OX=9606 GN=VIRMA PE=1 SV=2	VIRMA	2	2	1.160%	202022.63	4.9

Q6P2E9	sp|Q6P2E9|EDC4_HUMAN Enhancer of mRNA-decapping protein 4 OS=Homo sapiens OX=9606 GN=EDC4 PE=1 SV=1	EDC4	2	2	2.210%	151659.5	5.55
Q6UB35	sp|Q6UB35|C1TM_HUMAN Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Homo sapiens OX=9606 GN=MTHFD1L PE=1 SV=1	MTHFD1L	2	2	1.640%	105788.72	8.32
Q7Z3K3	sp|Q7Z3K3|POGZ_HUMAN Pogo transposable element with ZNF domain OS=Homo sapiens OX=9606 GN=POGZ PE=1 SV=2	POGZ	2	2	1.770%	155341.98	7.14
Q8IV32	sp|Q8IV32|CCD71_HUMAN Coiled-coil domain-containing protein 71 OS=Homo sapiens OX=9606 GN=CCDC71 PE=1 SV=3	CCDC71	2	2	3.850%	49647.53	11.8
Q8IVL1	sp|Q8IVL1|NAV2_HUMAN Neuron navigator 2 OS=Homo sapiens OX=9606 GN=NAV2 PE=1 SV=3	NAV2	2	2	0.440%	268164.34	9.13
Q8IYA6	sp|Q8IYA6|CKP2L_HUMAN Cytoskeleton-associated protein 2-like OS=Homo sapiens OX=9606 GN=CKAP2L PE=1 SV=4	CKAP2L	2	2	2.010%	83585.65	9.84
Q8N3K9	sp|Q8N3K9|CMYA5_HUMAN Cardiomyopathy-associated protein 5 OS=Homo sapiens OX=9606 GN=CMYA5 PE=1 SV=3	CMYA5	2	2	0.390%	449205.58	4.73
Q8N9T8	sp|Q8N9T8|KRI1_HUMAN Protein KRI1 homolog OS=Homo sapiens OX=9606 GN=KRI1 PE=1 SV=3	KRI1	2	2	4.130%	82597.07	5.06
Q8TEX9	sp|Q8TEX9|IPO4_HUMAN Importin-4 OS=Homo sapiens OX=9606 GN=IPO4 PE=1 SV=2	IPO4	2	2	1.850%	118713.99	4.88
Q8WUM0	sp|Q8WUM0|NU133_HUMAN Nuclear pore complex protein Nup133 OS=Homo sapiens OX=9606 GN=NUP133 PE=1 SV=2	NUP133	2	2	1.120%	128977.5	4.98
Q969X6	sp|Q969X6|UTP4_HUMAN U3 small nucleolar RNA-associated protein 4 homolog OS=Homo sapiens OX=9606 GN=UTP4 PE=1 SV=1	UTP4	2	2	4.960%	76889.31	9.03
Q96P70	sp|Q96P70|IPO9_HUMAN Importin-9 OS=Homo sapiens OX=9606 GN=IPO9 PE=1 SV=3	IPO9	2	2	2.790%	115961.54	4.71
Q96PY6	sp|Q96PY6|NEK1_HUMAN Serine/threonine-protein kinase Nek1 OS=Homo sapiens OX=9606 GN=NEK1 PE=1 SV=2	NEK1	2	2	1.030%	142826.71	5.67

Q96SB4	sp|Q96SB4|SRPK1_HUMAN SRSF protein kinase 1 OS=Homo sapiens OX=9606 GN=SRPK1 PE=1 SV=2	SRPK1	2	2	2.750%	74323.92	5.81
Q99714	sp|Q99714|HCD2_HUMAN 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens OX=9606 GN=HSD17B10 PE=1 SV=3	HSD17B10	2	2	11.880%	26922.78	7.65
Q9BQA1	sp|Q9BQA1|MEP50_HUMAN Methylosome protein 50 OS=Homo sapiens OX=9606 GN=WDR77 PE=1 SV=1	WDR77	2	2	6.430%	36723.97	5.03
Q9BTC0	sp|Q9BTC0|DIDO1_HUMAN Death-inducer obliterator 1 OS=Homo sapiens OX=9606 GN=DIDO1 PE=1 SV=5	DIDO1	2	2	1.290%	243869.76	8.09
Q9BV38	sp|Q9BV38|WDR18_HUMAN WD repeat-containing protein 18 OS=Homo sapiens OX=9606 GN=WDR18 PE=1 SV=2	WDR18	2	2	4.860%	47404.72	6.21
Q9BZI7	sp|Q9BZI7|REN3B_HUMAN Regulator of nonsense transcripts 3B OS=Homo sapiens OX=9606 GN=UPF3B PE=1 SV=1	UPF3B	2	2	4.760%	57761.35	9.48
Q9C0C9	sp|Q9C0C9|UBE2O_HUMAN (E3-independent) E2 ubiquitin-conjugating enzyme OS=Homo sapiens OX=9606 GN=UBE2O PE=1 SV=3	UBE2O	2	2	1.320%	141291.84	5.01
Q9H3P7	sp|Q9H3P7|GCP60_HUMAN Golgi resident protein GCP60 OS=Homo sapiens OX=9606 GN=ACBD3 PE=1 SV=4	ACBD3	2	2	5.490%	60592.67	5.02
Q9H501	sp|Q9H501|ESF1_HUMAN ESF1 homolog OS=Homo sapiens OX=9606 GN=ESF1 PE=1 SV=1	ESF1	2	2	2.470%	98794.99	5.01
Q9H6K5	sp|Q9H6K5|PRR36_HUMAN Proline-rich protein 36 OS=Homo sapiens OX=9606 GN=PRR36 PE=1 SV=2	PRR36	2	2	2.150%	132746.47	10.48
Q9H7B2	sp|Q9H7B2|RPF2_HUMAN Ribosome production factor 2 homolog OS=Homo sapiens OX=9606 GN=RPF2 PE=1 SV=2	RPF2	2	2	8.820%	35582.45	10
Q9NWH9	sp|Q9NWH9|SLTM_HUMAN SAFB-like transcription modulator OS=Homo sapiens OX=9606 GN=SLTM PE=1 SV=2	SLTM	2	2	2.320%	117147.01	7.69
Q9NZB2	sp|Q9NZB2|F120A_HUMAN Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens OX=9606 GN=FAM120A PE=1 SV=2	FAM120A	2	2	2.770%	121886.3	9.07

Q9UBU9	sp|Q9UBU9|NXF1_HUMAN Nuclear RNA export factor 1 OS=Homo sapiens OX=9606 GN=NXF1 PE=1 SV=1	NXF1	2	2	3.230%	70181.53	8.74
Q9UKI8	sp|Q9UKI8|TLK1_HUMAN Serine/threonine-protein kinase tousled-like 1 OS=Homo sapiens OX=9606 GN=TLK1 PE=1 SV=2	TLK1	2	2	1.700%	86698.62	8.88
Q9UPZ9	sp|Q9UPZ9|CILK1_HUMAN Serine/threonine-protein kinase ICK OS=Homo sapiens OX=9606 GN=CILK1 PE=1 SV=1	CILK1	2	2	2.060%	71425.88	9.79
Q9Y4W6	sp|Q9Y4W6|AFG32_HUMAN AFG3-like protein 2 OS=Homo sapiens OX=9606 GN=AFG3L2 PE=1 SV=2	AFG3L2	2	2	2.130%	88582.61	8.81
Q9Y6M1	sp|Q9Y6M1|IF2B2_HUMAN Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens OX=9606 GN=IGF2BP2 PE=1 SV=2	IGF2BP2	2	2	5.010%	66120.59	8.48
A0A024QZW2	tr|A0A024QZW2|A0A024QZW2_HUMAN Nucleolar protein 7, 27kDa, isoform CRA_a OS=Homo sapiens OX=9606 GN=NOL7 PE=4 SV=1	NOL7	2	2	6.230%	29426.04	9.68
A0A024QZW7	tr|A0A024QZW7|A0A024QZW7_HUMAN Nucleoporin 153kDa, isoform CRA_a OS=Homo sapiens OX=9606 GN=NUP153 PE=4 SV=1	NUP153	2	2	1.690%	153966.62	8.97
A0A024QZY3	tr|A0A024QZY3|A0A024QZY3_HUMAN Family with sequence similarity 50, member B, isoform CRA_a OS=Homo sapiens OX=9606 GN=FAM50B PE=4 SV=1	FAM50B	2	2	6.770%	38708.22	8.9
A0A024R222	tr|A0A024R222|A0A024R222_HUMAN Phosphoserine aminotransferase OS=Homo sapiens OX=9606 GN=PSAT1 PE=3 SV=1	PSAT1	2	2	5.410%	40422.21	7.56
A0A024R3G0	tr|A0A024R3G0|A0A024R3G0_HUMAN Hypoxia up-regulated 1, isoform CRA_a OS=Homo sapiens OX=9606 GN=HYOU1 PE=3 SV=1	HYOU1	2	2	3.700%	48984.27	9.69
A0A024R3J7	tr|A0A024R3J7|A0A024R3J7_HUMAN Dolichyl-diphosphooligosaccharide--protein glycotransferase OS=Homo sapiens OX=9606 GN=hCG_2032701 PE=3 SV=1	hCG_20327	2	2	2.700%	80427.56	7.88
A0A024R663	tr|A0A024R663|A0A024R663_HUMAN Kinectin 1 (Kinesin receptor), isoform CRA_a OS=Homo sapiens OX=9606 GN=KTN1 PE=4 SV=1	KTN1	2	2	1.030%	156273.39	5.52
A0A024R704	tr|A0A024R704|A0A024R704_HUMAN SFRS protein kinase 2, isoform CRA_b OS=Homo sapiens OX=9606 GN=SRPK2 PE=4 SV=1	SRPK2	2	2	3.050%	77525.77	4.87

A0A024R7X0	tr|A0A024R7X0|A0A024R7X0_HUMAN ADP-ribosylation factor guanine nucleotide-exchange factor 1(Brefeldin A-inhibited), isoform CRA_a OS=Homo sapiens OX=9606 GN=ARFGEF1 PE=4 SV=1	ARFGEF1	2	2	1.030%	208764.73	5.58
A0A087WV90	tr|A0A087WV90|A0A087WV90_HUMAN Dystrophin OS=Homo sapiens OX=9606 GN=DMD PE=1 SV=2	DMD	2	2	0.510%	271065.17	6
A0A087WVR3	tr|A0A087WVR3|A0A087WVR3_HUMAN RING-type E3 ubiquitin transferase OS=Homo sapiens OX=9606 GN=UHRF1 PE=1 SV=1	UHRF1	2	2	2.230%	91099.41	7.42
A0A087WZ11	tr|A0A087WZ11|A0A087WZ11_HUMAN Putative ATP-dependent RNA helicase DHX57 OS=Homo sapiens OX=9606 GN=DHX57 PE=1 SV=1	DHX57	2	2	3.810%	54082.29	5.09
A0A0B4J1W3	tr|A0A0B4J1W3|A0A0B4J1W3_HUMAN N-alpha-acetyltransferase 15, NatA auxiliary subunit OS=Homo sapiens OX=9606 GN=NAA15 PE=1 SV=1	NAA15	2	2	1.970%	101200.22	7.23
A0A0S2Z3G5	tr|A0A0S2Z3G5|A0A0S2Z3G5_HUMAN Caspase 10 apoptosis-related cysteine peptidase isoform 3 (Fragment) OS=Homo sapiens OX=9606 GN=CASP10 PE=2 SV=1	CASP10	2	2	2.090%	54565.23	5.97
A0A0S2Z3L2	tr|A0A0S2Z3L2|A0A0S2Z3L2_HUMAN P-type Ca(2+) transporter (Fragment) OS=Homo sapiens OX=9606 GN=ATP2A2 PE=2 SV=1	ATP2A2	2	2	2.690%	114755.63	5.23
A0A140TA25	tr|A0A140TA25|A0A140TA25_HUMAN Unconventional myosin-Ih OS=Homo sapiens OX=9606 GN=MYO1H PE=1 SV=1	MYO1H	2	2	1.250%	119980.32	9.24
A0A140VK70	tr|A0A140VK70|A0A140VK70_HUMAN 26S proteasome AAA-ATPase subunit RPT1 OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	2.770%	48633.3	5.71
A0A1B0GVU9	tr|A0A1B0GVU9|A0A1B0GVU9_HUMAN Glutaminyl-tRNA synthetase (Fragment) OS=Homo sapiens OX=9606 GN=QARS1 PE=1 SV=1	QARS1	2	2	2.580%	83782.2	7.19
A0A1L2BU38	tr|A0A1L2BU38|A0A1L2BU38_HUMAN Anti-staphylococcal enterotoxin E heavy chain variable region (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	14.400%	13601.04	9.01
A0A1W2PQ90	tr|A0A1W2PQ90|A0A1W2PQ90_HUMAN Zinc-hook domain-containing protein OS=Homo sapiens OX=9606 PE=3 SV=2		2	2	2.310%	142939.87	6.34

A0A286YF78	tr|A0A286YF78|A0A286YF78_HUMAN D-3-phosphoglycerate dehydrogenase (Fragment) OS=Homo sapiens OX=9606 GN=PHGDH PE=1 SV=1	PHGDH	2	2	6.880%	29580.95	8.4
A0A2R8YF43	tr|A0A2R8YF43|A0A2R8YF43_HUMAN Casein kinase II subunit alpha OS=Homo sapiens OX=9606 GN=CSNK2A1 PE=1 SV=1	CSNK2A1	2	2	7.440%	41790.2	7.19
A0A2U8J9D3	tr|A0A2U8J9D3|A0A2U8J9D3_HUMAN Ig heavy chain variable region (Fragment) OS=Homo sapiens OX=9606 GN=IgH PE=2 SV=1	IgH	2	2	16.000%	11463.85	7.97
A0A384P5W4	tr|A0A384P5W4|A0A384P5W4_HUMAN Epididymis secretory sperm binding protein OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	1.330%	186463.43	8.06
A0A3B3IT82	tr|A0A3B3IT82|A0A3B3IT82_HUMAN DNA helicase OS=Homo sapiens OX=9606 GN=BLM PE=1 SV=1	BLM	2	2	1.300%	156041.37	6.68
A0A4E0W6L3	tr|A0A4E0W6L3|A0A4E0W6L3_HUMAN AEP5A5 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	14.170%	13789.31	9.3
A0A590UJC4	tr|A0A590UJC4|A0A590UJC4_HUMAN Cullin-1 OS=Homo sapiens OX=9606 GN=CUL1 PE=1 SV=1	CUL1	2	2	2.650%	78372.83	8.83
A0A5C2G3H8	tr|A0A5C2G3H8|A0A5C2G3H8_HUMAN IGL c3679_light_IGKV4-1_IGKJ3 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	21.240%	12484.77	7.93
A0A5C2G7I4	tr|A0A5C2G7I4|A0A5C2G7I4_HUMAN IGH c572_heavy__IGHV3-21_IGHD5-18_IGHJ5 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	20.340%	12675.08	5.28
A0A5C2G8K2	tr|A0A5C2G8K2|A0A5C2G8K2_HUMAN IGH + IGL c124_heavy_IGHV3-43_IGHD6-13_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	9.240%	13253.67	5.26
A0A5C2GAD3	tr|A0A5C2GAD3|A0A5C2GAD3_HUMAN IGH c235_heavy__IGHV3-23_IGHD3-10_IGHJ5 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	15.630%	13899.17	4.79
A0A5C2GDW3	tr|A0A5C2GDW3|A0A5C2GDW3_HUMAN IGH + IGL c109_heavy_IGHV3-11_IGHD3-10_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	19.830%	13347.8	8.58
A0A5C2GG06	tr|A0A5C2GG06|A0A5C2GG06_HUMAN IG c1119_heavy_IGHV3-33_IGHD2-8_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	8.550%	13077.59	9.2

A0A5C2GHA7	tr|A0A5C2GHA7|A0A5C2GHA7_HUMAN IG c248_heavy_IGHV3-9_IGHD1-26_IGHJ3 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	19.670%	13415.91	7.09
A0A5C2GHD2	tr|A0A5C2GHD2|A0A5C2GHD2_HUMAN IGH + IGL c145_heavy_IGHV3-15_IGHD3-10_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	19.670%	13266.79	7
A0A5C2GMG8	tr|A0A5C2GMG8|A0A5C2GMG8_HUMAN IG c919_light_IGKV2-24_IGKJ2 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	10.710%	12318.85	9.44
A0A5C2GNS8	tr|A0A5C2GNS8|A0A5C2GNS8_HUMAN IG c400_heavy_IGHV3-49_IGHD5-18_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	11.670%	13132.61	8.64
A0A5C2GQE3	tr|A0A5C2GQE3|A0A5C2GQE3_HUMAN IG c1552_heavy_IGHV3-49_IGHD2-15_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	16.390%	13378.79	8.05
A0A5C2GSE6	tr|A0A5C2GSE6|A0A5C2GSE6_HUMAN IG c237_light_IGKV4-1_IGKJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	17.540%	12582.92	7.93
A0A5C2GUC4	tr|A0A5C2GUC4|A0A5C2GUC4_HUMAN IG c542_light_IGKV2D-29_IGKJ3 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	17.860%	12190.66	6.91
A0A5C2GUY1	tr|A0A5C2GUY1|A0A5C2GUY1_HUMAN IG c1609_heavy_IGHV3-21_IGHD3-10_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	20.000%	13042.33	8.57
A0A5C2GWE8	tr|A0A5C2GWE8|A0A5C2GWE8_HUMAN IG c769_light_IGKV1-5_IGKJ1 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	15.530%	11346.66	9.1
A0A5C2GY22	tr|A0A5C2GY22|A0A5C2GY22_HUMAN IG c1517_heavy_IGHV3-33_IGHD2-2_IGHJ6 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	18.900%	14038.61	8.84
A0A5C2GYK2	tr|A0A5C2GYK2|A0A5C2GYK2_HUMAN IG c1707_heavy_IGHV3-15_IGHD1-7_IGHJ5 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	11.570%	13202.73	8.67
A0A5F9ZI57	tr|A0A5F9ZI57|A0A5F9ZI57_HUMAN Ataxin-2 OS=Homo sapiens OX=9606 GN=ATXN2 PE=1 SV=1	ATXN2	2	2	1.820%	124586.52	9.21
A0A7I2V3Z0	tr|A0A7I2V3Z0|A0A7I2V3Z0_HUMAN ATP-dependent 6-phosphofructokinase OS=Homo sapiens OX=9606 GN=PFKP PE=1 SV=1	PFKP	2	2	2.820%	81798.95	7.49

A0A7I2V508	tr|A0A7I2V508|A0A7I2V508_HUMAN BCL2-associated athanogene 6 OS=Homo sapiens OX=9606 GN=BAG6 PE=1 SV=1	BAG6	2	2	1.960%	123451.04	5.45
A0A7P0T7V5	tr|A0A7P0T7V5|A0A7P0T7V5_HUMAN Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens OX=9606 GN=DYNC1H1 PE=1 SV=1	DYNC1H1	2	2	0.430%	505962.39	5.97
A0A7P0TA83	tr|A0A7P0TA83|A0A7P0TA83_HUMAN Reelin OS=Homo sapiens OX=9606 GN=RELN PE=1 SV=1	RELN	2	2	0.430%	388612.89	5.5
A0A7P0Z497	tr|A0A7P0Z497|A0A7P0Z497_HUMAN Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens OX=9606 GN=PPIB PE=1 SV=1	PPIB	2	2	8.290%	20209.98	9.19
A0A7S5BZ66	tr|A0A7S5BZ66|A0A7S5BZ66_HUMAN IGH c1208_heavy_IGHV3-33_IGHD3-22_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	16.260%	13697.22	8.53
A0A7S5BZX9	tr|A0A7S5BZX9|A0A7S5BZX9_HUMAN IGH c1628_heavy_IGHV3-15_IGHD2-21_IGHJ5 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	16.810%	12829.38	8.05
A0A7S5C2L8	tr|A0A7S5C2L8|A0A7S5C2L8_HUMAN IGH c3058_heavy_IGHV3-48_IGHD5-12_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	11.290%	13627.99	8.01
A0A804CBC2	tr|A0A804CBC2|A0A804CBC2_HUMAN Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=BAIAP2L2 PE=4 SV=1	BAIAP2L2	2	2	2.470%	43902.91	10.11
A0MNN4	tr|A0MNN4|A0MNN4_HUMAN CDW3/SMU1 OS=Homo sapiens OX=9606 GN=SMU1 PE=2 SV=1	SMU1	2	2	3.700%	57543.25	6.74
A2J1N8	tr|A2J1N8|A2J1N8_HUMAN Rheumatoid factor RF-ET11 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	17.890%	10208.35	9.39
A8K0T9	tr|A8K0T9|A8K0T9_HUMAN F-actin-capping protein subunit alpha OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	6.290%	32908.34	5.44
A8K494	tr|A8K494|A8K494_HUMAN Lactotransferrin OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	2.950%	78367.33	8.56

A8K6Q8	tr|A8K6Q8|A8K6Q8_HUMAN Transferrin receptor protein 1 OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	3.030%	84872.31	6.18
A9CP04	tr|A9CP04|A9CP04_HUMAN Non-specific serine/threonine protein kinase OS=Homo sapiens OX=9606 GN=Par1b PE=2 SV=1	Par1b	2	2	3.580%	78422.3	9.56
B2RDD7	tr|B2RDD7|B2RDD7_HUMAN Protein arginine N-methyltransferase 5 OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	2.510%	72709.1	5.88
B3KMZ6	tr|B3KMZ6|B3KMZ6_HUMAN SUMO-activating enzyme subunit 2 OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	3.750%	71160.64	5.15
B3KN57	tr|B3KN57|B3KN57_HUMAN Sorting nexin-2 OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	3.080%	58451.37	5.07
B3KS60	tr|B3KS60|B3KS60_HUMAN cDNA FLJ35566 fis, clone SPLEN2005474, highly similar to Homo sapiens CCR4-NOT transcription complex, subunit 1 (CNOT1), transcript variant 1, mRNA OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	6.050%	36049.54	7.16
B3KW21	tr|B3KW21|B3KW21_HUMAN cDNA FLJ41945 fis, clone PLACE6019676, highly similar to Coatomer subunit gamma OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	4.590%	67803.98	4.93
B4DKS0	tr|B4DKS0|B4DKS0_HUMAN Monocarboxylate transporter 1 OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	6.880%	51836.06	8.78
B4DMG8	tr|B4DMG8|B4DMG8_HUMAN Glutamate dehydrogenase OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	3.390%	55699.81	7.23
B4DNW3	tr|B4DNW3|B4DNW3_HUMAN cDNA FLJ51914, highly similar to Protein DEK OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	5.410%	40160.11	8.94
B4DWC0	tr|B4DWC0|B4DWC0_HUMAN cDNA FLJ58290, highly similar to Zinc finger MYM-type protein 6 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	1.830%	96934.54	8.72
B4DWH5	tr|B4DWH5|B4DWH5_HUMAN Calcium-activated neutral proteinase 1 OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	2.420%	75834.58	5.95

B4DZM3	tr|B4DZM3|B4DZM3_HUMAN cDNA FLJ61500, highly similar to NNP-1 protein OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	4.950%	46150.35	6.39
B4E266	tr|B4E266|B4E266_HUMAN Leucyl-tRNA synthetase OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	2.210%	129186.78	7.89
B7XCW9	tr|B7XCW9|B7XCW9_HUMAN ATP-binding cassette transporter A1 OS=Homo sapiens OX=9606 GN=ABCA1 PE=2 SV=1	ABCA1	2	2	0.490%	254352.21	6.47
B7Z1V9	tr|B7Z1V9|B7Z1V9_HUMAN cDNA FLJ53310, highly similar to Puromycin-sensitive aminopeptidase OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	4.020%	53151.62	6.25
B7Z9D5	tr|B7Z9D5|B7Z9D5_HUMAN cDNA FLJ50387 OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	5.080%	49377.32	9.16
B7ZA13	tr|B7ZA13|B7ZA13_HUMAN Calcium-transporting ATPase OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	1.160%	103068.19	5.65
B8ZZS4	tr|B8ZZS4|B8ZZS4_HUMAN Ankyrin repeat and zinc finger domain-containing protein 1 OS=Homo sapiens OX=9606 GN=ANKZF1 PE=1 SV=1	ANKZF1	2	2	3.290%	57572.08	9.59
B8ZZW2	tr|B8ZZW2|B8ZZW2_HUMAN GRIP and coiled-coil domain-containing protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=GCC2 PE=1 SV=1	GCC2	2	2	1.420%	107097.06	4.86
C7DJS2	tr|C7DJS2|C7DJS2_HUMAN GST class-pi (Fragment) OS=Homo sapiens OX=9606 GN=GSTP1 PE=2 SV=1	GSTP1	2	2	16.560%	16666.82	4.89
D6W539	tr|D6W539|D6W539_HUMAN Hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (Trifunctional protein), beta subunit, isoform CRA_b OS=Homo sapiens OX=9606 GN=HADHB PE=4 SV=1	HADHB	2	2	4.030%	40413.49	9.81
E2PSM9	tr|E2PSM9|E2PSM9_HUMAN cDNA FLJ12599 fis, clone NT2RM4001410 OS=Homo sapiens OX=9606 PE=1 SV=1		2	2	4.110%	40834.36	4.66
E5RI93	tr|E5RI93|E5RI93_HUMAN Zinc finger homeobox protein 4 (Fragment) OS=Homo sapiens OX=9606 GN=ZFHX4 PE=1 SV=2	ZFHX4	2	2	0.840%	183150.85	5.68

E5RK37	tr|E5RK37|E5RK37_HUMAN Carbonic anhydrase 2 OS=Homo sapiens OX=9606 GN=CA2 PE=1 SV=1	CA2	2	2	24.750%	11495.54	6.22
E9PRR7	tr|E9PRR7|E9PRR7_HUMAN Protein FRG1 (Fragment) OS=Homo sapiens OX=9606 GN=FRG1 PE=1 SV=1	FRG1	2	2	19.830%	12515.96	5.14
F5GYK2	tr|F5GYK2|F5GYK2_HUMAN Striatin-4 OS=Homo sapiens OX=9606 GN=STRN4 PE=1 SV=1	STRN4	2	2	3.310%	68583.76	5.06
F6VDE0	tr|F6VDE0|F6VDE0_HUMAN Probable global transcription activator SNF2L2 OS=Homo sapiens OX=9606 GN=SMARCA2 PE=1 SV=2	SMARCA2	2	2	0.860%	172590.35	6.68
F8VVU1	tr|F8VVU1|F8VVU1_HUMAN Advillin (Fragment) OS=Homo sapiens OX=9606 GN=AVIL PE=1 SV=1	AVIL	2	2	9.550%	17864.93	6.05
H0Y2V6	tr|H0Y2V6|H0Y2V6_HUMAN Centrosomal protein of 170 kDa (Fragment) OS=Homo sapiens OX=9606 GN=CEP170 PE=1 SV=1	CEP170	2	2	1.410%	171971.12	6.92
H0Y5B5	tr|H0Y5B5|H0Y5B5_HUMAN Protein polybromo-1 (Fragment) OS=Homo sapiens OX=9606 GN=PBRM1 PE=1 SV=1	PBRM1	2	2	1.380%	126291.14	6.51
H0YHC3	tr|H0YHC3|H0YHC3_HUMAN Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens OX=9606 GN=NAP1L1 PE=1 SV=1	NAP1L1	2	2	10.610%	23417.35	4.75
H0YHX9	tr|H0YHX9|H0YHX9_HUMAN Nascent polypeptide-associated complex subunit alpha OS=Homo sapiens OX=9606 GN=NACA PE=1 SV=2	NACA	2	2	11.490%	25278.74	4.51
H0YMU9	tr|H0YMU9|H0YMU9_HUMAN Annexin OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=1	ANXA2	2	2	8.700%	25568.7	5.68
H2EHT1	tr|H2EHT1|H2EHT1_HUMAN Cellular tumor antigen p53 OS=Homo sapiens OX=9606 GN=TP53 PE=2 SV=1	TP53	2	2	6.210%	39319.97	8.01
H7C1K6	tr|H7C1K6|H7C1K6_HUMAN Interferon-induced protein 44-like (Fragment) OS=Homo sapiens OX=9606 GN=IFI44L PE=1 SV=1	IFI44L	2	2	4.740%	26479.11	8.54
I6L9I5	tr|I6L9I5|I6L9I5_HUMAN CDC2 protein OS=Homo sapiens OX=9606 GN=CDC2 PE=2 SV=1	CDC2	2	2	9.780%	25938.85	8.41

M1VE91	tr|M1VE91|M1VE91_HUMAN KIF5B-RET(NM_020630)_K24R11 fusion protein OS=Homo sapiens OX=9606 GN=KIF5B-RET(NM_020630)_K24;R11 PE=2 SV=1	KIF5B-RET(	2	2	1.680%	155814.18	6.14
Q2NL95	tr|Q2NL95|Q2NL95_HUMAN RNA helicase (Fragment) OS=Homo sapiens OX=9606 GN=DDX19B PE=2 SV=1	DDX19B	2	2	4.450%	50643.66	7.14
Q53F09	tr|Q53F09|Q53F09_HUMAN Karyopherin alpha 3 variant (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	3.650%	57745.25	4.9
Q53HG7	tr|Q53HG7|Q53HG7_HUMAN Cortactin isoform a variant (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	4.550%	61557.37	5.24
Q53T99	tr|Q53T99|Q53T99_HUMAN Ribosome biogenesis protein WDR12 OS=Homo sapiens OX=9606 GN=WDR12 PE=2 SV=1	WDR12	2	2	9.930%	47707.42	5.57
Q59E88	tr|Q59E88|Q59E88_HUMAN DnaJ (Hsp40) homolog, subfamily A, member 3 variant (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	3.970%	52285.82	9.37
Q59EL4	tr|Q59EL4|Q59EL4_HUMAN PRPF4 protein variant (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	3.350%	60021.32	7.38
Q5TBI2	tr|Q5TBI2|Q5TBI2_HUMAN Uncharacterized protein C1orf131 (Fragment) OS=Homo sapiens OX=9606 GN=C1orf131 PE=1 SV=1	C1orf131	2	2	6.640%	28477.44	10.1
Q6AI02	tr|Q6AI02|Q6AI02_HUMAN Uncharacterized protein DKFZp686P168 OS=Homo sapiens OX=9606 GN=DKFZp686P168 PE=2 SV=1	DKFZp686P	2	2	0.970%	141020.59	5.33
Q6FHU2	tr|Q6FHU2|Q6FHU2_HUMAN Phosphoglycerate mutase (Fragment) OS=Homo sapiens OX=9606 GN=PGAM1 PE=2 SV=1	PGAM1	2	2	6.300%	28803.59	6.67
Q6I7N8	tr|Q6I7N8|Q6I7N8_HUMAN Lymphoid specific helicase variant9 OS=Homo sapiens OX=9606 GN=HELLS PE=2 SV=1	HELLS	2	2	2.970%	93961.34	8.36
Q6PUJ7	tr|Q6PUJ7|Q6PUJ7_HUMAN Prohibitin OS=Homo sapiens OX=9606 GN=HEL-215 PE=2 SV=1	HEL-215	2	2	5.880%	29819.76	5.57
Q8IXG0	tr|Q8IXG0|Q8IXG0_HUMAN Crn protein OS=Homo sapiens OX=9606 GN=crn PE=2 SV=1	crn	2	2	3.350%	83138.47	6.59

Q96DI9	tr|Q96DI9|Q96DI9_HUMAN POLDIP3 protein (Fragment) OS=Homo sapiens OX=9606 GN=POLDIP3 PE=2 SV=2	POLDIP3	2	2	4.800%	45658.25	10.04
Q96N31	tr|Q96N31|Q96N31_HUMAN cDNA FLJ31473 fis, clone NT2NE2001530 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	2	1.500%	89723.79	8.71
Q9NZ23	tr|Q9NZ23|Q9NZ23_HUMAN Drug-sensitive protein 1 OS=Homo sapiens OX=9606 GN=YA61 PE=2 SV=1	YA61	2	2	16.180%	14866.62	6.83
Q9UK43	tr|Q9UK43|Q9UK43_HUMAN Chondrosarcoma-associated protein 2 OS=Homo sapiens OX=9606 GN=CSA2 PE=2 SV=1	CSA2	2	2	2.870%	65585.45	6.26
V9HWE0	tr|V9HWE0|V9HWE0_HUMAN Annexin OS=Homo sapiens OX=9606 GN=HEL-S-7 PE=2 SV=1	HEL-S-7	2	2	6.560%	35936.34	4.94
V9HWF2	tr|V9HWF2|V9HWF2_HUMAN Malate dehydrogenase OS=Homo sapiens OX=9606 GN=HEL-S-32 PE=2 SV=1	HEL-S-32	2	2	5.390%	36425.7	6.91
V9HWK1	tr|V9HWK1|V9HWK1_HUMAN Triosephosphate isomerase OS=Homo sapiens OX=9606 GN=HEL-S-49 PE=2 SV=1	HEL-S-49	2	2	8.840%	26669.17	6.45
Q8WUA2	sp|Q8WUA2|PPIL4_HUMAN Peptidyl-prolyl cis-trans isomerase-like 4 OS=Homo sapiens OX=9606 GN=PPIL4 PE=1 SV=1	PPIL4	1	1	2.850%	57224.41	5.63
Q8WUJ3	sp|Q8WUJ3|CEMIP_HUMAN Cell migration-inducing and hyaluronan-binding protein OS=Homo sapiens OX=9606 GN=CEMIP PE=1 SV=2	CEMIP	1	1	0.370%	152995.98	7.98
Q8WVF5	sp|Q8WVF5|KCTD4_HUMAN BTB/POZ domain-containing protein KCTD4 OS=Homo sapiens OX=9606 GN=KCTD4 PE=1 SV=2	KCTD4	1	1	2.320%	29967.02	6.62
Q8WWI1	sp|Q8WWI1|LMO7_HUMAN LIM domain only protein 7 OS=Homo sapiens OX=9606 GN=LMO7 PE=1 SV=3	LMO7	1	1	0.650%	192693.39	8.34
Q8WXD2	sp|Q8WXD2|SCG3_HUMAN Secretogranin-3 OS=Homo sapiens OX=9606 GN=SCG3 PE=1 SV=3	SCG3	1	1	2.140%	53004.67	4.94
Q92830	sp|Q92830|KAT2A_HUMAN Histone acetyltransferase KAT2A OS=Homo sapiens OX=9606 GN=KAT2A PE=1 SV=3	KAT2A	1	1	1.790%	93924.48	9.18

Q92859	sp|Q92859|NEO1_HUMAN Neogenin OS=Homo sapiens OX=9606 GN=NEO1 PE=1 SV=2	NEO1	1	1	0.680%	160014.65	6.08
Q92966	sp|Q92966|SNPC3_HUMAN snRNA-activating protein complex subunit 3 OS=Homo sapiens OX=9606 GN=SNAPC3 PE=1 SV=1	SNAPC3	1	1	1.950%	46752.2	5.12
Q96AE4	sp|Q96AE4|FUBP1_HUMAN Far upstream element-binding protein 1 OS=Homo sapiens OX=9606 GN=FUBP1 PE=1 SV=3	FUBP1	1	1	0.780%	67559.59	7.18
Q96EZ8	sp|Q96EZ8|MCRS1_HUMAN Microspherule protein 1 OS=Homo sapiens OX=9606 GN=MCRS1 PE=1 SV=1	MCRS1	1	1	2.600%	51802.7	9.41
Q96FC7	sp|Q96FC7|PHIPL_HUMAN Phytanoyl-CoA hydroxylase-interacting protein-like OS=Homo sapiens OX=9606 GN=PHYHIPL PE=1 SV=3	PHYHIPL	1	1	1.860%	42485.62	5.97
Q96JK2	sp|Q96JK2|DCAF5_HUMAN DDB1- and CUL4-associated factor 5 OS=Homo sapiens OX=9606 GN=DCAF5 PE=1 SV=2	DCAF5	1	1	0.740%	103962.1	5.48
Q96K76	sp|Q96K76|UBP47_HUMAN Ubiquitin carboxyl-terminal hydrolase 47 OS=Homo sapiens OX=9606 GN=USP47 PE=1 SV=3	USP47	1	1	0.440%	157309.52	4.97
Q96LI9	sp|Q96LI9|CX058_HUMAN Uncharacterized protein CXorf58 OS=Homo sapiens OX=9606 GN=CXorf58 PE=2 SV=2	CXorf58	1	1	2.110%	38899.01	10.19
Q96MG2	sp|Q96MG2|JSPR1_HUMAN Junctional sarcoplasmic reticulum protein 1 OS=Homo sapiens OX=9606 GN=JSRP1 PE=1 SV=1	JSRP1	1	1	2.420%	36318.24	9.43
Q96NL6	sp|Q96NL6|SCLT1_HUMAN Sodium channel and clathrin linker 1 OS=Homo sapiens OX=9606 GN=SCLT1 PE=1 SV=2	SCLT1	1	1	0.870%	80909.5	5.83
Q96NU0	sp|Q96NU0|CNT3B_HUMAN Contactin-associated protein-like 3B OS=Homo sapiens OX=9606 GN=CNTNAP3B PE=2 SV=3	CNTNAP3B	1	1	1.480%	140412.96	7.19
Q96QI5	sp|Q96QI5|HS3S6_HUMAN Heparan sulfate glucosamine 3-O-sulfotransferase 6 OS=Homo sapiens OX=9606 GN=HS3ST6 PE=1 SV=2	HS3ST6	1	1	2.630%	37185.61	10.8
Q96R84	sp|Q96R84|OR1F2_HUMAN Putative olfactory receptor 1F2 OS=Homo sapiens OX=9606 GN=OR1F2P PE=5 SV=2	OR1F2P	1	1	4.170%	34943.17	8.92

Q96TA1	sp|Q96TA1|NIBA2_HUMAN Protein Niban 2 OS=Homo sapiens OX=9606 GN=NIBAN2 PE=1 SV=3	NIBAN2	1	1	0.800%	84136.88	5.82
Q99496	sp|Q99496|RING2_HUMAN E3 ubiquitin-protein ligase RING2 OS=Homo sapiens OX=9606 GN=RNF2 PE=1 SV=1	RNF2	1	1	3.270%	37654.97	6.38
Q99525	sp|Q99525|H4G_HUMAN Histone H4-like protein type G OS=Homo sapiens OX=9606 GN=H4C7 PE=1 SV=1	H4C7	1	1	9.180%	11008.98	11.06
Q99549	sp|Q99549|MPP8_HUMAN M-phase phosphoprotein 8 OS=Homo sapiens OX=9606 GN=MPHOSPH8 PE=1 SV=2	MPHOSPH8	1	1	0.810%	97181.07	5.81
Q99615	sp|Q99615|DNJC7_HUMAN DnaJ homolog subfamily C member 7 OS=Homo sapiens OX=9606 GN=DNAJC7 PE=1 SV=2	DNAJC7	1	1	2.230%	56440.25	6.56
Q99767	sp|Q99767|APBA2_HUMAN Amyloid-beta A4 precursor protein-binding family A member 2 OS=Homo sapiens OX=9606 GN=APBA2 PE=1 SV=3	APBA2	1	1	0.800%	82511.21	4.77
Q9BSC4	sp|Q9BSC4|NOL10_HUMAN Nucleolar protein 10 OS=Homo sapiens OX=9606 GN=NOL10 PE=1 SV=1	NOL10	1	1	1.160%	80300.57	8.64
Q9BUT9	sp|Q9BUT9|MCRI2_HUMAN MAPK regulated corepressor interacting protein 2 OS=Homo sapiens OX=9606 GN=MCRIP2 PE=1 SV=2	MCRIP2	1	1	5.000%	17827.78	9.5
Q9BUY5	sp|Q9BUY5|ZN426_HUMAN Zinc finger protein 426 OS=Homo sapiens OX=9606 GN=ZNF426 PE=1 SV=1	ZNF426	1	1	2.170%	63105.36	7.96
Q9BW85	sp|Q9BW85|YJU2_HUMAN Splicing factor YJU2 OS=Homo sapiens OX=9606 GN=YJU2 PE=1 SV=1	YJU2	1	1	1.860%	37085.36	5.75
Q9BXJ2	sp|Q9BXJ2|C1QT7_HUMAN Complement C1q tumor necrosis factor-related protein 7 OS=Homo sapiens OX=9606 GN=C1QTNF7 PE=2 SV=1	C1QTNF7	1	1	2.420%	30682.98	5.11
Q9BXN1	sp|Q9BXN1|ASPN_HUMAN Asporin OS=Homo sapiens OX=9606 GN=ASPN PE=1 SV=2	ASPN	1	1	2.630%	43416.69	6.61
Q9BXY0	sp|Q9BXY0|MAK16_HUMAN Protein MAK16 homolog OS=Homo sapiens OX=9606 GN=MAK16 PE=1 SV=2	MAK16	1	1	4.330%	35368.2	5.27

Q9BY44	sp|Q9BY44|EIF2A_HUMAN Eukaryotic translation initiation factor 2A OS=Homo sapiens OX=9606 GN=EIF2A PE=1 SV=3	EIF2A	1	1	1.540%	64989.32	9.01
Q9BYD6	sp|Q9BYD6|RM01_HUMAN 39S ribosomal protein L1, mitochondrial OS=Homo sapiens OX=9606 GN=MRPL1 PE=1 SV=2	MRPL1	1	1	5.230%	36908.27	8.88
Q9BYG3	sp|Q9BYG3|MK67I_HUMAN MKI67 FHA domain-interacting nucleolar phosphoprotein OS=Homo sapiens OX=9606 GN=NIFK PE=1 SV=1	NIFK	1	1	4.780%	34221.78	9.88
Q9C093	sp|Q9C093|SPEF2_HUMAN Sperm flagellar protein 2 OS=Homo sapiens OX=9606 GN=SPEF2 PE=1 SV=2	SPEF2	1	1	0.490%	209808.29	5.4
Q9GZT8	sp|Q9GZT8|NIF3L_HUMAN NIF3-like protein 1 OS=Homo sapiens OX=9606 GN=NIF3L1 PE=1 SV=2	NIF3L1	1	1	1.590%	41967.57	6.19
Q9GZW5	sp|Q9GZW5|SCND2_HUMAN Putative SCAN domain-containing protein SCAND2P OS=Homo sapiens OX=9606 GN=SCAND2P PE=5 SV=2	SCAND2P	1	1	2.610%	34216.68	10.67
Q9H422	sp|Q9H422|HIPK3_HUMAN Homeodomain-interacting protein kinase 3 OS=Homo sapiens OX=9606 GN=HIPK3 PE=1 SV=1	HIPK3	1	1	0.490%	133741.64	7.16
Q9H7T3	sp|Q9H7T3|CJ095_HUMAN Uncharacterized protein C10orf95 OS=Homo sapiens OX=9606 GN=C10orf95 PE=1 SV=1	C10orf95	1	1	3.500%	26269.61	11.69
Q9H967	sp|Q9H967|WDR76_HUMAN WD repeat-containing protein 76 OS=Homo sapiens OX=9606 GN=WDR76 PE=1 SV=2	WDR76	1	1	1.760%	69768.47	9.35
Q9HB71	sp|Q9HB71|CYBP_HUMAN Calcyclin-binding protein OS=Homo sapiens OX=9606 GN=CACYBP PE=1 SV=2	CACYBP	1	1	3.070%	26209.63	8.28
Q9HCD5	sp|Q9HCD5|NCOA5_HUMAN Nuclear receptor coactivator 5 OS=Homo sapiens OX=9606 GN=NCOA5 PE=1 SV=2	NCOA5	1	1	2.590%	65535.72	9.62
Q9HCM2	sp|Q9HCM2|PLXA4_HUMAN Plexin-A4 OS=Homo sapiens OX=9606 GN=PLXNA4 PE=1 SV=4	PLXNA4	1	1	0.260%	212452.68	6.42
Q9HD43	sp|Q9HD43|PTPRH_HUMAN Receptor-type tyrosine-protein phosphatase H OS=Homo sapiens OX=9606 GN=PTPRH PE=1 SV=4	PTPRH	1	1	0.630%	122351.51	5.16

Q9NPF5	sp|Q9NPF5|DMAP1_HUMAN DNA methyltransferase 1-associated protein 1 OS=Homo sapiens OX=9606 GN=DMAP1 PE=1 SV=1	DMAP1	1	1	2.570%	52991.95	9.51
Q9NTJ4	sp|Q9NTJ4|MA2C1_HUMAN Alpha-mannosidase 2C1 OS=Homo sapiens OX=9606 GN=MAN2C1 PE=1 SV=1	MAN2C1	1	1	0.670%	115833.89	6.1
Q9NUP9	sp|Q9NUP9|LIN7C_HUMAN Protein lin-7 homolog C OS=Homo sapiens OX=9606 GN=LIN7C PE=1 SV=1	LIN7C	1	1	3.050%	21833.72	8.52
Q9NVH1	sp|Q9NVH1|DJC11_HUMAN DnaJ homolog subfamily C member 11 OS=Homo sapiens OX=9606 GN=DNAJC11 PE=1 SV=2	DNAJC11	1	1	1.610%	63277.32	8.54
Q9NWU2	sp|Q9NWU2|GID8_HUMAN Glucose-induced degradation protein 8 homolog OS=Homo sapiens OX=9606 GN=GID8 PE=1 SV=1	GID8	1	1	4.820%	26748.26	4.92
Q9NY12	sp|Q9NY12|GAR1_HUMAN H/ACA ribonucleoprotein complex subunit 1 OS=Homo sapiens OX=9606 GN=GAR1 PE=1 SV=1	GAR1	1	1	3.230%	22347.61	10.91
Q9NY61	sp|Q9NY61|AATF_HUMAN Protein AATF OS=Homo sapiens OX=9606 GN=AATF PE=1 SV=1	AATF	1	1	2.500%	63132.18	4.83
Q9NY93	sp|Q9NY93|DDX56_HUMAN Probable ATP-dependent RNA helicase DDX56 OS=Homo sapiens OX=9606 GN=DDX56 PE=1 SV=1	DDX56	1	1	2.560%	61588.79	9.34
Q9NYS7	sp|Q9NYS7|WSB2_HUMAN WD repeat and SOCS box-containing protein 2 OS=Homo sapiens OX=9606 GN=WSB2 PE=2 SV=1	WSB2	1	1	1.730%	45285.65	8.36
Q9P241	sp|Q9P241|AT10D_HUMAN Phospholipid-transporting ATPase VD OS=Homo sapiens OX=9606 GN=ATP10D PE=1 SV=3	ATP10D	1	1	0.770%	160272.06	6.78
Q9P265	sp|Q9P265|DIP2B_HUMAN Disco-interacting protein 2 homolog B OS=Homo sapiens OX=9606 GN=DIP2B PE=1 SV=3	DIP2B	1	1	1.080%	171489.66	8.43
Q9P299	sp|Q9P299|COPZ2_HUMAN Coatomer subunit zeta-2 OS=Homo sapiens OX=9606 GN=COPZ2 PE=2 SV=1	COPZ2	1	1	3.810%	23547.68	5.08
Q9P2I0	sp|Q9P2I0|CPSF2_HUMAN Cleavage and polyadenylation specificity factor subunit 2 OS=Homo sapiens OX=9606 GN=CPSF2 PE=1 SV=2	CPSF2	1	1	1.020%	88485.75	4.98

Q9P2Q2	sp|Q9P2Q2|FRM4A_HUMAN FERM domain-containing protein 4A OS=Homo sapiens OX=9606 GN=FRMD4A PE=1 SV=3	FRMD4A	1	1	1.060%	115456.98	8.98
Q9UBC2	sp|Q9UBC2|EP15R_HUMAN Epidermal growth factor receptor substrate 15-like 1 OS=Homo sapiens OX=9606 GN=EPS15L1 PE=1 SV=1	EPS15L1	1	1	0.930%	94253.92	4.93
Q9UBX3	sp|Q9UBX3|DIC_HUMAN Mitochondrial dicarboxylate carrier OS=Homo sapiens OX=9606 GN=SLC25A10 PE=1 SV=2	SLC25A10	1	1	2.790%	31282.12	9.62
Q9UDW1	sp|Q9UDW1|QCR9_HUMAN Cytochrome b-c1 complex subunit 9 OS=Homo sapiens OX=9606 GN=UQCR10 PE=1 SV=3	UQCR10	1	1	11.110%	7308.4	9.45
Q9UGP4	sp|Q9UGP4|LIMD1_HUMAN LIM domain-containing protein 1 OS=Homo sapiens OX=9606 GN=LIMD1 PE=1 SV=1	LIMD1	1	1	0.740%	72189.47	6.2
Q9UHP6	sp|Q9UHP6|RSP14_HUMAN Radial spoke head 14 homolog OS=Homo sapiens OX=9606 GN=RSPH14 PE=1 SV=1	RSPH14	1	1	2.870%	38591.64	6.43
Q9UJV9	sp|Q9UJV9|DDX41_HUMAN Probable ATP-dependent RNA helicase DDX41 OS=Homo sapiens OX=9606 GN=DDX41 PE=1 SV=2	DDX41	1	1	1.130%	69836.86	6.4
Q9UJX2	sp|Q9UJX2|CDC23_HUMAN Cell division cycle protein 23 homolog OS=Homo sapiens OX=9606 GN=CDC23 PE=1 SV=3	CDC23	1	1	1.010%	68833.38	6.59
Q9UKB1	sp|Q9UKB1|FBW1B_HUMAN F-box/WD repeat-containing protein 11 OS=Homo sapiens OX=9606 GN=FBXW11 PE=1 SV=1	FBXW11	1	1	2.210%	62090.21	6.73
Q9UKJ3	sp|Q9UKJ3|GPTC8_HUMAN G patch domain-containing protein 8 OS=Homo sapiens OX=9606 GN=GPATCH8 PE=1 SV=2	GPATCH8	1	1	0.400%	164195.41	8.81
Q9UKL3	sp|Q9UKL3|C8AP2_HUMAN CASP8-associated protein 2 OS=Homo sapiens OX=9606 GN=CASP8AP2 PE=1 SV=1	CASP8AP2	1	1	0.400%	222655.25	6.14
Q9UKN8	sp|Q9UKN8|TF3C4_HUMAN General transcription factor 3C polypeptide 4 OS=Homo sapiens OX=9606 GN=GTF3C4 PE=1 SV=2	GTF3C4	1	1	1.090%	91981.34	6.21
Q9ULI4	sp|Q9ULI4|KI26A_HUMAN Kinesin-like protein KIF26A OS=Homo sapiens OX=9606 GN=KIF26A PE=1 SV=3	KIF26A	1	1	0.320%	194587.47	9.12

Q9ULN7	sp|Q9ULN7|PNM8B_HUMAN Paraneoplastic antigen-like protein 8B OS=Homo sapiens OX=9606 GN=PNMA8B PE=2 SV=4	PNMA8B	1	1	0.940%	68614.35	5.35
Q9UMQ3	sp|Q9UMQ3|BARX2_HUMAN Homeobox protein BarH-like 2 OS=Homo sapiens OX=9606 GN=BARX2 PE=1 SV=3	BARX2	1	1	2.510%	31187.38	8.65
Q9UPP1	sp|Q9UPP1|PHF8_HUMAN Histone lysine demethylase PHF8 OS=Homo sapiens OX=9606 GN=PHF8 PE=1 SV=3	PHF8	1	1	0.660%	117862.7	8.92
Q9UPU7	sp|Q9UPU7|TBD2B_HUMAN TBC1 domain family member 2B OS=Homo sapiens OX=9606 GN=TBC1D2B PE=1 SV=2	TBC1D2B	1	1	1.040%	109879.15	5.85
Q9UQ07	sp|Q9UQ07|MOK_HUMAN MAPK/MAK/MRK overlapping kinase OS=Homo sapiens OX=9606 GN=MOK PE=2 SV=1	MOK	1	1	1.430%	48013.26	9.64
Q9Y2I7	sp|Q9Y2I7|FYV1_HUMAN 1-phosphatidylinositol 3-phosphate 5-kinase OS=Homo sapiens OX=9606 GN=PIKFYVE PE=1 SV=3	PIKFYVE	1	1	0.380%	237133.52	6.24
Q9Y2P4	sp|Q9Y2P4|S27A6_HUMAN Long-chain fatty acid transport protein 6 OS=Homo sapiens OX=9606 GN=SLC27A6 PE=1 SV=1	SLC27A6	1	1	0.810%	70110.77	8.75
Q9Y2Y9	sp|Q9Y2Y9|KLF13_HUMAN Krueppel-like factor 13 OS=Homo sapiens OX=9606 GN=KLF13 PE=1 SV=1	KLF13	1	1	2.430%	31179.55	9.63
Q9Y3B8	sp|Q9Y3B8|ORN_HUMAN Oligoribonuclease, mitochondrial OS=Homo sapiens OX=9606 GN=REXO2 PE=1 SV=3	REXO2	1	1	2.530%	26832.47	6.4
Q9Y3F4	sp|Q9Y3F4|STRAP_HUMAN Serine-threonine kinase receptor-associated protein OS=Homo sapiens OX=9606 GN=STRAP PE=1 SV=1	STRAP	1	1	3.140%	38437.86	4.98
Q9Y4B6	sp|Q9Y4B6|DCAF1_HUMAN DDB1- and CUL4-associated factor 1 OS=Homo sapiens OX=9606 GN=DCAF1 PE=1 SV=3	DCAF1	1	1	0.600%	169005.36	4.92
Q9Y4C8	sp|Q9Y4C8|RBM19_HUMAN Probable RNA-binding protein 19 OS=Homo sapiens OX=9606 GN=RBM19 PE=1 SV=3	RBM19	1	1	1.250%	107330.45	6.13
Q9Y4K1	sp|Q9Y4K1|CRBG1_HUMAN Beta/gamma crystallin domain-containing protein 1 OS=Homo sapiens OX=9606 GN=CRYBG1 PE=1 SV=3	CRYBG1	1	1	0.810%	188673.6	5.61

Q9Y4K4	sp|Q9Y4K4|M4K5_HUMAN Mitogen-activated protein kinase kinase kinase kinase 5 OS=Homo sapiens OX=9606 GN=MAP4K5 PE=1 SV=2	MAP4K5	1	1	1.060%	95022.89	7.97
Q9Y4P3	sp|Q9Y4P3|TBL2_HUMAN Transducin beta-like protein 2 OS=Homo sapiens OX=9606 GN=TBL2 PE=1 SV=1	TBL2	1	1	2.910%	49797.3	9.52
Q9Y5A9	sp|Q9Y5A9|YTHD2_HUMAN YTH domain-containing family protein 2 OS=Homo sapiens OX=9606 GN=YTHDF2 PE=1 SV=2	YTHDF2	1	1	1.550%	62333.4	8.87
Q9Y5I4	sp|Q9Y5I4|PCDC2_HUMAN Protocadherin alpha-C2 OS=Homo sapiens OX=9606 GN=PCDHAC2 PE=2 SV=1	PCDHAC2	1	1	0.700%	109448.74	5.26
Q9Y661	sp|Q9Y661|HS3S4_HUMAN Heparan sulfate glucosamine 3-O-sulfotransferase 4 OS=Homo sapiens OX=9606 GN=HS3ST4 PE=2 SV=3	HS3ST4	1	1	1.750%	49798.52	8.82
Q9Y697	sp|Q9Y697|NFS1_HUMAN Cysteine desulfurase, mitochondrial OS=Homo sapiens OX=9606 GN=NFS1 PE=1 SV=3	NFS1	1	1	1.530%	50195.12	8.54
Q9Y6B6	sp|Q9Y6B6|SAR1B_HUMAN GTP-binding protein SAR1b OS=Homo sapiens OX=9606 GN=SAR1B PE=1 SV=1	SAR1B	1	1	5.560%	22409.63	5.76
A0A024QZ30	tr|A0A024QZ30|A0A024QZ30_HUMAN Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens OX=9606 GN=SDHA PE=3 SV=1	SDHA	1	1	1.960%	72690.72	7.06
A0A024QZB1	tr|A0A024QZB1|A0A024QZB1_HUMAN HCG1998636, isoform CRA_a OS=Homo sapiens OX=9606 GN=hCG_1998636 PE=4 SV=1	hCG_19986	1	1	1.390%	111488.48	5.25
A0A024QZN8	tr|A0A024QZN8|A0A024QZN8_HUMAN Hect domain and RLD 4, isoform CRA_b OS=Homo sapiens OX=9606 GN=HERC4 PE=4 SV=1	HERC4	1	1	0.570%	117695.62	5.86
A0A024QZR5	tr|A0A024QZR5|A0A024QZR5_HUMAN Adaptor-related protein complex 3, mu 1 subunit, isoform CRA_a OS=Homo sapiens OX=9606 GN=AP3M1 PE=3 SV=1	AP3M1	1	1	1.910%	46938.61	6.47
A0A024R0R1	tr|A0A024R0R1|A0A024R0R1_HUMAN Rho guanine nucleotide exchange factor (GEF) 1, isoform CRA_e OS=Homo sapiens OX=9606 GN=ARHGEF1 PE=4 SV=1	ARHGEF1	1	1	1.100%	102434.12	5.47
A0A024R2T9	tr|A0A024R2T9|A0A024R2T9_HUMAN Ubiquitin specific peptidase 19, isoform CRA_a OS=Homo sapiens OX=9606 GN=USP19 PE=4 SV=1	USP19	1	1	0.760%	145671.16	5.94

A0A024R3C3	tr|A0A024R3C3|A0A024R3C3_HUMAN Cysteine and histidine-rich domain (CHORD)-containing 1, isoform CRA_b OS=Homo sapiens OX=9606 GN=CHORDC1 PE=4 SV=1	CHORDC1	1	1	4.790%	35329.88	7.53
A0A024R4N6	tr|A0A024R4N6|A0A024R4N6_HUMAN Zinc finger protein 577, isoform CRA_b OS=Homo sapiens OX=9606 GN=ZNF577 PE=4 SV=1	ZNF577	1	1	1.240%	54937.95	9.39
A0A024R4V6	tr|A0A024R4V6|A0A024R4V6_HUMAN Mannosyltransferase OS=Homo sapiens OX=9606 GN=ALG12 PE=3 SV=1	ALG12	1	1	1.840%	54654.03	9.63
A0A024R5H2	tr|A0A024R5H2|A0A024R5H2_HUMAN FCH and double SH3 domains 2, isoform CRA_a OS=Homo sapiens OX=9606 GN=FCHSD2 PE=4 SV=1	FCHSD2	1	1	0.880%	77750.97	5.4
A0A024R6W0	tr|A0A024R6W0|A0A024R6W0_HUMAN Aspartate aminotransferase OS=Homo sapiens OX=9606 GN=GOT2 PE=3 SV=1	GOT2	1	1	1.630%	47475.03	9.14
A0A024R7B0	tr|A0A024R7B0|A0A024R7B0_HUMAN Ubiquitin-like protein 5 OS=Homo sapiens OX=9606 GN=UBL5 PE=2 SV=1	UBL5	1	1	10.960%	8546.83	8.58
A0A024R7F2	tr|A0A024R7F2|A0A024R7F2_HUMAN Peroxiredoxin 2, isoform CRA_d OS=Homo sapiens OX=9606 GN=PRDX2 PE=4 SV=1	PRDX2	1	1	7.040%	15818.33	9.14
A0A024R994	tr|A0A024R994|A0A024R994_HUMAN Copine III, isoform CRA_a OS=Homo sapiens OX=9606 GN=CPNE3 PE=3 SV=1	CPNE3	1	1	1.680%	60129.96	5.6
A0A024R9K7	tr|A0A024R9K7|A0A024R9K7_HUMAN ER membrane protein complex subunit 7 OS=Homo sapiens OX=9606 GN=C15orf24 PE=3 SV=1	C15orf24	1	1	4.380%	35416.45	9.64
A0A024R9P1	tr|A0A024R9P1|A0A024R9P1_HUMAN RNA-binding protein with serine-rich domain 1 OS=Homo sapiens OX=9606 GN=hCG_2026745 PE=3 SV=1	hCG_20267	1	1	2.300%	34108.79	11.81
A0A024R9W7	tr|A0A024R9W7|A0A024R9W7_HUMAN Transmembrane protein 33, isoform CRA_a OS=Homo sapiens OX=9606 GN=TMEM33 PE=3 SV=1	TMEM33	1	1	4.860%	27977.84	9.76
A0A024RAV6	tr|A0A024RAV6|A0A024RAV6_HUMAN Potassium inwardly-rectifying channel, subfamily J, member 8, isoform CRA_a OS=Homo sapiens OX=9606 GN=KCNJ8 PE=3 SV=1	KCNJ8	1	1	1.420%	47967.38	9.38
A0A024RBQ0	tr|A0A024RBQ0|A0A024RBQ0_HUMAN Calcium/calmodulin-dependent protein kinase kinase 2, beta, isoform CRA_f OS=Homo sapiens OX=9606 GN=CAMKK2 PE=4 SV=1	CAMKK2	1	1	1.020%	64745.1	6.25

A0A024RBQ9	tr|A0A024RBQ9|A0A024RBQ9_HUMAN Dynein regulatory complex protein 10 OS=Homo sapiens OX=9606 GN=IQCD PE=3 SV=1	IQCD	1	1	2.880%	40094.05	9.37
A0A024RE18	tr|A0A024RE18|A0A024RE18_HUMAN Prominin 2, isoform CRA_a OS=Homo sapiens OX=9606 GN=PROM2 PE=3 SV=1	PROM2	1	1	1.080%	91910.05	5.86
A0A075B764	tr|A0A075B764|A0A075B764_HUMAN Neuroblastoma breakpoint family member 12 OS=Homo sapiens OX=9606 GN=NBPF12 PE=4 SV=1	NBPF12	1	1	0.720%	128033.99	4.79
A0A087WV68	tr|A0A087WV68|A0A087WV68_HUMAN TAR DNA-binding protein 43 (Fragment) OS=Homo sapiens OX=9606 GN=TARDBP PE=1 SV=1	TARDBP	1	1	5.190%	23977.09	8.64
A0A087WVC6	tr|A0A087WVC6|A0A087WVC6_HUMAN Protein-tyrosine-phosphatase OS=Homo sapiens OX=9606 GN=PTPRJ PE=1 SV=1	PTPRJ	1	1	1.190%	146556.5	5.41
A0A087WW81	tr|A0A087WW81|A0A087WW81_HUMAN Rootletin (Fragment) OS=Homo sapiens OX=9606 GN=CROCC PE=1 SV=6	CROCC	1	1	1.070%	95739.41	5.22
A0A087WWF4	tr|A0A087WWF4|A0A087WWF4_HUMAN Kanadaptin (Fragment) OS=Homo sapiens OX=9606 GN=SLC4A1AP PE=1 SV=1	SLC4A1AP	1	1	3.300%	30977.97	4.52
A0A087WWK1	tr|A0A087WWK1|A0A087WWK1_HUMAN Zinc finger protein 518A (Fragment) OS=Homo sapiens OX=9606 GN=ZNF518A PE=1 SV=1	ZNF518A	1	1	2.070%	39603.25	9.45
A0A087WXH1	tr|A0A087WXH1|A0A087WXH1_HUMAN Protein lifeguard 4 OS=Homo sapiens OX=9606 GN=TMBIM4 PE=3 SV=1	TMBIM4	1	1	2.380%	23716.75	6.96
A0A087WXK8	tr|A0A087WXK8|A0A087WXK8_HUMAN Chromosome 20 open reading frame 129 OS=Homo sapiens OX=9606 GN=FAM83D PE=1 SV=1	FAM83D	1	1	1.460%	67663.64	6.49
A0A087WYF0	tr|A0A087WYF0|A0A087WYF0_HUMAN Nucleolar protein of 40 kDa OS=Homo sapiens OX=9606 GN=ZCCHC17 PE=1 SV=1	ZCCHC17	1	1	6.880%	18290.01	11.1
A0A087WYN0	tr|A0A087WYN0|A0A087WYN0_HUMAN Transporter OS=Homo sapiens OX=9606 GN=SLC6A6 PE=1 SV=1	SLC6A6	1	1	2.610%	52024.62	9.49
A0A087X0J6	tr|A0A087X0J6|A0A087X0J6_HUMAN UPF0193 protein EVG1 OS=Homo sapiens OX=9606 GN=C22orf23 PE=4 SV=1	C22orf23	1	1	3.570%	22299.43	9.68

A0A087X234	tr|A0A087X234|A0A087X234_HUMAN Tubulin polyglutamylase TTLL7 OS=Homo sapiens OX=9606 GN=TTLL7 PE=1 SV=1	TTLL7	1	1	2.210%	63576.58	9.44
A0A087X2E4	tr|A0A087X2E4|A0A087X2E4_HUMAN Contactin-associated protein-like 3B (Fragment) OS=Homo sapiens OX=9606 GN=CNTNAP3B PE=4 SV=1	CNTNAP3B	1	1	3.590%	18681.91	6.06
A0A0A0MQS3	tr|A0A0A0MQS3|A0A0A0MQS3_HUMAN Leydig cell tumor 10 kDa protein homolog (Fragment) OS=Homo sapiens OX=9606 GN=C19orf53 PE=1 SV=1	C19orf53	1	1	6.250%	8873.32	12.02
A0A0A0MR18	tr|A0A0A0MR18|A0A0A0MR18_HUMAN Doublesex- and mab-3-related transcription factor 2 OS=Homo sapiens OX=9606 GN=DMRT2 PE=1 SV=1	DMRT2	1	1	1.480%	45224.87	8.72
A0A0A0MRB5	tr|A0A0A0MRB5|A0A0A0MRB5_HUMAN MAP kinase-activating death domain protein OS=Homo sapiens OX=9606 GN=MADD PE=1 SV=1	MADD	1	1	0.500%	176552.59	5.78
A0A0A0MS31	tr|A0A0A0MS31|A0A0A0MS31_HUMAN Caspase-8 OS=Homo sapiens OX=9606 GN=CASP8 PE=1 SV=1	CASP8	1	1	2.880%	32487	5.76
A0A0A0MS84	tr|A0A0A0MS84|A0A0A0MS84_HUMAN Centrosomal protein of 83 kDa OS=Homo sapiens OX=9606 GN=CEP83 PE=1 SV=1	CEP83	1	1	1.480%	56054.76	6.03
A0A0A0MTM4	tr|A0A0A0MTM4|A0A0A0MTM4_HUMAN Zinc finger protein 793 OS=Homo sapiens OX=9606 GN=ZNF793 PE=4 SV=1	ZNF793	1	1	3.930%	34421.17	9.77
A0A0A7EP75	tr|A0A0A7EP75|A0A0A7EP75_HUMAN Truncated UNCX homeobox protein transcript variant 2 OS=Homo sapiens OX=9606 GN=UNCX PE=2 SV=1	UNCX	1	1	4.980%	23613.33	8.6
A0A0B4J253	tr|A0A0B4J253|A0A0B4J253_HUMAN Dolichyl-phosphate-mannose--protein mannosyltransferase OS=Homo sapiens OX=9606 GN=TMTC2 PE=1 SV=1	TMTC2	1	1	1.200%	93566.01	9.11
A0A0B4J296	tr|A0A0B4J296|A0A0B4J296_HUMAN Elongin-B OS=Homo sapiens OX=9606 GN=ELOB PE=1 SV=1	ELOB	1	1	10.610%	7756.11	10.03
A0A0C4DFS8	tr|A0A0C4DFS8|A0A0C4DFS8_HUMAN Nicotinamide phosphoribosyltransferase OS=Homo sapiens OX=9606 GN=NAMPT PE=1 SV=1	NAMPT	1	1	1.900%	41864.09	6.04
A0A0C4DG62	tr|A0A0C4DG62|A0A0C4DG62_HUMAN ADP-ribosylation factor-like protein 6-interacting protein 4 OS=Homo sapiens OX=9606 GN=ARL6IP4 PE=1 SV=1	ARL6IP4	1	1	4.130%	24591.39	10.94

A0A0D9SG96	tr|A0A0D9SG96|A0A0D9SG96_HUMAN Neurexin-1-beta (Fragment) OS=Homo sapiens OX=9606 GN=NRXN1 PE=1 SV=1	NRXN1	1	1	6.620%	14656.28	4.62
A0A0F7WAP3	tr|A0A0F7WAP3|A0A0F7WAP3_HUMAN Calreticulin (Fragment) OS=Homo sapiens OX=9606 GN=CALR PE=4 SV=1	CALR	1	1	13.640%	8439	11.61
A0A0G2JQK5	tr|A0A0G2JQK5|A0A0G2JQK5_HUMAN Nucleoredoxin (Fragment) OS=Homo sapiens OX=9606 GN=NXN PE=1 SV=1	NXN	1	1	9.170%	12832.4	5.65
A0A0G2R1R6	tr|A0A0G2R1R6|A0A0G2R1R6_HUMAN MHC class II antigen (Fragment) OS=Homo sapiens OX=9606 GN=HLA-DQB1 PE=4 SV=1	HLA-DQB1	1	1	6.740%	10501.56	9.03
A0A0S2Z3B0	tr|A0A0S2Z3B0|A0A0S2Z3B0_HUMAN Argininosuccinate lyase isoform 3 (Fragment) OS=Homo sapiens OX=9606 GN=ASL PE=2 SV=1	ASL	1	1	4.460%	39788.91	5.87
A0A0S2Z3E8	tr|A0A0S2Z3E8|A0A0S2Z3E8_HUMAN Fibrinopeptide A (Fragment) OS=Homo sapiens OX=9606 GN=FGA PE=1 SV=1	FGA	1	1	1.610%	47384.01	8.55
A0A0S2Z3F2	tr|A0A0S2Z3F2|A0A0S2Z3F2_HUMAN V-raf murine sarcoma 3611 viral oncogene-like protein isoform 2 (Fragment) OS=Homo sapiens OX=9606 GN=ARAF PE=2 SV=1	ARAF	1	1	1.150%	67999.06	9.2
A0A0S2Z3N8	tr|A0A0S2Z3N8|A0A0S2Z3N8_HUMAN 7-dehydrocholesterol reductase isoform 4 (Fragment) OS=Homo sapiens OX=9606 GN=DHCR7 PE=2 SV=1	DHCR7	1	1	4.240%	18221.98	9.47
A0A0S2Z519	tr|A0A0S2Z519|A0A0S2Z519_HUMAN HCLS1 associated protein X-1 isoform 5 OS=Homo sapiens OX=9606 GN=HAX1 PE=2 SV=1	HAX1	1	1	11.290%	7248.57	11.54
A0A0S2Z6F0	tr|A0A0S2Z6F0|A0A0S2Z6F0_HUMAN Histocompatibility 13 isoform 2 OS=Homo sapiens OX=9606 GN=HM13 PE=1 SV=1	HM13	1	1	2.030%	38067.19	6.38
A0A0U1RQR3	tr|A0A0U1RQR3|A0A0U1RQR3_HUMAN InaD-like protein (Fragment) OS=Homo sapiens OX=9606 GN=PATJ PE=1 SV=1	PATJ	1	1	5.040%	14913.6	6.81
A0A125QYY8	tr|A0A125QYY8|A0A125QYY8_HUMAN IBM-B1 light chain variable region (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	11.610%	12166.61	8.68
A0A126GW78	tr|A0A126GW78|A0A126GW78_HUMAN Olfactory receptor OS=Homo sapiens OX=9606 GN=OR5AC2 PE=3 SV=1	OR5AC2	1	1	2.270%	35285.93	9.13

A0A126LB01	tr|A0A126LB01|A0A126LB01_HUMAN Protease/assembly protein OS=Homo sapiens OX=9606 GN=U53 PE=3 SV=1	U53	1	1	0.950%	58517.74	5.44
A0A126LB07	tr|A0A126LB07|A0A126LB07_HUMAN Major capsid protein OS=Homo sapiens OX=9606 GN=U57 PE=3 SV=1	U57	1	1	1.260%	151991.7	6.21
A0A140VJE2	tr|A0A140VJE2|A0A140VJE2_HUMAN Testicular tissue protein Li 16 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.770%	71157.72	6.55
A0A140VJE6	tr|A0A140VJE6|A0A140VJE6_HUMAN Guanylate cyclase OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	0.470%	118917.84	6.19
A0A140VJJ4	tr|A0A140VJJ4|A0A140VJJ4_HUMAN Family with sequence similarity 71, member B OS=Homo sapiens OX=9606 GN=FAM71B PE=2 SV=1	FAM71B	1	1	1.160%	64755.03	9.52
A0A140VJZ8	tr|A0A140VJZ8|A0A140VJZ8_HUMAN Testicular tissue protein Li 225 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.120%	102933.41	5.52
A0A140VK57	tr|A0A140VK57|A0A140VK57_HUMAN Metalloproteinase inhibitor 2 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	3.640%	24399.02	7.46
A0A1B0GTY9	tr|A0A1B0GTY9|A0A1B0GTY9_HUMAN Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH7A1 PE=1 SV=1	ALDH7A1	1	1	2.920%	51853	8.25
A0A1B0GUM1	tr|A0A1B0GUM1|A0A1B0GUM1_HUMAN Pleckstrin homology domain-containing family A member 7 (Fragment) OS=Homo sapiens OX=9606 GN=PLEKHA7 PE=1 SV=1	PLEKHA7	1	1	1.930%	58700.68	9.09
A0A1B0GWC0	tr|A0A1B0GWC0|A0A1B0GWC0_HUMAN Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens OX=9606 GN=CPT2 PE=1 SV=1	CPT2	1	1	1.080%	72648.77	8.84
A0A1P0AYU5	tr|A0A1P0AYU5|A0A1P0AYU5_HUMAN Sidoreflexin OS=Homo sapiens OX=9606 GN=SFXN3 PE=1 SV=1	SFXN3	1	1	1.850%	35978.49	9.25
A0A1U9X8P6	tr|A0A1U9X8P6|A0A1U9X8P6_HUMAN TRIM26 OS=Homo sapiens OX=9606 PE=4 SV=1		1	1	2.040%	62179.21	4.98
A0A1U9X982	tr|A0A1U9X982|A0A1U9X982_HUMAN PRRC2A OS=Homo sapiens OX=9606 PE=4 SV=1		1	1	0.370%	228838.29	9.47

A0A1U9XBC2	tr|A0A1U9XBC2|A0A1U9XBC2_HUMAN Mediator of DNA damage checkpoint protein 1 OS=Homo sapiens OX=9606 PE=4 SV=1		1	1	0.810%	226642.53	5.38
A0A1W2PP04	tr|A0A1W2PP04|A0A1W2PP04_HUMAN RNA-binding motif protein, X-linked 2 OS=Homo sapiens OX=9606 GN=RBMX2 PE=1 SV=1	RBMX2	1	1	3.620%	31522.07	9.45
A0A1W2PPE0	tr|A0A1W2PPE0|A0A1W2PPE0_HUMAN Golgi SNAP receptor complex member 2 OS=Homo sapiens OX=9606 GN=GOSR2 PE=4 SV=1	GOSR2	1	1	13.640%	7354.36	9.15
A0A1W2PPR3	tr|A0A1W2PPR3|A0A1W2PPR3_HUMAN Elongator complex protein 4 OS=Homo sapiens OX=9606 GN=ELP4 PE=1 SV=1	ELP4	1	1	9.900%	10403.62	10.51
A0A1W2PQS4	tr|A0A1W2PQS4|A0A1W2PQS4_HUMAN Glial fibrillary acidic protein (Fragment) OS=Homo sapiens OX=9606 GN=GFAP PE=1 SV=1	GFAP	1	1	32.350%	3605.04	6.93
A0A1W2PS79	tr|A0A1W2PS79|A0A1W2PS79_HUMAN ADP-ribosylation factor-like 9, isoform CRA_b OS=Homo sapiens OX=9606 GN=ARL9 PE=1 SV=2	ARL9	1	1	2.260%	30158.03	8.82
A0A1X7SBU6	tr|A0A1X7SBU6|A0A1X7SBU6_HUMAN Adhesion G-protein-coupled receptor V1 (Fragment) OS=Homo sapiens OX=9606 GN=ADGRV1 PE=1 SV=1	ADGRV1	1	1	0.420%	288346.02	4.68
A0A286LWX1	tr|A0A286LWX1|A0A286LWX1_HUMAN Aldehyde oxidase 1 OS=Homo sapiens OX=9606 GN=AOX1 PE=2 SV=1	AOX1	1	1	0.450%	147829.19	6.72
A0A2R4CIF1	tr|A0A2R4CIF1|A0A2R4CIF1_HUMAN Dioxin-inducible cytochrome p450 (Fragment) OS=Homo sapiens OX=9606 GN=CYP1B1 PE=3 SV=1	CYP1B1	1	1	3.080%	21996.06	7.07
A0A2R8Y481	tr|A0A2R8Y481|A0A2R8Y481_HUMAN Spastin (Fragment) OS=Homo sapiens OX=9606 GN=SPAST PE=1 SV=1	SPAST	1	1	2.220%	49610.09	9.31
A0A2R8Y4Z8	tr|A0A2R8Y4Z8|A0A2R8Y4Z8_HUMAN Coiled-coil domain-containing protein 9 OS=Homo sapiens OX=9606 GN=CCDC9 PE=1 SV=1	CCDC9	1	1	1.190%	65306.31	5.22
A0A2R8Y5P9	tr|A0A2R8Y5P9|A0A2R8Y5P9_HUMAN Protein Shroom3 OS=Homo sapiens OX=9606 GN=SHROOM3 PE=1 SV=1	SHROOM3	1	1	0.470%	208047.19	8.16
A0A2R8YCJ0	tr|A0A2R8YCJ0|A0A2R8YCJ0_HUMAN Girdin (Fragment) OS=Homo sapiens OX=9606 GN=CCDC88A PE=4 SV=1	CCDC88A	1	1	53.330%	1577.65	4.09

A0A2R8YD35	tr|A0A2R8YD35|A0A2R8YD35_HUMAN Histone deacetylase 6 (Fragment) OS=Homo sapiens OX=9606 GN=HDAC6 PE=1 SV=1	HDAC6	1	1	14.550%	12225.97	4.93
A0A2R8YD63	tr|A0A2R8YD63|A0A2R8YD63_HUMAN DNA topoisomerase 2-binding protein 1 OS=Homo sapiens OX=9606 GN=TOPBP1 PE=1 SV=1	TOPBP1	1	1	0.530%	170131.04	6.52
A0A2R8YFH3	tr|A0A2R8YFH3|A0A2R8YFH3_HUMAN Protein SERAC1 OS=Homo sapiens OX=9606 GN=SERAC1 PE=1 SV=1	SERAC1	1	1	1.770%	70471.33	7.07
A0A2R8YFH5	tr|A0A2R8YFH5|A0A2R8YFH5_HUMAN Protein transport protein SEC23 OS=Homo sapiens OX=9606 GN=SEC23B PE=1 SV=1	SEC23B	1	1	1.600%	84471.91	6.54
A0A2S1ZR87	tr|A0A2S1ZR87|A0A2S1ZR87_HUMAN Structural maintenance of chromosomes 6 OS=Homo sapiens OX=9606 GN=SMC6 PE=2 SV=1	SMC6	1	1	0.820%	126324.16	6.57
A0A2U3TZV9	tr|A0A2U3TZV9|A0A2U3TZV9_HUMAN Girdin OS=Homo sapiens OX=9606 GN=CCDC88A PE=1 SV=1	CCDC88A	1	1	0.390%	207881.98	5.73
A0A2U8BR37	tr|A0A2U8BR37|A0A2U8BR37_HUMAN SR-related CTD associated factor 1 transcript variant 4 OS=Homo sapiens OX=9606 GN=SCAF1 PE=2 SV=1	SCAF1	1	1	1.370%	39836.67	8.88
A0A2X0SFX5	tr|A0A2X0SFX5|A0A2X0SFX5_HUMAN ARHGEF16 (Fragment) OS=Homo sapiens OX=9606 GN=ARHGEF16 PE=4 SV=1	ARHGEF16	1	1	1.550%	80330.35	6.9
A0A2X0SSL3	tr|A0A2X0SSL3|A0A2X0SSL3_HUMAN FARP2 (Fragment) OS=Homo sapiens OX=9606 GN=FARP2 PE=4 SV=1	FARP2	1	1	1.330%	120113.36	8.96
A0A343GKA1	tr|A0A343GKA1|A0A343GKA1_HUMAN NADH-ubiquinone oxidoreductase chain 4 OS=Homo sapiens OX=9606 GN=ND4 PE=3 SV=1	ND4	1	1	2.180%	50208.73	9.4
A0A384MEG1	tr|A0A384MEG1|A0A384MEG1_HUMAN Fascin OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	3.250%	54529.35	6.84
A0A384N6B9	tr|A0A384N6B9|A0A384N6B9_HUMAN Epididymis secretory sperm binding protein OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	3.550%	38650.74	6.33
A0A3B3ITX7	tr|A0A3B3ITX7|A0A3B3ITX7_HUMAN Acylglycerol kinase, mitochondrial OS=Homo sapiens OX=9606 GN=AGK PE=1 SV=1	AGK	1	1	6.070%	23422.87	9.05

A0A494C0E5	tr|A0A494C0E5|A0A494C0E5_HUMAN Matrix metalloproteinase-21 (Fragment) OS=Homo sapiens OX=9606 GN=MMP21 PE=4 SV=1	MMP21	1	1	7.140%	9197.23	6.56
A0A494C0S9	tr|A0A494C0S9|A0A494C0S9_HUMAN C3 and PZP-like alpha-2-macroglobulin domain-containing protein 8 OS=Homo sapiens OX=9606 GN=CPAMD8 PE=1 SV=1	CPAMD8	1	1	0.310%	211282.69	6.16
A0A494C142	tr|A0A494C142|A0A494C142_HUMAN BRCA1-associated RING domain protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=BARD1 PE=1 SV=1	BARD1	1	1	1.390%	47645.72	9.15
A0A494C1T7	tr|A0A494C1T7|A0A494C1T7_HUMAN Protein kinase C delta type (Fragment) OS=Homo sapiens OX=9606 GN=PRKCD PE=1 SV=1	PRKCD	1	1	1.690%	33662.69	8.89
A0A4D6J698	tr|A0A4D6J698|A0A4D6J698_HUMAN Mena delta 11a OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	3.860%	63923.68	6.12
A0A590UJ94	tr|A0A590UJ94|A0A590UJ94_HUMAN Unconventional myosin-VIIa (Fragment) OS=Homo sapiens OX=9606 GN=MYO7A PE=1 SV=1	MYO7A	1	1	0.560%	123258.8	9.11
A0A590UJD6	tr|A0A590UJD6|A0A590UJD6_HUMAN Egl nine homolog 1 (Fragment) OS=Homo sapiens OX=9606 GN=EGLN1 PE=1 SV=1	EGLN1	1	1	8.640%	8806.95	8.64
A0A590UJN8	tr|A0A590UJN8|A0A590UJN8_HUMAN DNA mismatch repair protein Msh3 OS=Homo sapiens OX=9606 GN=MSH3 PE=1 SV=1	MSH3	1	1	0.840%	119735.36	6.8
A0A590UJY2	tr|A0A590UJY2|A0A590UJY2_HUMAN Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Homo sapiens OX=9606 GN=GNAS PE=1 SV=1	GNAS	1	1	2.950%	27931.57	7.6
A0A5C2FSX6	tr|A0A5C2FSX6|A0A5C2FSX6_HUMAN IGL c18_light_IGKV1-5_IGKJ1 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	7.480%	11736.96	8.66
A0A5C2FVY3	tr|A0A5C2FVY3|A0A5C2FVY3_HUMAN IGL c1171_light_IGKV3-11_IGKJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	7.480%	11757.08	8.7
A0A5C2FXS1	tr|A0A5C2FXS1|A0A5C2FXS1_HUMAN IGL c1434_light_IGKV1-12_IGKJ1 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	14.950%	11557.89	9.07
A0A5C2FXT9	tr|A0A5C2FXT9|A0A5C2FXT9_HUMAN IGL c435_light_IGKV1D-39_IGKJ1 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	14.950%	11533.74	9.3

A0A5C2FYN4	tr|A0A5C2FYN4|A0A5C2FYN4_HUMAN IGL c1340_light_IGKV1-17_IGKJ1 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	14.020%	11716.03	9.01
A0A5C2G0Z7	tr|A0A5C2G0Z7|A0A5C2G0Z7_HUMAN IGL c1605_light_IGKV3-15_IGKJ2 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	7.410%	11653.85	8.07
A0A5C2G171	tr|A0A5C2G171|A0A5C2G171_HUMAN IGL c2899_light_IGKV1-39_IGKJ1 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	14.810%	11843.13	8.68
A0A5C2G4Y6	tr|A0A5C2G4Y6|A0A5C2G4Y6_HUMAN IGL c2597_light_IGKV1-27_IGKJ2 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	14.950%	11421.7	8.98
A0A5C2G5L1	tr|A0A5C2G5L1|A0A5C2G5L1_HUMAN IGH c7_heavy__IGHV3-30_IGHD3-22_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	9.170%	13313.79	8.62
A0A5C2G606	tr|A0A5C2G606|A0A5C2G606_HUMAN IGH c389_heavy__IGHV4-39_IGHD6-25_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	5.040%	12815.13	7.94
A0A5C2G6P5	tr|A0A5C2G6P5|A0A5C2G6P5_HUMAN IGH c609_heavy__IGHV5-51_IGHD3-9_IGHJ5 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	15.200%	13959.4	7
A0A5C2G781	tr|A0A5C2G781|A0A5C2G781_HUMAN IGL c3567_light_IGKV1-39_IGKJ2 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	14.950%	11472.57	7.95
A0A5C2G8H9	tr|A0A5C2G8H9|A0A5C2G8H9_HUMAN IGL c2753_light_IGKV3-20_IGKJ1 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	8.330%	11677.87	8.08
A0A5C2G9I2	tr|A0A5C2G9I2|A0A5C2G9I2_HUMAN IGL c12_light_IGKV3-11_IGKJ2 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	7.340%	12064.43	8.7
A0A5C2GA72	tr|A0A5C2GA72|A0A5C2GA72_HUMAN IGH c165_heavy__IGHV4-34_IGHD3-10_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	7.200%	13892.37	8.91
A0A5C2GAL3	tr|A0A5C2GAL3|A0A5C2GAL3_HUMAN IGH + IGL c296_heavy_IGHV3-33_IGHD3-3_IGHJ6 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	9.090%	13513.02	8.49
A0A5C2GB35	tr|A0A5C2GB35|A0A5C2GB35_HUMAN IGH + IGL c416_light_IGKV3-15_IGKJ1 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	17.590%	11874.19	8.74

A0A5C2GBI6	tr|A0A5C2GBI6|A0A5C2GBI6_HUMAN IGH + IGL c551_heavy_IGHV4-34_IGHD5-18_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	11.570%	13338.81	7.99
A0A5C2GDJ7	tr|A0A5C2GDJ7|A0A5C2GDJ7_HUMAN IGH + IGL c170_light_IGKV3-11_IGKJ5 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	14.950%	11565.77	6.86
A0A5C2GFC9	tr|A0A5C2GFC9|A0A5C2GFC9_HUMAN IG c153_heavy_IGHV3-23_IGHD1-7_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	18.330%	12852.14	6.85
A0A5C2GFK2	tr|A0A5C2GFK2|A0A5C2GFK2_HUMAN IG c360_heavy_IGHV4-31_IGHD4-4_IGHJ5 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	5.790%	13162.5	9.18
A0A5C2GH22	tr|A0A5C2GH22|A0A5C2GH22_HUMAN IG c1145_light_IGKV2-30_IGKJ3 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	6.250%	12331.73	9.62
A0A5C2GJU4	tr|A0A5C2GJU4|A0A5C2GJU4_HUMAN IGH + IGL c287_light_IGKV1-8_IGKJ1 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	14.950%	11710.93	9.1
A0A5C2GKE5	tr|A0A5C2GKE5|A0A5C2GKE5_HUMAN IG c125_light_IGKV3-11_IGKJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	7.410%	11518.79	8.07
A0A5C2GKS6	tr|A0A5C2GKS6|A0A5C2GKS6_HUMAN IG c155_heavy_IGHV1-2_IGHD7-27_IGHJ5 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	10.570%	13483.77	4.9
A0A5C2GKZ8	tr|A0A5C2GKZ8|A0A5C2GKZ8_HUMAN IG c192_heavy_IGHV4-61_IGHD3-10_IGHJ6 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	4.880%	13517.82	8.56
A0A5C2GR10	tr|A0A5C2GR10|A0A5C2GR10_HUMAN IG c1154_heavy_IGHV3-66_IGHD3-16_IGHJ6 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	4.000%	13612.01	7.93
A0A5C2GSP8	tr|A0A5C2GSP8|A0A5C2GSP8_HUMAN IG c1510_heavy_IGHV3-7_IGHD5-12_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	10.570%	13326.93	8.9
A0A5C2GU88	tr|A0A5C2GU88|A0A5C2GU88_HUMAN IG c1084_light_IGLV2-23_IGLJ2 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	7.270%	11255.19	7.96
A0A5C2GXB2	tr|A0A5C2GXB2|A0A5C2GXB2_HUMAN IG c1079_light_IGKV3-20_IGKJ2 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	7.410%	11834.04	6.06

A0A669KB49	tr|A0A669KB49|A0A669KB49_HUMAN Msx2-interacting protein (Fragment) OS=Homo sapiens OX=9606 GN=SPEN PE=1 SV=1	SPEN	1	1	1.140%	81280	8.76
A0A669KB83	tr|A0A669KB83|A0A669KB83_HUMAN Alpha-galactosidase (Fragment) OS=Homo sapiens OX=9606 GN=GLA PE=1 SV=1	GLA	1	1	3.520%	22365.8	4.74
A0A6B9DHC0	tr|A0A6B9DHC0|A0A6B9DHC0_HUMAN MHC class II antigen (Fragment) OS=Homo sapiens OX=9606 GN=DPA1 PE=3 SV=1	DPA1	1	1	3.690%	24573.56	4.69
A0A6H0MUP3	tr|A0A6H0MUP3|A0A6H0MUP3_HUMAN NADH-ubiquinone oxidoreductase chain 1 OS=Homo sapiens OX=9606 GN=ND1 PE=3 SV=1	ND1	1	1	1.570%	34715.1	6.11
A0A6I8PRT6	tr|A0A6I8PRT6|A0A6I8PRT6_HUMAN Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens OX=9606 GN=GFPT1 PE=1 SV=1	GFPT1	1	1	14.040%	6765.73	9.36
A0A6I8PRV8	tr|A0A6I8PRV8|A0A6I8PRV8_HUMAN Cadherin EGF LAG seven-pass G-type receptor 1 (Fragment) OS=Homo sapiens OX=9606 GN=CELSR1 PE=1 SV=1	CELSR1	1	1	1.830%	34610.9	7.37
A0A6M4C8X9	tr|A0A6M4C8X9|A0A6M4C8X9_HUMAN Docking protein 3 OS=Homo sapiens OX=9606 GN=DOK3 PE=4 SV=1	DOK3	1	1	4.390%	24736.77	8.54
A0A6Q8PFE7	tr|A0A6Q8PFE7|A0A6Q8PFE7_HUMAN Heat shock protein beta-1 OS=Homo sapiens OX=9606 GN=HSPB1 PE=1 SV=1	HSPB1	1	1	8.200%	13827.43	6.83
A0A6Q8PGX2	tr|A0A6Q8PGX2|A0A6Q8PGX2_HUMAN DNA-binding protein SMUBP-2 OS=Homo sapiens OX=9606 GN=IGHMBP2 PE=1 SV=1	IGHMBP2	1	1	2.800%	51105.89	8.61
A0A6Q8PH17	tr|A0A6Q8PH17|A0A6Q8PH17_HUMAN Sodium/potassium-transporting ATPase subunit beta-1-interacting protein OS=Homo sapiens OX=9606 GN=NKAIN3 PE=1 SV=1	NKAIN3	1	1	7.290%	28089.64	6.73
A0A6Q8PHM1	tr|A0A6Q8PHM1|A0A6Q8PHM1_HUMAN Myelin regulatory factor (Fragment) OS=Homo sapiens OX=9606 GN=MYRF PE=1 SV=1	MYRF	1	1	0.530%	101784.46	8.94
A0A7I2RAZ6	tr|A0A7I2RAZ6|A0A7I2RAZ6_HUMAN C-myc promoter-binding protein OS=Homo sapiens OX=9606 GN=DENND4A PE=1 SV=1	DENND4A	1	1	0.260%	213772.47	6.7
A0A7I2V3K7	tr|A0A7I2V3K7|A0A7I2V3K7_HUMAN DnaJ homolog subfamily B member 1 OS=Homo sapiens OX=9606 GN=DNAJB1 PE=1 SV=1	DNAJB1	1	1	2.560%	30184.22	8.97

A0A7I2V3V7	tr|A0A7I2V3V7|A0A7I2V3V7_HUMAN Synaptobrevin homolog YKT6 OS=Homo sapiens OX=9606 GN=YKT6 PE=1 SV=1	YKT6	1	1	2.400%	27815.68	7
A0A7I2V3X2	tr|A0A7I2V3X2|A0A7I2V3X2_HUMAN Acyl-coenzyme A oxidase OS=Homo sapiens OX=9606 GN=ACOXL PE=1 SV=1	ACOXL	1	1	1.800%	68823.84	9.08
A0A7I2V5H2	tr|A0A7I2V5H2|A0A7I2V5H2_HUMAN Pitrilysin metalloproteinase 1 OS=Homo sapiens OX=9606 GN=PITRM1 PE=1 SV=1	PITRM1	1	1	0.700%	112814.97	6.22
A0A7I2V5P9	tr|A0A7I2V5P9|A0A7I2V5P9_HUMAN Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens OX=9606 GN=EIF3E PE=1 SV=1	EIF3E	1	1	2.100%	39189.46	6.33
A0A7P0T7Z8	tr|A0A7P0T7Z8|A0A7P0T7Z8_HUMAN Jouberin OS=Homo sapiens OX=9606 GN=AHI1 PE=1 SV=1	AHI1	1	1	0.760%	135610.05	6.63
A0A7P0T8I3	tr|A0A7P0T8I3|A0A7P0T8I3_HUMAN UPF0688 protein C1orf174 OS=Homo sapiens OX=9606 GN=C1orf174 PE=1 SV=1	C1orf174	1	1	5.710%	11280.72	9.64
A0A7S5BYA5	tr|A0A7S5BYA5|A0A7S5BYA5_HUMAN IGH c476_heavy_IGHV3-73_IGHD4-17_IGHJ5 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	7.500%	12793.17	8.07
A0A7S5C089	tr|A0A7S5C089|A0A7S5C089_HUMAN IGH c1798_heavy_IGHV4-39_IGHD6-19_IGHJ3 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	6.610%	13057.51	7.93
A0A7S5C0A0	tr|A0A7S5C0A0|A0A7S5C0A0_HUMAN IGH c1823_heavy_IGHV4-39_IGHD2-21_IGHJ5 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	13.560%	13216.73	7.96
A0A7S5C0L7	tr|A0A7S5C0L7|A0A7S5C0L7_HUMAN IGH c934_heavy_IGHV3-48_IGHD5-12_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	17.740%	13656.98	4.62
A0A7S5C127	tr|A0A7S5C127|A0A7S5C127_HUMAN IGH c2263_heavy_IGHV1-69_IGHD3-9_IGHJ6 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	6.750%	17501.41	9.33
A0A7S5C1H7	tr|A0A7S5C1H7|A0A7S5C1H7_HUMAN IGH c10_heavy_IGHV1-2_IGHD2-2_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	11.400%	12649.08	9.33
A0A7S5C2W0	tr|A0A7S5C2W0|A0A7S5C2W0_HUMAN IGH c2360_heavy_IGHV1-69_IGHD6-19_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	11.570%	12851.28	7.97

A0A7S5EU20	tr|A0A7S5EU20|A0A7S5EU20_HUMAN IGH c1456_heavy_IGHV4-34_IGHD2-8_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	11.850%	15236.02	8.96
A0A7S5EUG8	tr|A0A7S5EUG8|A0A7S5EUG8_HUMAN IGH c2146_heavy_IGHV4-39_IGHD3-10_IGHJ2 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	9.760%	13356.95	9.43
A0A7S5EX76	tr|A0A7S5EX76|A0A7S5EX76_HUMAN IGH c1949_heavy_IGHV3-15_IGHD1-26_IGHJ3 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	15.570%	12979.41	8.66
A0A7T0LN63	tr|A0A7T0LN63|A0A7T0LN63_HUMAN Immunglobulin heavy chain variable region (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	4.100%	13431.76	9.26
A0A804CL36	tr|A0A804CL36|A0A804CL36_HUMAN Cullin-4B OS=Homo sapiens OX=9606 GN=CUL4B PE=4 SV=1	CUL4B	1	1	0.950%	96263	7.55
A0A804HIM6	tr|A0A804HIM6|A0A804HIM6_HUMAN Histone-lysine N-methyltransferase 2C (Fragment) OS=Homo sapiens OX=9606 GN=KMT2C PE=4 SV=1	KMT2C	1	1	0.380%	172563.92	5.92
A0A804HJ97	tr|A0A804HJ97|A0A804HJ97_HUMAN Beta-hexosaminidase subunit alpha OS=Homo sapiens OX=9606 GN=HEXA PE=4 SV=1	HEXA	1	1	3.110%	29123.76	5.96
A1A4B9	tr|A1A4B9|A1A4B9_HUMAN CLMN protein (Fragment) OS=Homo sapiens OX=9606 GN=CLMN PE=2 SV=1	CLMN	1	1	1.470%	74987.57	4.68
A1LMA8	tr|A1LMA8|A1LMA8_HUMAN Contactin 6, isoform CRA_a OS=Homo sapiens OX=9606 GN=CNTN6 PE=4 SV=1	CNTN6	1	1	0.580%	113954.81	5.73
A2NUW5	tr|A2NUW5|A2NUW5_HUMAN T-cell gamma protein (Fragment) OS=Homo sapiens OX=9606 PE=1 SV=1		1	1	6.020%	15177.12	9.14
A2RRN2	tr|A2RRN2|A2RRN2_HUMAN CAPS2 protein OS=Homo sapiens OX=9606 GN=CAPS2 PE=2 SV=1	CAPS2	1	1	3.430%	23448.35	5.38
A2RUF7	tr|A2RUF7|A2RUF7_HUMAN Phosphatidylinositol-4-phosphate 3-kinase OS=Homo sapiens OX=9606 GN=PIK3C2B PE=2 SV=1	PIK3C2B	1	1	0.430%	184765.71	6.95
A4D0Z4	tr|A4D0Z4|A4D0Z4_HUMAN GRIP and coiled-coil domain containing 1 OS=Homo sapiens OX=9606 GN=GCC1 PE=4 SV=1	GCC1	1	1	0.900%	87809.63	5.35

A4D1P7	tr|A4D1P7|A4D1P7_HUMAN Ribonuclease H OS=Homo sapiens OX=9606 GN=KIAA1466 PE=4 SV=1	KIAA1466	1	1	1.050%	53489.46	9.2
A5YM41	tr|A5YM41|A5YM41_HUMAN MTSS1 protein OS=Homo sapiens OX=9606 GN=MTSS1 PE=2 SV=1	MTSS1	1	1	0.960%	79080.3	6.01
A6NDF3	tr|A6NDF3|A6NDF3_HUMAN Protein PBDC1 OS=Homo sapiens OX=9606 GN=PBDC1 PE=1 SV=2	PBDC1	1	1	3.450%	26643.55	9.38
A6NNK5	tr|A6NNK5|A6NNK5_HUMAN TP53-binding protein 1 OS=Homo sapiens OX=9606 GN=TP53BP1 PE=1 SV=2	TP53BP1	1	1	0.360%	209017	4.58
A8K0P8	tr|A8K0P8|A8K0P8_HUMAN U3 small nucleolar RNA-associated protein 25 homolog OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.060%	87055.92	5.49
A8K4W5	tr|A8K4W5|A8K4W5_HUMAN cDNA FLJ76813, highly similar to Homo sapiens acetyl-Coenzyme A acetyltransferase 2 (acetoacetyl Coenzyme A thiolase), mRNA OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	2.770%	41378.44	6.47
A8K5C4	tr|A8K5C4|A8K5C4_HUMAN cDNA FLJ76290, highly similar to Homo sapiens TIA1 cytotoxic granule-associated RNA bindingprotein-like 1 (TIAL1), transcript variant 1, mRNA OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	2.930%	41576.22	7.62
A8K5W7	tr|A8K5W7|A8K5W7_HUMAN Isoleucyl-tRNA synthetase OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	0.850%	105939.31	6.01
A8K5Y7	tr|A8K5Y7|A8K5Y7_HUMAN cDNA FLJ78655, highly similar to Homo sapiens exportin 5 (XPO5), mRNA OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	0.830%	136308.83	5.63
A8K6Q9	tr|A8K6Q9|A8K6Q9_HUMAN cDNA FLJ75882, highly similar to Homo sapiens spastic paraplegia 20, spartin (Troyer syndrome) (SPG20), mRNA OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.800%	72831.17	5.72
A8K732	tr|A8K732|A8K732_HUMAN cDNA FLJ78771, highly similar to Homo sapiens discs, large homolog 7 (Drosophila), mRNA OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.770%	95129.92	9.11
A8K7A2	tr|A8K7A2|A8K7A2_HUMAN cDNA FLJ78084, highly similar to Homo sapiens cell division cycle associated 8, mRNA OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	3.210%	31310.54	9.88

A8K7W3	tr|A8K7W3|A8K7W3_HUMAN cDNA FLJ75780, highly similar to Homo sapiens SGT1, suppressor of G2 allele of SKP1 (SUGT1), mRNA OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	3.600%	37833.13	5.06
A8K897	tr|A8K897|A8K897_HUMAN Nuclear pore complex protein Nup93 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.340%	93381.11	5.54
A8K8W7	tr|A8K8W7|A8K8W7_HUMAN Hormone-sensitive lipase OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	0.840%	116582.53	6.25
A8K9T9	tr|A8K9T9|A8K9T9_HUMAN Formylglycinamide ribonucleotide amidotransferase OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	0.820%	144641.61	5.52
B1AK63	tr|B1AK63|B1AK63_HUMAN Chromatin modification-related protein MEAF6 OS=Homo sapiens OX=9606 GN=MEAF6 PE=1 SV=1	MEAF6	1	1	4.140%	19163.78	9.05
B1AK87	tr|B1AK87|B1AK87_HUMAN F-actin-capping protein subunit beta OS=Homo sapiens OX=9606 GN=CAPZB PE=1 SV=2	CAPZB	1	1	3.690%	27439.79	5.33
B2R748	tr|B2R748|B2R748_HUMAN Interleukin-1 receptor-associated kinase-like 2 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.020%	65255.74	5.7
B2R7U5	tr|B2R7U5|B2R7U5_HUMAN cDNA, FLJ93607 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	3.230%	21355.63	7.59
B2R886	tr|B2R886|B2R886_HUMAN Dendritic cell-derived ubiquitin-like protein, isoform CRA_a OS=Homo sapiens OX=9606 GN=DC-UbP PE=1 SV=1	DC-UbP	1	1	2.630%	21548.17	5.17
B2RAQ9	tr|B2RAQ9|B2RAQ9_HUMAN Proteasome subunit beta OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	4.330%	29931.09	7.58
B2RB99	tr|B2RB99|B2RB99_HUMAN Replication termination factor 2 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	2.290%	33798.16	8.87
B2RD60	tr|B2RD60|B2RD60_HUMAN cDNA, FLJ96471, highly similar to Homo sapiens GABA(A) receptor-associated protein like 1(GABARAPL1), mRNA OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	5.980%	14071.9	8.69

B2RDG4	tr|B2RDG4|B2RDG4_HUMAN cDNA, FLJ96597 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	3.540%	57432.28	8.9
B2RNG4	tr|B2RNG4|B2RNG4_HUMAN RING-type E3 ubiquitin transferase OS=Homo sapiens OX=9606 GN=TRIM6-TRIM34 PE=2 SV=1	TRIM6-TRIM	1	1	0.950%	97728.26	7.89
B2RWN9	tr|B2RWN9|B2RWN9_HUMAN DOPEY1 protein OS=Homo sapiens OX=9606 GN=DOPEY1 PE=2 SV=1	DOPEY1	1	1	0.240%	276435.43	5.9
B3KM90	tr|B3KM90|B3KM90_HUMAN cDNA FLJ10529 fis, clone NT2RP2000965, highly similar to Targeting protein for Xklp2 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.490%	69757.52	9.39
B3KMD8	tr|B3KMD8|B3KMD8_HUMAN Transcription initiation factor TFIID 150 kDa subunit OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.980%	57036.67	9.04
B3KMI9	tr|B3KMI9|B3KMI9_HUMAN cDNA FLJ11140 fis, clone PLACE1006488, highly similar to Signal recognition particle 68 kDa protein OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	2.440%	41372.41	8.92
B3KMK0	tr|B3KMK0|B3KMK0_HUMAN Nuclear pore complex protein OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.180%	69205.48	5.26
B3KMW4	tr|B3KMW4|B3KMW4_HUMAN Phosphoinositide 5-phosphatase OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.600%	85641.5	5.55
B3KN43	tr|B3KN43|B3KN43_HUMAN 39S ribosomal protein L27, mitochondrial OS=Homo sapiens OX=9606 GN=MRPL27 PE=1 SV=1	MRPL27	1	1	12.770%	9911.39	11.65
B3KN52	tr|B3KN52|B3KN52_HUMAN cDNA FLJ13606 fis, clone PLACE1010579, highly similar to Homo sapiens GULP, engulfment adaptor PTB domain containing 1 (GULP1), mRNA OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	2.630%	34460.06	8.04
B3KNC3	tr|B3KNC3|B3KNC3_HUMAN Nucleolar complex protein 2 homolog OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.340%	84916.47	5.46
B3KNS8	tr|B3KNS8|B3KNS8_HUMAN cDNA FLJ30322 fis, clone BRACE2006703, highly similar to Surfeit locus protein 6 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.660%	41507.94	10.6

B3KPB2	tr|B3KPB2|B3KPB2_HUMAN Centromere protein T OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	0.890%	60363.96	6.22
B3KQG6	tr|B3KQG6|B3KQG6_HUMAN cDNA FLJ90427 fis, clone NT2RP3000481, highly similar to Importin-7 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.250%	82514.9	4.49
B3KQI2	tr|B3KQI2|B3KQI2_HUMAN cDNA FLJ90497 fis, clone NT2RP3003874, highly similar to Myosin Ib OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	2.620%	44809.57	10.07
B3KQY9	tr|B3KQY9|B3KQY9_HUMAN DNA-directed RNA polymerase OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.530%	58819.14	6.91
B3KTL1	tr|B3KTL1|B3KTL1_HUMAN cDNA FLJ38439 fis, clone FEBRA2016739, highly similar to Alpha-N-acetylgalactosaminidealpha-2,6-sialyltransferase 5 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	6.160%	16649.91	10.02
B3KV46	tr|B3KV46|B3KV46_HUMAN Dihydrofolate reductase OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	3.740%	21593.77	7.75
B3KXF4	tr|B3KXF4|B3KXF4_HUMAN cDNA FLJ45324 fis, clone BRHIP3006449, highly similar to Catenin delta-2 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.640%	87158.06	8.63
B3KXN0	tr|B3KXN0|B3KXN0_HUMAN cDNA FLJ45747 fis, clone LIVER2008465 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	2.550%	31443.27	8.69
B4DEH8	tr|B4DEH8|B4DEH8_HUMAN Polyadenylate-binding protein 2 OS=Homo sapiens OX=9606 GN=PABPN1 PE=1 SV=1	PABPN1	1	1	6.550%	18990.08	9.3
B4DEQ8	tr|B4DEQ8|B4DEQ8_HUMAN cDNA FLJ60443, moderately similar to Protocadherin-8 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	0.660%	96866.54	5.48
B4DFE8	tr|B4DFE8|B4DFE8_HUMAN Creatine kinase OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	3.940%	28335.18	7.01
B4DFQ5	tr|B4DFQ5|B4DFQ5_HUMAN cDNA FLJ58134, highly similar to Cleavage stimulation factor 77 kDa subunit OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.120%	72184.4	7.56

B4DGF8	tr|B4DGF8|B4DGF8_HUMAN cDNA FLJ57877, highly similar to Cleavage and polyadenylation specificity factor 7 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.730%	51105.34	7.33
B4DGV9	tr|B4DGV9|B4DGV9_HUMAN cDNA FLJ55891, highly similar to Sterol regulatory element-binding protein 1 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	0.650%	114594.05	9.08
B4DHP3	tr|B4DHP3|B4DHP3_HUMAN cDNA FLJ56346, highly similar to Regulator of nonsense transcripts 2 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	3.360%	34039.95	4.46
B4DHU9	tr|B4DHU9|B4DHU9_HUMAN Glycylpeptide N-tetradecanoyltransferase OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.440%	56524.55	9.38
B4DID5	tr|B4DID5|B4DID5_HUMAN Transaldolase OS=Homo sapiens OX=9606 GN=TALDO1 PE=2 SV=1	TALDO1	1	1	5.190%	17073.37	6.61
B4DJ66	tr|B4DJ66|B4DJ66_HUMAN 26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens OX=9606 GN=PSMD13 PE=2 SV=1	PSMD13	1	1	3.220%	35346.55	5.68
B4DJN0	tr|B4DJN0|B4DJN0_HUMAN cDNA FLJ51641, highly similar to Nicastrin OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	2.440%	50288.33	5.45
B4DJX9	tr|B4DJX9|B4DJX9_HUMAN Syntaxin 16, isoform CRA_c OS=Homo sapiens OX=9606 GN=STX16 PE=2 SV=1	STX16	1	1	4.320%	16277.58	5.09
B4DKC2	tr|B4DKC2|B4DKC2_HUMAN cDNA FLJ55802, highly similar to Protein RUFY3 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.990%	51401.25	5.05
B4DKZ7	tr|B4DKZ7|B4DKZ7_HUMAN cDNA FLJ55704, highly similar to Transcriptional repressor p66 alpha OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	2.750%	46806.31	10.25
B4DLL7	tr|B4DLL7|B4DLL7_HUMAN cDNA FLJ57319, highly similar to Sorting nexin-17 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.550%	43573.16	6.41
B4DMB4	tr|B4DMB4|B4DMB4_HUMAN Synaptobrevin-like 1, isoform CRA_a OS=Homo sapiens OX=9606 GN=SYBL1 PE=2 SV=1	SYBL1	1	1	10.920%	13338.64	8.86
B4DMF3	tr|B4DMF3|B4DMF3_HUMAN cDNA FLJ58122, highly similar to Kinesin-like protein KIF1B OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	0.680%	99184.65	5.54

B4DNM8	tr|B4DNM8|B4DNM8_HUMAN Procollagen-proline 3-dioxygenase OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	2.160%	68987.52	4.93
B4DQD4	tr|B4DQD4|B4DQD4_HUMAN cDNA FLJ58389, highly similar to N-myc-interactor OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	3.950%	17358.43	4.98
B4DR88	tr|B4DR88|B4DR88_HUMAN RNA helicase OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	1.110%	72189.74	8.7
B4DSL9	tr|B4DSL9|B4DSL9_HUMAN cDNA FLJ58748, highly similar to U3 small nucleolar RNA-associated protein 6homolog OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	3.030%	39077.5	6.15
B4DSQ1	tr|B4DSQ1|B4DSQ1_HUMAN Microtubule-associated protein OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	4.420%	26119.53	10.75
B4DSS6	tr|B4DSS6|B4DSS6_HUMAN cDNA FLJ56649, highly similar to Homo sapiens serine/threonine kinase 11 interacting protein (STK11IP), mRNA OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	5.790%	13061.86	6.82
B4DSU7	tr|B4DSU7|B4DSU7_HUMAN cDNA FLJ60866, highly similar to Protein FAM13C1 OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	1.390%	56416.42	6.22
B4DSU9	tr|B4DSU9|B4DSU9_HUMAN cDNA FLJ58421, highly similar to Cleavage and polyadenylation specificity factor 6 OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	8.330%	33572.3	5.85
B4DTH9	tr|B4DTH9|B4DTH9_HUMAN cDNA FLJ53190, highly similar to Beta-glucuronidase OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	1.670%	41466.73	7.73
B4DV84	tr|B4DV84|B4DV84_HUMAN cDNA FLJ56159, highly similar to 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	2.890%	59385	6.92
B4DW39	tr|B4DW39|B4DW39_HUMAN cDNA FLJ60915, highly similar to Fc receptor-like protein 5 OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	0.980%	67633.85	6.85
B4DWF8	tr|B4DWF8|B4DWF8_HUMAN cDNA FLJ53414, highly similar to Nuclear pore complex protein Nup98-Nup96precursor OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	1.950%	70941.67	6.02
B4DX19	tr|B4DX19|B4DX19_HUMAN Paraoxonase OS=Homo sapiens OX=9606 PE=2 SV=1	1	1	3.100%	39720.75	4.79

B4DXJ8	tr|B4DXJ8|B4DXJ8_HUMAN cDNA FLJ54970, highly similar to Zinc finger protein 462 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.730%	53093.17	6.51
B4DY32	tr|B4DY32|B4DY32_HUMAN Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	2.300%	54861.1	5.97
B4DYI0	tr|B4DYI0|B4DYI0_HUMAN cDNA FLJ51573, highly similar to Golgin subfamily A member 1 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	0.900%	76853.79	5.11
B4DZ26	tr|B4DZ26|B4DZ26_HUMAN cDNA FLJ52371 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	0.480%	115111.41	6.12
B4E002	tr|B4E002|B4E002_HUMAN cDNA FLJ59804, moderately similar to BCoR protein OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	5.110%	19603.26	8.69
B4E0B7	tr|B4E0B7|B4E0B7_HUMAN Condensin complex subunit 1 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	0.740%	152235.91	6.32
B4E1K8	tr|B4E1K8|B4E1K8_HUMAN Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens OX=9606 GN=EIF3D PE=2 SV=1	EIF3D	1	1	1.770%	52826.91	5.6
B4E1S3	tr|B4E1S3|B4E1S3_HUMAN cDNA FLJ57860, highly similar to Transmembrane protein 109 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	5.130%	24983.42	9.63
B4E1U2	tr|B4E1U2|B4E1U2_HUMAN cDNA FLJ53421, highly similar to Homo sapiens guanylate binding protein family, member 6 (GBP6), mRNA OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.160%	69197.18	5.83
B4E290	tr|B4E290|B4E290_HUMAN cDNA FLJ50039, highly similar to Homo sapiens solute carrier family 25, member 24, transcript variant 1, mRNA OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.260%	53295.8	6.22
B4E2M7	tr|B4E2M7|B4E2M7_HUMAN Tektin OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.840%	30983.94	5.79
B4E3V9	tr|B4E3V9|B4E3V9_HUMAN cDNA FLJ50388, highly similar to Protein FAN OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.440%	48199.57	8.94
B5MDQ0	tr|B5MDQ0|B5MDQ0_HUMAN DNA excision repair protein ERCC-6-like OS=Homo sapiens OX=9606 GN=ERCC6L PE=1 SV=1	ERCC6L	1	1	1.240%	126981.78	5.27

B5MEB3	tr|B5MEB3|B5MEB3_HUMAN Calcineurin binding protein 1, isoform CRA_c OS=Homo sapiens OX=9606 GN=CABIN1 PE=1 SV=1	CABIN1	1	1	1.530%	63323.53	6.33
B7Z1C8	tr|B7Z1C8|B7Z1C8_HUMAN cDNA FLJ52250, highly similar to NEDD8 ultimate buster 1 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	3.660%	19263.15	9.84
B7Z1J1	tr|B7Z1J1|B7Z1J1_HUMAN cDNA FLJ59585 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	9.940%	17861.76	9.4
B7Z3A4	tr|B7Z3A4|B7Z3A4_HUMAN cDNA FLJ56906, highly similar to RNA-binding protein 16 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	0.520%	148866.15	9.14
B7Z3E3	tr|B7Z3E3|B7Z3E3_HUMAN Reticulon OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.200%	100822.75	4.84
B7Z4G9	tr|B7Z4G9|B7Z4G9_HUMAN cDNA FLJ59344, highly similar to Membrane protein MLC1 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	2.040%	37414.34	6.82
B7Z570	tr|B7Z570|B7Z570_HUMAN cDNA FLJ53078, highly similar to Splicing factor, arginine/serine-rich 1 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	8.390%	16219.76	11.09
B7Z6I9	tr|B7Z6I9|B7Z6I9_HUMAN Nitric-oxide synthase (NADPH) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	0.900%	111164.48	6.33
B7Z6Q2	tr|B7Z6Q2|B7Z6Q2_HUMAN Zinc finger protein 346 OS=Homo sapiens OX=9606 GN=ZNF346 PE=1 SV=1	ZNF346	1	1	6.670%	15050.9	8.35
B7Z6Q9	tr|B7Z6Q9|B7Z6Q9_HUMAN Cholecystokinin-12 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	14.410%	11598.42	11.16
B7Z7A2	tr|B7Z7A2|B7Z7A2_HUMAN Phosphodiesterase OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.400%	57468.33	6.86
B7Z8N7	tr|B7Z8N7|B7Z8N7_HUMAN Cytoplasmic FMR1-interacting protein OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	0.980%	142586.3	6.63
B7Z9I1	tr|B7Z9I1|B7Z9I1_HUMAN Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 PE=1 SV=1		1	1	3.120%	42426.11	6.1

B7ZAE8	tr|B7ZAE8|B7ZAE8_HUMAN cDNA, FLJ79162, highly similar to Protocadherin-11 X-linked (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.340%	99034.41	4.71
B7ZB79	tr|B7ZB79|B7ZB79_HUMAN Frizzled-6 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.040%	75319.31	8.25
B7ZKP0	tr|B7ZKP0|B7ZKP0_HUMAN Uncharacterized protein OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.720%	37882.28	8.43
B7ZKX2	tr|B7ZKX2|B7ZKX2_HUMAN Uncharacterized protein OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	0.790%	117665.05	9.49
B7ZME4	tr|B7ZME4|B7ZME4_HUMAN TXNDC16 protein OS=Homo sapiens OX=9606 GN=TXNDC16 PE=2 SV=1	TXNDC16	1	1	1.220%	93039.17	5.1
B7ZMH4	tr|B7ZMH4|B7ZMH4_HUMAN ODZ1 protein OS=Homo sapiens OX=9606 GN=ODZ1 PE=2 SV=1	ODZ1	1	1	0.260%	305872.78	6.02
B9EFN7	tr|B9EFN7|B9EFN7_HUMAN NADH-ubiquinone oxidoreductase chain 5 OS=Homo sapiens OX=9606 GN=NADH5 PE=3 SV=1	NADH5	1	1	1.160%	66968.69	9.14
B9EGR7	tr|B9EGR7|B9EGR7_HUMAN ARHGEF5 OS=Homo sapiens OX=9606 GN=ARHGEF5 PE=2 SV=1	ARHGEF5	1	1	0.380%	176637.23	5.39
C9IYC5	tr|C9IYC5|C9IYC5_HUMAN Sorting nexin-8 (Fragment) OS=Homo sapiens OX=9606 GN=SNX8 PE=1 SV=1	SNX8	1	1	14.290%	4858.68	6.01
C9IZ80	tr|C9IZ80|C9IZ80_HUMAN Basic leucine zipper and W2 domain-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=BZW1 PE=1 SV=1	BZW1	1	1	2.040%	33454.07	7.63
C9IZK7	tr|C9IZK7|C9IZK7_HUMAN WD repeat-containing protein 43 (Fragment) OS=Homo sapiens OX=9606 GN=WDR43 PE=1 SV=1	WDR43	1	1	4.280%	20925	8.66
C9IZN5	tr|C9IZN5|C9IZN5_HUMAN Complex I subunit B13 OS=Homo sapiens OX=9606 GN=NDUFA5 PE=1 SV=2	NDUFA5	1	1	6.120%	11169.13	7.75
C9IZR8	tr|C9IZR8|C9IZR8_HUMAN Engulfment and cell motility protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=ELMO1 PE=1 SV=1	ELMO1	1	1	3.590%	18622.93	4.7

C9J1C5	tr|C9J1C5|C9J1C5_HUMAN 40S ribosomal protein S27 OS=Homo sapiens OX=9606 GN=RPS27L PE=3 SV=1	RPS27L	1	1	15.380%	5646.62	9.12
C9J2C4	tr|C9J2C4|C9J2C4_HUMAN DnaJ homolog subfamily B member 6 (Fragment) OS=Homo sapiens OX=9606 GN=DNAJB6 PE=1 SV=1	DNAJB6	1	1	4.390%	25376.59	6.46
C9J470	tr|C9J470|C9J470_HUMAN Condensin complex subunit 2 (Fragment) OS=Homo sapiens OX=9606 GN=NCAPH PE=1 SV=8	NCAPH	1	1	1.810%	68010.64	4.79
C9J4N6	tr|C9J4N6|C9J4N6_HUMAN Isocitrate dehydrogenase [NADP] cytoplasmic (Fragment) OS=Homo sapiens OX=9606 GN=IDH1 PE=1 SV=1	IDH1	1	1	5.730%	17719.3	8.48
C9J6F6	tr|C9J6F6|C9J6F6_HUMAN Aquaporin OS=Homo sapiens OX=9606 GN=AQP12A PE=3 SV=1	AQP12A	1	1	1.630%	32644.61	8.09
C9J8P0	tr|C9J8P0|C9J8P0_HUMAN Calcium/calmodulin-dependent protein kinase type 1B (Fragment) OS=Homo sapiens OX=9606 GN=PNCK PE=1 SV=1	PNCK	1	1	6.380%	10362.03	10.11
C9JER0	tr|C9JER0|C9JER0_HUMAN POM121 and ZP3 fusion protein OS=Homo sapiens OX=9606 GN=POMZP3 PE=4 SV=1	POMZP3	1	1	5.190%	17273.84	9.63
C9JHK9	tr|C9JHK9|C9JHK9_HUMAN ATP-binding cassette sub-family F member 2 (Fragment) OS=Homo sapiens OX=9606 GN=ABCF2 PE=1 SV=1	ABCF2	1	1	2.920%	26929.57	6.34
C9JKA9	tr|C9JKA9|C9JKA9_HUMAN Kinesin-like protein KIF15 OS=Homo sapiens OX=9606 GN=KIF15 PE=1 SV=1	KIF15	1	1	1.170%	120338.01	5.44
C9JMZ3	tr|C9JMZ3|C9JMZ3_HUMAN Aminopeptidase B (Fragment) OS=Homo sapiens OX=9606 GN=RNPEP PE=1 SV=1	RNPEP	1	1	3.490%	38998.29	4.92
C9JPA8	tr|C9JPA8|C9JPA8_HUMAN Golgi to ER traffic protein 4 homolog (Fragment) OS=Homo sapiens OX=9606 GN=GET4 PE=1 SV=2	GET4	1	1	6.760%	16542.55	5.46
C9JYT6	tr|C9JYT6|C9JYT6_HUMAN Semaphorin-3D OS=Homo sapiens OX=9606 GN=SEMA3D PE=1 SV=1	SEMA3D	1	1	2.040%	33634.14	6.15
C9JZR2	tr|C9JZR2|C9JZR2_HUMAN Catenin delta-1 OS=Homo sapiens OX=9606 GN=CTNND1 PE=1 SV=2	CTNND1	1	1	0.750%	104847.32	6.41

D3DWL0	tr|D3DWL0|D3DWL0_HUMAN Plectin 1, intermediate filament binding protein 500kDa, isoform CRA_b OS=Homo sapiens OX=9606 GN=PLEC1 PE=4 SV=1	PLEC1	1	1	0.480%	234116.41	5.7
D6RAE5	tr|D6RAE5|D6RAE5_HUMAN DNA polymerase kappa OS=Homo sapiens OX=9606 GN=POLK PE=1 SV=1	POLK	1	1	3.540%	45316.5	8.09
D6RBC8	tr|D6RBC8|D6RBC8_HUMAN Spermatogenesis-associated protein 24 OS=Homo sapiens OX=9606 GN=SPATA24 PE=1 SV=1	SPATA24	1	1	3.010%	18253.88	9.68
D6RD36	tr|D6RD36|D6RD36_HUMAN Regulator of G-protein-signaling 8 (Fragment) OS=Homo sapiens OX=9606 GN=RGS8 PE=1 SV=1	RGS8	1	1	14.040%	6452.41	10.04
D6REZ7	tr|D6REZ7|D6REZ7_HUMAN Nuclear receptor subfamily 1 group I member 3 OS=Homo sapiens OX=9606 GN=NR1I3 PE=3 SV=1	NR1I3	1	1	3.300%	31371.33	7.77
D6RJ99	tr|D6RJ99|D6RJ99_HUMAN DNA damage-inducible transcript 4-like protein (Fragment) OS=Homo sapiens OX=9606 GN=DDIT4L PE=3 SV=1	DDIT4L	1	1	3.950%	20020.85	6.14
D6RJE8	tr|D6RJE8|D6RJE8_HUMAN Eukaryotic peptide chain release factor subunit 1 (Fragment) OS=Homo sapiens OX=9606 GN=ETF1 PE=1 SV=8	ETF1	1	1	10.920%	13231.26	8.56
D6W625	tr|D6W625|D6W625_HUMAN Chromatin assembly factor 1, subunit A (P150), isoform CRA_a OS=Homo sapiens OX=9606 GN=CHAF1A PE=3 SV=1	CHAF1A	1	1	1.050%	106936.71	5.69
D9ZGF8	tr|D9ZGF8|D9ZGF8_HUMAN Rho-associated protein kinase OS=Homo sapiens OX=9606 GN=ROCK1 PE=3 SV=1	ROCK1	1	1	0.660%	158242.01	5.69
E2QRN4	tr|E2QRN4|E2QRN4_HUMAN DBIRD complex subunit ZNF326 OS=Homo sapiens OX=9606 GN=ZNF326 PE=1 SV=1	ZNF326	1	1	15.090%	5967.54	4.88
E5RFP7	tr|E5RFP7|E5RFP7_HUMAN N-acetyltransferase ESCO2 (Fragment) OS=Homo sapiens OX=9606 GN=ESCO2 PE=1 SV=1	ESCO2	1	1	5.260%	15325.24	9.13
E5RHY6	tr|E5RHY6|E5RHY6_HUMAN Serine/threonine-protein kinase Sgk3 (Fragment) OS=Homo sapiens OX=9606 GN=SGK3 PE=1 SV=1	SGK3	1	1	3.610%	19706.43	9.57
E5RIM3	tr|E5RIM3|E5RIM3_HUMAN Phospholipase A-2-activating protein OS=Homo sapiens OX=9606 GN=PLAA PE=1 SV=1	PLAA	1	1	2.790%	66733.65	5.66

E7ENQ1	tr|E7ENQ1|E7ENQ1_HUMAN Mitogen-activated protein kinase kinase kinase kinase 4 OS=Homo sapiens OX=9606 GN=MAP4K4 PE=1 SV=1	MAP4K4	1	1	0.610%	132164.34	7.22
E7EPD2	tr|E7EPD2|E7EPD2_HUMAN Signal transducer and activator of transcription 1-alpha/beta (Fragment) OS=Homo sapiens OX=9606 GN=STAT1 PE=1 SV=2	STAT1	1	1	3.180%	45026.88	6.29
E7ERI8	tr|E7ERI8|E7ERI8_HUMAN CLIP-associating protein 2 OS=Homo sapiens OX=9606 GN=CLASP2 PE=1 SV=1	CLASP2	1	1	1.060%	165625.78	8.5
E7EUY5	tr|E7EUY5|E7EUY5_HUMAN Single-stranded DNA-binding protein, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=SSBP1 PE=1 SV=1	SSBP1	1	1	11.110%	15712.73	9.84
E7EW71	tr|E7EW71|E7EW71_HUMAN Mu-type opioid receptor (Fragment) OS=Homo sapiens OX=9606 GN=OPRM1 PE=1 SV=8	OPRM1	1	1	4.940%	17265.73	9
E9PB51	tr|E9PB51|E9PB51_HUMAN RNA-binding protein 4 (Fragment) OS=Homo sapiens OX=9606 GN=RBM4 PE=1 SV=1	RBM4	1	1	4.170%	26286.25	7.12
E9PFI7	tr|E9PFI7|E9PFI7_HUMAN Poly [ADP-ribose] polymerase OS=Homo sapiens OX=9606 GN=PARP8 PE=1 SV=1	PARP8	1	1	0.840%	93380.01	8.6
E9PJ40	tr|E9PJ40|E9PJ40_HUMAN Receptor-binding cancer antigen-expressed on SiSo cells (Fragment) OS=Homo sapiens OX=9606 GN=EBAG9 PE=1 SV=1	EBAG9	1	1	19.510%	4514.21	10.43
E9PLJ3	tr|E9PLJ3|E9PLJ3_HUMAN Cofilin, non-muscle isoform (Fragment) OS=Homo sapiens OX=9606 GN=CFL1 PE=1 SV=1	CFL1	1	1	13.920%	9090.44	8.5
E9PP00	tr|E9PP00|E9PP00_HUMAN Probable ribonuclease ZC3H12C OS=Homo sapiens OX=9606 GN=ZC3H12C PE=1 SV=1	ZC3H12C	1	1	1.290%	95877.27	6.4
E9PP83	tr|E9PP83|E9PP83_HUMAN E3 ubiquitin-protein ligase TRIM68 (Fragment) OS=Homo sapiens OX=9606 GN=TRIM68 PE=1 SV=1	TRIM68	1	1	4.230%	16856.02	7.78
E9PR30	tr|E9PR30|E9PR30_HUMAN 40S ribosomal protein S30 OS=Homo sapiens OX=9606 GN=FAU PE=1 SV=1	FAU	1	1	10.200%	10904.68	11.56
F1T0H9	tr|F1T0H9|F1T0H9_HUMAN Uncharacterized protein OS=Homo sapiens OX=9606 GN=EYS PE=2 SV=1	EYS	1	1	16.440%	7623.68	5.99

F5GWJ5	tr|F5GWJ5|F5GWJ5_HUMAN Roundabout homolog 3 OS=Homo sapiens OX=9606 GN=ROBO3 PE=1 SV=1	ROBO3	1	1	0.510%	146054.87	6.88
F5GXQ8	tr|F5GXQ8|F5GXQ8_HUMAN Nesprin-1 OS=Homo sapiens OX=9606 GN=SYNE1 PE=1 SV=1	SYNE1	1	1	0.490%	166123.48	6.18
F5GZ28	tr|F5GZ28|F5GZ28_HUMAN DNA ligase OS=Homo sapiens OX=9606 GN=LIG1 PE=1 SV=1	LIG1	1	1	0.710%	93946.48	5.77
F5GZS6	tr|F5GZS6|F5GZS6_HUMAN 4F2 cell-surface antigen heavy chain OS=Homo sapiens OX=9606 GN=SLC3A2 PE=1 SV=1	SLC3A2	1	1	2.170%	64871.72	4.97
F5H1Y3	tr|F5H1Y3|F5H1Y3_HUMAN Flap endonuclease 1 (Fragment) OS=Homo sapiens OX=9606 GN=FEN1 PE=1 SV=1	FEN1	1	1	6.670%	18274.78	6.84
F5H1Y4	tr|F5H1Y4|F5H1Y4_HUMAN Golgi-associated PDZ and coiled-coil motif containing protein transcript variant 3 OS=Homo sapiens OX=9606 GN=GOPC PE=1 SV=2	GOPC	1	1	1.720%	44789.93	5.46
F5H2T0	tr|F5H2T0|F5H2T0_HUMAN IkappaB kinase complex-associated protein OS=Homo sapiens OX=9606 GN=ELP1 PE=1 SV=1	ELP1	1	1	1.220%	111474.11	5.87
F5H3Y4	tr|F5H3Y4|F5H3Y4_HUMAN Probable ATP-dependent RNA helicase DHX37 (Fragment) OS=Homo sapiens OX=9606 GN=DHX37 PE=1 SV=2	DHX37	1	1	0.600%	110690.59	7.25
F5H4D1	tr|F5H4D1|F5H4D1_HUMAN Adenylate cyclase OS=Homo sapiens OX=9606 GN=ADCY7 PE=1 SV=1	ADCY7	1	1	0.820%	81477.44	8.94
F5H5R4	tr|F5H5R4|F5H5R4_HUMAN Mas-related G-protein-coupled receptor member F OS=Homo sapiens OX=9606 GN=MRGPRF PE=1 SV=1	MRGPRF	1	1	7.690%	10613.88	5.53
F8VPN9	tr|F8VPN9|F8VPN9_HUMAN Vezatin (Fragment) OS=Homo sapiens OX=9606 GN=VEZT PE=1 SV=1	VEZT	1	1	6.740%	10197.72	4.98
F8VT91	tr|F8VT91|F8VT91_HUMAN SPATS2-like protein (Fragment) OS=Homo sapiens OX=9606 GN=SPATS2L PE=1 SV=1	SPATS2L	1	1	2.660%	20885.36	9.39
F8VU08	tr|F8VU08|F8VU08_HUMAN Hematopoietically-expressed homeobox protein HHEX OS=Homo sapiens OX=9606 GN=HHEX PE=1 SV=1	HHEX	1	1	6.120%	11252.95	4.51

F8VU51	tr|F8VU51|F8VU51_HUMAN YLP motif-containing protein 1 OS=Homo sapiens OX=9606 GN=YLPM1 PE=1 SV=1	YLPM1	1	1	0.900%	160739.95	6.11
F8VV63	tr|F8VV63|F8VV63_HUMAN Uncharacterized protein C12orf42 OS=Homo sapiens OX=9606 GN=C12orf42 PE=4 SV=1	C12orf42	1	1	3.410%	31951.79	9.79
F8W122	tr|F8W122|F8W122_HUMAN Phosphatidylinositol phosphatase PTPRQ (Fragment) OS=Homo sapiens OX=9606 GN=PTPRQ PE=4 SV=1	PTPRQ	1	1	1.810%	37137.45	9.4
F8W7R3	tr|F8W7R3|F8W7R3_HUMAN Fanconi anemia group I protein OS=Homo sapiens OX=9606 GN=FANCI PE=1 SV=1	FANCI	1	1	1.370%	123240.36	5.9
F8WAQ4	tr|F8WAQ4|F8WAQ4_HUMAN BTB/POZ domain-containing protein 3 OS=Homo sapiens OX=9606 GN=BTBD3 PE=1 SV=1	BTBD3	1	1	14.000%	5692.32	9.52
F8WBU7	tr|F8WBU7|F8WBU7_HUMAN Calcium/calmodulin-dependent protein kinase type 1B OS=Homo sapiens OX=9606 GN=PNCK PE=1 SV=1	PNCK	1	1	7.320%	9381.49	11.65
F8WFB6	tr|F8WFB6|F8WFB6_HUMAN Apoptosis-inducing factor 3 OS=Homo sapiens OX=9606 GN=AIFM3 PE=1 SV=1	AIFM3	1	1	9.920%	13223.7	7.01
G1UI16	tr|G1UI16|G1UI16_HUMAN SCC-112 protein, isoform CRA_b OS=Homo sapiens OX=9606 GN=PDS5A PE=2 SV=1	PDS5A	1	1	0.970%	150828.47	8.15
G1UI22	tr|G1UI22|G1UI22_HUMAN Afadin OS=Homo sapiens OX=9606 GN=MLLT4 PE=2 SV=1	MLLT4	1	1	0.560%	201817.36	6.11
G3V121	tr|G3V121|G3V121_HUMAN Coiled-coil domain-containing protein 25 OS=Homo sapiens OX=9606 GN=CCDC25 PE=1 SV=1	CCDC25	1	1	10.470%	9950.16	5.91
G3V1B6	tr|G3V1B6|G3V1B6_HUMAN MICOS complex subunit MIC26 OS=Homo sapiens OX=9606 GN=APOO PE=1 SV=1	APOO	1	1	17.540%	13101.09	6.72
G3V1L9	tr|G3V1L9|G3V1L9_HUMAN Tight junction protein ZO-1 OS=Homo sapiens OX=9606 GN=TJP1 PE=1 SV=2	TJP1	1	1	0.430%	208292.23	6.8
G3V1M5	tr|G3V1M5|G3V1M5_HUMAN Transmembrane protein 134 OS=Homo sapiens OX=9606 GN=TMEM134 PE=1 SV=1	TMEM134	1	1	9.240%	12154.02	4.39

G3V3A5	tr|G3V3A5|G3V3A5_HUMAN Tetratricopeptide repeat protein 6 OS=Homo sapiens OX=9606 GN=TTC6 PE=1 SV=1	TTC6	1	1	0.530%	216441.93	8.94
G3V4I8	tr|G3V4I8|G3V4I8_HUMAN G patch domain-containing protein 2-like (Fragment) OS=Homo sapiens OX=9606 GN=GPATCH2L PE=4 SV=2	GPATCH2L	1	1	19.350%	3161.62	12.18
G8JL96	tr|G8JL96|G8JL96_HUMAN Protein-tyrosine-phosphatase OS=Homo sapiens OX=9606 GN=PTPRS PE=1 SV=2	PTPRS	1	1	0.730%	168427.78	6.23
G8JLH2	tr|G8JLH2|G8JLH2_HUMAN M-phase inducer phosphatase OS=Homo sapiens OX=9606 GN=CDC25B PE=1 SV=1	CDC25B	1	1	3.270%	55959.64	6.53
G8YXX4	tr|G8YXX4|G8YXX4_HUMAN CD19-ligand protein OS=Homo sapiens OX=9606 GN=Bbtx1 PE=4 SV=1	Bbtx1	1	1	1.230%	53376.62	8.24
H0Y3V3	tr|H0Y3V3|H0Y3V3_HUMAN Adhesion G protein-coupled receptor L2 (Fragment) OS=Homo sapiens OX=9606 GN=ADGRL2 PE=1 SV=1	ADGRL2	1	1	1.270%	52311.07	5.93
H0Y4C5	tr|H0Y4C5|H0Y4C5_HUMAN NGFI-A-binding protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=NAB1 PE=1 SV=1	NAB1	1	1	2.500%	27655.88	8.8
H0Y534	tr|H0Y534|H0Y534_HUMAN Kinesin-like protein KIF16B (Fragment) OS=Homo sapiens OX=9606 GN=KIF16B PE=1 SV=8	KIF16B	1	1	5.950%	22632.45	5.42
H0Y5P8	tr|H0Y5P8|H0Y5P8_HUMAN BTB/POZ domain-containing protein KCTD3 (Fragment) OS=Homo sapiens OX=9606 GN=KCTD3 PE=1 SV=1	KCTD3	1	1	5.950%	18139.33	9.04
H0Y7V4	tr|H0Y7V4|H0Y7V4_HUMAN Dynein axonemal heavy chain 8 OS=Homo sapiens OX=9606 GN=DNAH8 PE=1 SV=1	DNAH8	1	1	0.170%	478865.43	5.8
H0Y7Z8	tr|H0Y7Z8|H0Y7Z8_HUMAN Probable ATP-dependent RNA helicase DDX59 (Fragment) OS=Homo sapiens OX=9606 GN=DDX59 PE=1 SV=1	DDX59	1	1	8.510%	10539.89	6.56
H0Y7Z9	tr|H0Y7Z9|H0Y7Z9_HUMAN Protein-tyrosine-phosphatase (Fragment) OS=Homo sapiens OX=9606 GN=PTPRF PE=1 SV=1	PTPRF	1	1	0.900%	150351.41	6.19
H0Y863	tr|H0Y863|H0Y863_HUMAN Pseudouridylate synthase 7 homolog (Fragment) OS=Homo sapiens OX=9606 GN=PUS7 PE=1 SV=1	PUS7	1	1	4.550%	15050.07	9.24

H0Y8H7	tr|H0Y8H7|H0Y8H7_HUMAN Rap guanine nucleotide exchange factor 2 (Fragment) OS=Homo sapiens OX=9606 GN=RAPGEF2 PE=1 SV=8	RAPGEF2	1	1	3.020%	28493.41	8.91
H0Y8S9	tr|H0Y8S9|H0Y8S9_HUMAN Methionine synthase reductase (Fragment) OS=Homo sapiens OX=9606 GN=MTRR PE=1 SV=1	MTRR	1	1	2.960%	40969.78	4.97
H0Y938	tr|H0Y938|H0Y938_HUMAN Coatomer subunit beta' OS=Homo sapiens OX=9606 GN=COPB2 PE=1 SV=2	COPB2	1	1	0.670%	101532.12	5.55
H0YA88	tr|H0YA88|H0YA88_HUMAN DNA polymerase nu (Fragment) OS=Homo sapiens OX=9606 GN=POLN PE=1 SV=1	POLN	1	1	1.150%	58361.79	9.25
H0YAD4	tr|H0YAD4|H0YAD4_HUMAN Zinc finger and BTB domain-containing protein 49 (Fragment) OS=Homo sapiens OX=9606 GN=ZBTB49 PE=4 SV=1	ZBTB49	1	1	4.100%	13778.22	7.08
H0YAF7	tr|H0YAF7|H0YAF7_HUMAN Neurolysin, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=NLN PE=1 SV=2	NLN	1	1	3.890%	31718.67	5.7
H0YBR0	tr|H0YBR0|H0YBR0_HUMAN Trafficking protein particle complex subunit 9 (Fragment) OS=Homo sapiens OX=9606 GN=TRAPPC9 PE=1 SV=1	TRAPPC9	1	1	0.600%	110088.67	6.39
H0YC14	tr|H0YC14|H0YC14_HUMAN Heat shock factor protein 4 (Fragment) OS=Homo sapiens OX=9606 GN=HSF4 PE=4 SV=1	HSF4	1	1	10.390%	8061.73	5.28
H0YCB4	tr|H0YCB4|H0YCB4_HUMAN Transcription factor p65 (Fragment) OS=Homo sapiens OX=9606 GN=RELA PE=1 SV=1	RELA	1	1	8.330%	8254.38	11.4
H0YDD8	tr|H0YDD8|H0YDD8_HUMAN 60S acidic ribosomal protein P2 (Fragment) OS=Homo sapiens OX=9606 GN=RPLP2 PE=1 SV=1	RPLP2	1	1	14.130%	8985.74	4.38
H0YDM2	tr|H0YDM2|H0YDM2_HUMAN Protein SOGA1 (Fragment) OS=Homo sapiens OX=9606 GN=SOGA1 PE=1 SV=1	SOGA1	1	1	1.180%	142114.17	5.94
H0YDV8	tr|H0YDV8|H0YDV8_HUMAN CD44 antigen (Fragment) OS=Homo sapiens OX=9606 GN=CD44 PE=1 SV=2	CD44	1	1	3.140%	21179.39	5.7
H0YE80	tr|H0YE80|H0YE80_HUMAN Ankyrin repeat domain-containing protein 42 (Fragment) OS=Homo sapiens OX=9606 GN=ANKRD42 PE=1 SV=1	ANKRD42	1	1	4.230%	16191.27	8.44

H0YEQ1	tr|H0YEQ1|H0YEQ1_HUMAN E3 ubiquitin-protein ligase RNF169 (Fragment) OS=Homo sapiens OX=9606 GN=RNF169 PE=1 SV=1	RNF169	1	1	12.660%	8988.05	9.3
H0YF54	tr|H0YF54|H0YF54_HUMAN von Willebrand factor A domain-containing protein 3B (Fragment) OS=Homo sapiens OX=9606 GN=VWA3B PE=1 SV=1	VWA3B	1	1	7.620%	11731.12	5.79
H0YFM3	tr|H0YFM3|H0YFM3_HUMAN Transmembrane 7 superfamily member 3 (Fragment) OS=Homo sapiens OX=9606 GN=TM7SF3 PE=1 SV=1	TM7SF3	1	1	4.000%	21870.68	9.08
H0YFT0	tr|H0YFT0|H0YFT0_HUMAN Transmembrane 7 superfamily member 3 (Fragment) OS=Homo sapiens OX=9606 GN=TM7SF3 PE=1 SV=1	TM7SF3	1	1	7.640%	16059.44	7.93
H0YG18	tr|H0YG18|H0YG18_HUMAN Mesothelin-like protein (Fragment) OS=Homo sapiens OX=9606 GN=MSLNL PE=3 SV=1	MSLNL	1	1	0.660%	79712.4	7.07
H0YG99	tr|H0YG99|H0YG99_HUMAN Forkhead box protein M1 (Fragment) OS=Homo sapiens OX=9606 GN=FOXM1 PE=1 SV=1	FOXM1	1	1	5.340%	22942.46	9.84
H0YGG4	tr|H0YGG4|H0YGG4_HUMAN Translation initiation factor eIF-2B subunit alpha (Fragment) OS=Homo sapiens OX=9606 GN=EIF2B1 PE=1 SV=1	EIF2B1	1	1	3.950%	16816.03	6.48
H0YGL3	tr|H0YGL3|H0YGL3_HUMAN T-cell differentiation antigen CD6 (Fragment) OS=Homo sapiens OX=9606 GN=CD6 PE=1 SV=8	CD6	1	1	3.240%	19895.72	5.96
H0YJ97	tr|H0YJ97|H0YJ97_HUMAN Thyroid receptor-interacting protein 11 (Fragment) OS=Homo sapiens OX=9606 GN=TRIP11 PE=1 SV=1	TRIP11	1	1	0.350%	195699.6	5.15
H0YJC6	tr|H0YJC6|H0YJC6_HUMAN Inositol 1,4,5-triphosphate receptor-associated 2 (Fragment) OS=Homo sapiens OX=9606 GN=IRAG2 PE=1 SV=1	IRAG2	1	1	14.430%	10947.42	5.6
H0YJR4	tr|H0YJR4|H0YJR4_HUMAN SH2 domain-containing adapter protein E (Fragment) OS=Homo sapiens OX=9606 GN=SHE PE=4 SV=1	SHE	1	1	21.950%	4472.91	9.11
H0YJS4	tr|H0YJS4|H0YJS4_HUMAN Eukaryotic translation initiation factor 2 subunit 1 (Fragment) OS=Homo sapiens OX=9606 GN=EIF2S1 PE=1 SV=1	EIF2S1	1	1	2.780%	28865.02	8.71
H0YLT0	tr|H0YLT0|H0YLT0_HUMAN Gamma-secretase subunit APH-1B (Fragment) OS=Homo sapiens OX=9606 GN=APH1B PE=1 SV=1	APH1B	1	1	3.150%	24320.23	9.1

H0YLW8	tr|H0YLW8|H0YLW8_HUMAN Proline-serine-threonine phosphatase-interacting protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=PSTPIP1 PE=1 SV=8	PSTPIP1	1	1	3.850%	24612.57	9.08
H0YN97	tr|H0YN97|H0YN97_HUMAN Treslin (Fragment) OS=Homo sapiens OX=9606 GN=TICRR PE=1 SV=1	TICRR	1	1	2.800%	23234.58	5.14
H3BM37	tr|H3BM37|H3BM37_HUMAN Neuropilin and tolloid-like protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=NETO2 PE=1 SV=2	NETO2	1	1	1.370%	41377.81	8.01
H3BMW3	tr|H3BMW3|H3BMW3_HUMAN Neutral alpha-glucosidase C (Fragment) OS=Homo sapiens OX=9606 GN=GANC PE=1 SV=8	GANC	1	1	10.450%	7846.69	5.04
H3BQV0	tr|H3BQV0|H3BQV0_HUMAN KLRC4-KLRK1 readthrough (Fragment) OS=Homo sapiens OX=9606 GN=KLRC4-KLRK1 PE=4 SV=1	KLRC4-KLR	1	1	9.330%	17167.85	9.09
H3BQZ6	tr|H3BQZ6|H3BQZ6_HUMAN Synaptotagmin XVII OS=Homo sapiens OX=9606 GN=SYT17 PE=1 SV=2	SYT17	1	1	2.040%	44126.53	8.2
H3BRS6	tr|H3BRS6|H3BRS6_HUMAN ADP-dependent glucokinase (Fragment) OS=Homo sapiens OX=9606 GN=ADPGK PE=1 SV=1	ADPGK	1	1	2.450%	21804.54	5.34
H3BT55	tr|H3BT55|H3BT55_HUMAN Calpain-15 (Fragment) OS=Homo sapiens OX=9606 GN=CAPN15 PE=4 SV=1	CAPN15	1	1	16.070%	11887.65	12
H3BUN0	tr|H3BUN0|H3BUN0_HUMAN E3 ubiquitin-protein ligase RBBP6 (Fragment) OS=Homo sapiens OX=9606 GN=RBBP6 PE=1 SV=1	RBBP6	1	1	5.330%	32969.36	5.76
H3BUT7	tr|H3BUT7|H3BUT7_HUMAN RNA exonuclease 5 (Fragment) OS=Homo sapiens OX=9606 GN=REXO5 PE=1 SV=1	REXO5	1	1	3.490%	19557.22	8.69
H3BUZ4	tr|H3BUZ4|H3BUZ4_HUMAN E3 ubiquitin-protein ligase (Fragment) OS=Homo sapiens OX=9606 GN=UBR1 PE=1 SV=1	UBR1	1	1	8.450%	8119.04	9.66
H7BXG7	tr|H7BXG7|H7BXG7_HUMAN Protein transport protein Sec31A OS=Homo sapiens OX=9606 GN=SEC31A PE=1 SV=1	SEC31A	1	1	0.930%	105703.26	8.61
H7BY35	tr|H7BY35|H7BY35_HUMAN Ryanodine receptor 2 OS=Homo sapiens OX=9606 GN=RYR2 PE=1 SV=2	RYR2	1	1	0.140%	562603.37	5.81

H7BYK1	tr|H7BYK1|H7BYK1_HUMAN Testin (Fragment) OS=Homo sapiens OX=9606 GN=TES PE=1 SV=1	TES	1	1	8.850%	21878.26	7.9
H7BZJ3	tr|H7BZJ3|H7BZJ3_HUMAN Protein disulfide-isomerase A3 (Fragment) OS=Homo sapiens OX=9606 GN=PDIA3 PE=1 SV=1	PDIA3	1	1	11.380%	13519.17	6.79
H7BZX9	tr|H7BZX9|H7BZX9_HUMAN Polypeptide N-acetylgalactosaminyltransferase 17 (Fragment) OS=Homo sapiens OX=9606 GN=GALNT17 PE=1 SV=1	GALNT17	1	1	2.660%	20875.65	5.77
H7C0E7	tr|H7C0E7|H7C0E7_HUMAN Protein ARV1 (Fragment) OS=Homo sapiens OX=9606 GN=ARV1 PE=1 SV=1	ARV1	1	1	3.090%	33110.34	8.46
H7C102	tr|H7C102|H7C102_HUMAN Mucin-20 (Fragment) OS=Homo sapiens OX=9606 GN=MUC20 PE=1 SV=1	MUC20	1	1	7.030%	13314.99	9.97
H7C1U0	tr|H7C1U0|H7C1U0_HUMAN Acylamino-acid-releasing enzyme (Fragment) OS=Homo sapiens OX=9606 GN=APEH PE=1 SV=1	APEH	1	1	1.950%	34582.96	6.1
H7C204	tr|H7C204|H7C204_HUMAN Rabenosyn-5 (Fragment) OS=Homo sapiens OX=9606 GN=RBSN PE=1 SV=1	RBSN	1	1	4.490%	18255.98	8.49
H7C2F9	tr|H7C2F9|H7C2F9_HUMAN R3H domain-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=R3HDM1 PE=1 SV=1	R3HDM1	1	1	2.460%	33120.67	5.61
H7C2M5	tr|H7C2M5|H7C2M5_HUMAN Radial spoke head 14 homolog (Fragment) OS=Homo sapiens OX=9606 GN=RSPH14 PE=1 SV=1	RSPH14	1	1	16.420%	7402.49	8.99
H7C3C1	tr|H7C3C1|H7C3C1_HUMAN Interleukin-1 receptor-associated kinase 1 (Fragment) OS=Homo sapiens OX=9606 GN=IRAK1 PE=1 SV=1	IRAK1	1	1	2.750%	22566.91	5.54
H7C3C5	tr|H7C3C5|H7C3C5_HUMAN Polyribonucleotide nucleotidyltransferase 1, mitochondrial (Fragment) OS=Homo sapiens OX=9606 GN=PNPT1 PE=1 SV=1	PNPT1	1	1	6.470%	15862.12	5.09
H7C3N7	tr|H7C3N7|H7C3N7_HUMAN TP53-binding protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=TP53BP1 PE=1 SV=1	TP53BP1	1	1	4.690%	20771.69	4.56
H7C4F6	tr|H7C4F6|H7C4F6_HUMAN Importin subunit alpha OS=Homo sapiens OX=9606 GN=KPNA4 PE=1 SV=2	KPNA4	1	1	3.320%	56836.13	4.97

H7C5G6	tr|H7C5G6|H7C5G6_HUMAN Uncharacterized protein KIAA2012 OS=Homo sapiens OX=9606 GN=KIAA2012 PE=1 SV=8	KIAA2012	1	1	0.510%	136119.6	8.09
H7C5N0	tr|H7C5N0|H7C5N0_HUMAN Helicase SKI2W (Fragment) OS=Homo sapiens OX=9606 GN=SKIV2L PE=1 SV=1	SKIV2L	1	1	10.260%	16873.23	6.09
H9KV28	tr|H9KV28|H9KV28_HUMAN Protein diaphanous homolog 1 OS=Homo sapiens OX=9606 GN=DIAPH1 PE=1 SV=2	DIAPH1	1	1	0.900%	136850.66	5.16
I3L0S1	tr|I3L0S1|I3L0S1_HUMAN Phosphoribosyl pyrophosphate synthase-associated protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=PRPSAP2 PE=1 SV=1	PRPSAP2	1	1	5.380%	28638.44	5.38
I3L1L6	tr|I3L1L6|I3L1L6_HUMAN RNA helicase (Fragment) OS=Homo sapiens OX=9606 GN=DHX33 PE=1 SV=1	DHX33	1	1	1.620%	69255.09	8.45
I3L203	tr|I3L203|I3L203_HUMAN Misshapen-like kinase 1 (Fragment) OS=Homo sapiens OX=9606 GN=MINK1 PE=4 SV=1	MINK1	1	1	13.210%	5528.3	5.58
I3L2C7	tr|I3L2C7|I3L2C7_HUMAN Gem-associated protein 4 OS=Homo sapiens OX=9606 GN=GEMIN4 PE=1 SV=1	GEMIN4	1	1	1.050%	118820.58	5.81
I3L362	tr|I3L362|I3L362_HUMAN RNA N6-adenosine-methyltransferase METTL16 OS=Homo sapiens OX=9606 GN=METTL16 PE=1 SV=1	METTL16	1	1	2.980%	18979.52	8.72
I3L390	tr|I3L390|I3L390_HUMAN Telomerase-binding protein EST1A (Fragment) OS=Homo sapiens OX=9606 GN=SMG6 PE=1 SV=2	SMG6	1	1	2.880%	23279.22	4.38
I3L3P8	tr|I3L3P8|I3L3P8_HUMAN Rabankyrin-5 OS=Homo sapiens OX=9606 GN=ANKFY1 PE=1 SV=1	ANKFY1	1	1	14.490%	8017.2	5.82
J3KNQ2	tr|J3KNQ2|J3KNQ2_HUMAN Fibronectin type III domain-containing protein 1 (Fragment) OS=Homo sapiens OX=9606 GN=FNDC1 PE=1 SV=1	FNDC1	1	1	0.340%	194428.47	9.25
J3KR05	tr|J3KR05|J3KR05_HUMAN Protein cordon-bleu (Fragment) OS=Homo sapiens OX=9606 GN=COBL PE=1 SV=1	COBL	1	1	0.790%	122452.39	6.3
J3KRT0	tr|J3KRT0|J3KRT0_HUMAN Core-binding factor subunit beta (Fragment) OS=Homo sapiens OX=9606 GN=CBFB PE=1 SV=2	CBFB	1	1	2.530%	22521.51	11.98

J3QKW7	tr|J3QKW7|J3QKW7_HUMAN Developmentally-regulated GTP-binding protein 2 OS=Homo sapiens OX=9606 GN=DRG2 PE=1 SV=1	DRG2	1	1	2.870%	26623.76	9.55
J3QSB5	tr|J3QSB5|J3QSB5_HUMAN 60S ribosomal protein L36 OS=Homo sapiens OX=9606 GN=RPL36 PE=1 SV=1	RPL36	1	1	10.640%	10788.73	11.61
J3QW41	tr|J3QW41|J3QW41_HUMAN cDNA FLJ50748, highly similar to Rho GDP-dissociation inhibitor 1 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	3.370%	20326.63	5.12
J7HWJ8	tr|J7HWJ8|J7HWJ8_HUMAN Cytochrome b OS=Homo sapiens OX=9606 GN=CYTB PE=3 SV=1	CYTB	1	1	1.840%	42585	7.83
K4P1Y1	tr|K4P1Y1|K4P1Y1_HUMAN Organic anion transporting polypeptide (Fragment) OS=Homo sapiens OX=9606 GN=SLCO1B1 PE=4 SV=1	SLCO1B1	1	1	4.790%	20774.09	9.21
K7EIW9	tr|K7EIW9|K7EIW9_HUMAN Pleckstrin homology domain-containing family J member 1 OS=Homo sapiens OX=9606 GN=PLEKHJ1 PE=1 SV=1	PLEKHJ1	1	1	4.670%	16959.44	11.17
K7EK20	tr|K7EK20|K7EK20_HUMAN Coactivator-associated arginine methyltransferase 1 (Fragment) OS=Homo sapiens OX=9606 GN=CARM1 PE=1 SV=1	CARM1	1	1	10.830%	12542.88	6.26
K7EM56	tr|K7EM56|K7EM56_HUMAN 40S ribosomal protein S15 OS=Homo sapiens OX=9606 GN=RPS15 PE=1 SV=2	RPS15	1	1	4.460%	12990.28	10.88
K7EMU8	tr|K7EMU8|K7EMU8_HUMAN DNA (cytosine-5)-methyltransferase 1 OS=Homo sapiens OX=9606 GN=DNMT1 PE=1 SV=1	DNMT1	1	1	10.110%	10283.95	7.71
K7EPJ5	tr|K7EPJ5|K7EPJ5_HUMAN E3 ubiquitin-protein ligase MGRN1 (Fragment) OS=Homo sapiens OX=9606 GN=MGRN1 PE=1 SV=1	MGRN1	1	1	1.680%	65083.12	5.39
K7EPT8	tr|K7EPT8|K7EPT8_HUMAN Glial fibrillary acidic protein (Fragment) OS=Homo sapiens OX=9606 GN=GFAP PE=1 SV=2	GFAP	1	1	14.670%	8266.39	9.87
K7ER00	tr|K7ER00|K7ER00_HUMAN Phenylalanine--tRNA ligase OS=Homo sapiens OX=9606 GN=FARSA PE=1 SV=1	FARSA	1	1	2.550%	62394.53	7.37
K7ERC0	tr|K7ERC0|K7ERC0_HUMAN Cilia- and flagella-associated protein 52 (Fragment) OS=Homo sapiens OX=9606 GN=CFAP52 PE=1 SV=1	CFAP52	1	1	10.750%	10720.4	8.7

K7ERT2	tr|K7ERT2|K7ERT2_HUMAN Mitogen-activated protein kinase kinase kinase kinase 1 (Fragment) OS=Homo sapiens OX=9606 GN=MAP4K1 PE=1 SV=1	MAP4K1	1	1	10.140%	7415.5	4.64
K7ES30	tr|K7ES30|K7ES30_HUMAN Zinc finger protein 180 OS=Homo sapiens OX=9606 GN=ZNF180 PE=4 SV=2	ZNF180	1	1	15.380%	7345.52	12.01
K7ESD3	tr|K7ESD3|K7ESD3_HUMAN Zinc finger and SCAN domain-containing protein 5B (Fragment) OS=Homo sapiens OX=9606 GN=ZSCAN5B PE=4 SV=2	ZSCAN5B	1	1	7.300%	15767.93	6.08
L0R5D0	tr|L0R5D0|L0R5D0_HUMAN Alternative protein SRGAP1 OS=Homo sapiens OX=9606 GN=SRGAP1 PE=4 SV=1	SRGAP1	1	1	12.050%	9230.77	9.45
L8EBE5	tr|L8EBE5|L8EBE5_HUMAN Alternative protein SPRED1 OS=Homo sapiens OX=9606 GN=SPRED1 PE=4 SV=1	SPRED1	1	1	7.890%	8378.11	9.4
M0QXE6	tr|M0QXE6|M0QXE6_HUMAN DNA-directed DNA polymerase (Fragment) OS=Homo sapiens OX=9606 GN=POLD1 PE=1 SV=1	POLD1	1	1	3.460%	31660.2	8.49
M0QYD4	tr|M0QYD4|M0QYD4_HUMAN Putative L-aspartate dehydrogenase (Fragment) OS=Homo sapiens OX=9606 GN=ASPDH PE=1 SV=1	ASPDH	1	1	11.760%	5473.19	9.69
M0QYZ2	tr|M0QYZ2|M0QYZ2_HUMAN AP complex subunit sigma OS=Homo sapiens OX=9606 GN=AP2S1 PE=1 SV=1	AP2S1	1	1	5.060%	18928.78	7.66
M0R1W7	tr|M0R1W7|M0R1W7_HUMAN Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=4 SV=1		1	1	11.110%	7546.45	4.82
M0R2J6	tr|M0R2J6|M0R2J6_HUMAN Zinc finger protein 548 OS=Homo sapiens OX=9606 GN=ZNF548 PE=4 SV=1	ZNF548	1	1	23.400%	5583.1	6.56
M0R3G9	tr|M0R3G9|M0R3G9_HUMAN 5'-3' exonuclease PLD3 (Fragment) OS=Homo sapiens OX=9606 GN=PLD3 PE=1 SV=1	PLD3	1	1	7.040%	7657.24	4.7
O43455	tr|O43455|O43455_HUMAN Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=4 SV=1		1	1	8.990%	10023.35	5.4
Q05BG9	tr|Q05BG9|Q05BG9_HUMAN P2X purinoceptor OS=Homo sapiens OX=9606 GN=P2RX6 PE=2 SV=1	P2RX6	1	1	1.800%	43214.57	6.59

Q05CP8	tr|Q05CP8|Q05CP8_HUMAN CCDC6 protein (Fragment) OS=Homo sapiens OX=9606 GN=CCDC6 PE=2 SV=1	CCDC6	1	1	1.800%	38163.11	9.42
Q05DA9	tr|Q05DA9|Q05DA9_HUMAN SFRS17A protein (Fragment) OS=Homo sapiens OX=9606 GN=SFRS17A PE=2 SV=1	SFRS17A	1	1	3.080%	33554.28	8.49
Q05DB9	tr|Q05DB9|Q05DB9_HUMAN Polynucleotide adenylyltransferase (Fragment) OS=Homo sapiens OX=9606 GN=PAPOLG PE=2 SV=1	PAPOLG	1	1	1.210%	57003.78	8.85
Q05DM0	tr|Q05DM0|Q05DM0_HUMAN HMMR protein (Fragment) OS=Homo sapiens OX=9606 GN=HMMR PE=2 SV=1	HMMR	1	1	3.910%	59164.58	5.62
Q12984	tr|Q12984|Q12984_HUMAN Uncharacterized protein OS=Homo sapiens OX=9606 PE=4 SV=1		1	1	1.730%	40903.01	11.42
Q13537	tr|Q13537|Q13537_HUMAN Putative transposase OS=Homo sapiens OX=9606 PE=4 SV=2		1	1	2.420%	51665.88	8.89
Q13590	tr|Q13590|Q13590_HUMAN Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	7.020%	12634.76	10.3
Q2NLC9	tr|Q2NLC9|Q2NLC9_HUMAN PURA protein (Fragment) OS=Homo sapiens OX=9606 GN=PURA PE=2 SV=1	PURA	1	1	3.000%	34165.96	9.3
Q2XND8	tr|Q2XND8|Q2XND8_HUMAN Cytochrome P450 OS=Homo sapiens OX=9606 GN=CYP2D6 PE=3 SV=1	CYP2D6	1	1	1.610%	55775.85	6.61
Q495F8	tr|Q495F8|Q495F8_HUMAN Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens OX=9606 GN=USP26 PE=2 SV=1	USP26	1	1	0.770%	103996.83	8.91
Q49AK0	tr|Q49AK0|Q49AK0_HUMAN LTA4H protein OS=Homo sapiens OX=9606 GN=LTA4H PE=2 SV=1	LTA4H	1	1	8.720%	17202.64	8.95
Q4VBY4	tr|Q4VBY4|Q4VBY4_HUMAN MAP1B protein (Fragment) OS=Homo sapiens OX=9606 GN=MAP1B PE=2 SV=1	MAP1B	1	1	1.380%	82059.63	8.68
Q504W7	tr|Q504W7|Q504W7_HUMAN Phosphoinositide 5-phosphatase OS=Homo sapiens OX=9606 GN=OCRL PE=2 SV=1	OCRL	1	1	1.120%	103179.38	6.34

Q506M0	tr|Q506M0|Q506M0_HUMAN Regulator of G-protein signalling 12 OS=Homo sapiens OX=9606 GN=RGS12 PE=2 SV=1	RGS12	1	1	0.990%	76757.2	8.3
Q50L08	tr|Q50L08|Q50L08_HUMAN Bitter taste receptor T2R1 (Fragment) OS=Homo sapiens OX=9606 GN=Hosa(Japanese)-T2R1 PE=3 SV=1	Hosa(Japan	1	1	2.790%	28844.79	9.82
Q53GE1	tr|Q53GE1|Q53GE1_HUMAN RAN binding protein 3 isoform RANBP3-a variant (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.070%	59674.58	4.71
Q562F2	tr|Q562F2|Q562F2_HUMAN Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit OS=Homo sapiens OX=9606 GN=PPP2R5E PE=2 SV=1	PPP2R5E	1	1	1.930%	54680.71	6.51
Q59EV6	tr|Q59EV6|Q59EV6_HUMAN Carboxypeptidase (Fragment) OS=Homo sapiens OX=9606 GN=PPGB PE=1 SV=1	PPGB	1	1	1.210%	56119.18	6.17
Q59F74	tr|Q59F74|Q59F74_HUMAN CD72 antigen variant (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	8.640%	8500.52	5.21
Q59FM0	tr|Q59FM0|Q59FM0_HUMAN Complex I-42kD (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	3.730%	27039.66	9.12
Q59FV6	tr|Q59FV6|Q59FV6_HUMAN Actin-like protein 3 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.900%	42257.78	5.59
Q59G16	tr|Q59G16|Q59G16_HUMAN SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c2 isoform b variant (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	0.950%	127375.36	5.38
Q59G42	tr|Q59G42|Q59G42_HUMAN Eukaryotic translation initiation factor 4 gamma, 2 variant (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.060%	105826.89	7.08
Q59GS6	tr|Q59GS6|Q59GS6_HUMAN Diacylglycerol kinase (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	2.640%	68332.02	5.7
Q59HG5	tr|Q59HG5|Q59HG5_HUMAN Zinc finger protein 192 variant (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	3.170%	49854.25	8.92
Q5JPB9	tr|Q5JPB9|Q5JPB9_HUMAN Uncharacterized protein DKFZp686N2317 (Fragment) OS=Homo sapiens OX=9606 GN=DKFZp686N2317 PE=2 SV=1	DKFZp686N	1	1	7.000%	11768.46	8.89

Q5JRC6	tr|Q5JRC6|Q5JRC6_HUMAN PHD finger protein 6 OS=Homo sapiens OX=9606 GN=PHF6 PE=1 SV=1	PHF6	1	1	2.780%	36430.04	9.24
Q5M7Z5	tr|Q5M7Z5|Q5M7Z5_HUMAN GRHPR protein (Fragment) OS=Homo sapiens OX=9606 GN=GRHPR PE=2 SV=1	GRHPR	1	1	2.930%	36823.76	5.95
Q5QPM7	tr|Q5QPM7|Q5QPM7_HUMAN Proteasome inhibitor PI31 subunit OS=Homo sapiens OX=9606 GN=PSMF1 PE=1 SV=2	PSMF1	1	1	6.460%	28956.43	5.98
Q5RLJ0	tr|Q5RLJ0|Q5RLJ0_HUMAN RNA transcription, translation and transport factor protein OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	3.280%	27968.6	6
Q5T0F3	tr|Q5T0F3|Q5T0F3_HUMAN Nucleolar GTP-binding protein 2 OS=Homo sapiens OX=9606 GN=GNL2 PE=2 SV=1	GNL2	1	1	1.780%	83653.92	9.27
Q5TA58	tr|Q5TA58|Q5TA58_HUMAN Protein argonaute-1 OS=Homo sapiens OX=9606 GN=AGO1 PE=1 SV=1	AGO1	1	1	1.020%	88877.66	9.31
Q5TEE2	tr|Q5TEE2|Q5TEE2_HUMAN Histone deacetylase (Fragment) OS=Homo sapiens OX=9606 GN=HDAC1 PE=1 SV=1	HDAC1	1	1	4.270%	24544.41	8.33
Q5U0K8	tr|Q5U0K8|Q5U0K8_HUMAN Sodium channel, voltage-gated, type II, beta OS=Homo sapiens OX=9606 GN=SCN2B PE=2 SV=1	SCN2B	1	1	2.330%	24325.59	5.98
Q66K91	tr|Q66K91|Q66K91_HUMAN Small nuclear ribonucleoprotein-associated protein OS=Homo sapiens OX=9606 GN=SNRPB PE=1 SV=1	SNRPB	1	1	3.030%	23655.74	10.91
Q68CX1	tr|Q68CX1|Q68CX1_HUMAN Uncharacterized protein DKFZp761D0422 (Fragment) OS=Homo sapiens OX=9606 GN=DKFZp761D0422 PE=2 SV=1	DKFZp761D	1	1	1.200%	93226.88	5.76
Q68DB7	tr|Q68DB7|Q68DB7_HUMAN Mothers against decapentaplegic homolog OS=Homo sapiens OX=9606 GN=DKFZp781O1323 PE=2 SV=1	DKFZp781O	1	1	2.150%	52257.68	7.63
Q6AI59	tr|Q6AI59|Q6AI59_HUMAN Uncharacterized protein DKFZp781H0795 (Fragment) OS=Homo sapiens OX=9606 GN=DKFZp781H0795 PE=2 SV=1	DKFZp781H	1	1	0.920%	192922.34	8.63
Q6AZW6	tr|Q6AZW6|Q6AZW6_HUMAN Activating transcription factor 6 beta OS=Homo sapiens OX=9606 GN=ATF6B PE=2 SV=1	ATF6B	1	1	2.420%	76720.35	5.9

Q6DHZ8	tr|Q6DHZ8|Q6DHZ8_HUMAN Activity-dependent neuroprotector homeobox OS=Homo sapiens OX=9606 GN=ADNP PE=2 SV=1	ADNP	1	1	1.630%	123445.39	7.08
Q6FHF5	tr|Q6FHF5|Q6FHF5_HUMAN Proliferating cell nuclear antigen (Fragment) OS=Homo sapiens OX=9606 GN=PCNA PE=2 SV=1	PCNA	1	1	7.280%	28705.38	4.57
Q6FHZ7	tr|Q6FHZ7|Q6FHZ7_HUMAN Perilipin OS=Homo sapiens OX=9606 GN=ADFP PE=2 SV=1	ADFP	1	1	1.600%	48074.87	6.34
Q6I9T8	tr|Q6I9T8|Q6I9T8_HUMAN Serine/threonine-protein phosphatase OS=Homo sapiens OX=9606 GN=PPP2CA PE=2 SV=1	PPP2CA	1	1	2.590%	35549.74	5.3
Q6IB71	tr|Q6IB71|Q6IB71_HUMAN Proteasome subunit alpha type OS=Homo sapiens OX=9606 GN=PSMA3 PE=2 SV=1	PSMA3	1	1	4.710%	28414.88	5.19
Q6IEG3	tr|Q6IEG3|Q6IEG3_HUMAN Programmed cell death 7, isoform CRA_a OS=Homo sapiens OX=9606 GN=PDCD7 PE=2 SV=1	PDCD7	1	1	1.440%	54699.29	9.97
Q6IRT1	tr|Q6IRT1|Q6IRT1_HUMAN S-(hydroxymethyl)glutathione dehydrogenase OS=Homo sapiens OX=9606 GN=ADH5 PE=2 SV=2	ADH5	1	1	1.870%	39723.81	7.45
Q6LBZ0	tr|Q6LBZ0|Q6LBZ0_HUMAN Proto-oncogene c-sis for PDGF B chain (platelet-derived growth factor) (Fragment) OS=Homo sapiens OX=9606 PE=3 SV=1		1	1	21.430%	4708.18	4.44
Q6MZV5	tr|Q6MZV5|Q6MZV5_HUMAN Coatomer subunit delta OS=Homo sapiens OX=9606 GN=DKFZp686M09245 PE=2 SV=1	DKFZp686M	1	1	1.990%	61597.56	5.63
Q6N0B1	tr|Q6N0B1|Q6N0B1_HUMAN Succinate-CoA ligase subunit beta (Fragment) OS=Homo sapiens OX=9606 GN=DKFZp686D0880 PE=2 SV=1	DKFZp686D	1	1	1.480%	51199.53	6.26
Q6NWZ1	tr|Q6NWZ1|Q6NWZ1_HUMAN CKAP4 protein (Fragment) OS=Homo sapiens OX=9606 GN=CKAP4 PE=2 SV=1	CKAP4	1	1	2.000%	67817.36	9.34
Q6T775	tr|Q6T775|Q6T775_HUMAN Kallikrein 2 isoform 5 preproprotein OS=Homo sapiens OX=9606 GN=KLK2 PE=2 SV=1	KLK2	1	1	3.330%	19672.19	5.73
Q6ZU41	tr|Q6ZU41|Q6ZU41_HUMAN cDNA FLJ44011 fis, clone TESTI4024420, highly similar to Rattus norvegicus presynaptic cytomatrix protein (Pclo) OS=Homo sapiens OX=9606 PE=2		1	1	0.890%	113426.69	9.1

	SV=1						
Q6ZUY9	tr|Q6ZUY9|Q6ZUY9_HUMAN cDNA FLJ43200 fis, clone FEBRA2007793 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	4.260%	20707.57	11.65
Q71VF8	tr|Q71VF8|Q71VF8_HUMAN Beta-spectrin (Fragment) OS=Homo sapiens OX=9606 GN=HSpTB1 PE=4 SV=1	HSpTB1	1	1	5.410%	13034.65	5.8
Q7L2M4	tr|Q7L2M4|Q7L2M4_HUMAN Transmembrane channel-like protein (Fragment) OS=Homo sapiens OX=9606 GN=TMC6 PE=2 SV=1	TMC6	1	1	2.340%	57780.33	8.89
Q86TA8	tr|Q86TA8|Q86TA8_HUMAN Uncharacterized protein DKFZp451M091 OS=Homo sapiens OX=9606 GN=DKFZp451M091 PE=2 SV=1	DKFZp451M	1	1	1.200%	131650.48	5.68
Q8IXF7	tr|Q8IXF7|Q8IXF7_HUMAN HAWMS1 protein OS=Homo sapiens OX=9606 GN=hAWMS1 PE=2 SV=1	hAWMS1	1	1	11.430%	8389.94	10.13
Q8IY71	tr|Q8IY71|Q8IY71_HUMAN MRPS17 protein (Fragment) OS=Homo sapiens OX=9606 GN=MRPS17 PE=2 SV=1	MRPS17	1	1	6.340%	15707.17	9.86
Q8NAY2	tr|Q8NAY2|Q8NAY2_HUMAN cDNA FLJ34557 fis, clone KIDNE2001160 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	8.960%	14098.95	9.67
Q8NC75	tr|Q8NC75|Q8NC75_HUMAN cDNA FLJ90437 fis, clone NT2RP3000838, weakly similar to TRICHOHYALIN OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	1.140%	69847.39	8.92
Q8NGM3	tr|Q8NGM3|Q8NGM3_HUMAN HCG1641819 OS=Homo sapiens OX=9606 GN=hCG_1641819 PE=4 SV=1	hCG_16418	1	1	5.150%	22151.91	9.17
Q8TE01	tr|Q8TE01|Q8TE01_HUMAN DERP12 (Dermal papilla derived protein 12) OS=Homo sapiens OX=9606 GN=derp12 PE=2 SV=1	derp12	1	1	3.500%	38192.09	6.2
Q8TEF1	tr|Q8TEF1|Q8TEF1_HUMAN FLJ00246 protein (Fragment) OS=Homo sapiens OX=9606 GN=FLJ00246 PE=2 SV=1	FLJ00246	1	1	0.400%	157809.37	4.96
Q8WYY4	tr|Q8WYY4|Q8WYY4_HUMAN Uncharacterized protein OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	7.630%	12929.9	11.47

Q96CQ6	tr|Q96CQ6|Q96CQ6_HUMAN Uncharacterized protein (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	14.750%	6848.73	5.41
Q96G78	tr|Q96G78|Q96G78_HUMAN EXOSC10 protein (Fragment) OS=Homo sapiens OX=9606 GN=EXOSC10 PE=2 SV=2	EXOSC10	1	1	14.750%	6964.16	12.01
Q96J05	tr|Q96J05|Q96J05_HUMAN ECT2 protein OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	4.400%	20333.08	9.79
Q96NY3	tr|Q96NY3|Q96NY3_HUMAN DnaJ-like protein (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	2.910%	31474.69	5.63
Q9H2I3	tr|Q9H2I3|Q9H2I3_HUMAN DC41 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	6.860%	12540.99	9.7
Q9H2M6	tr|Q9H2M6|Q9H2M6_HUMAN DC30 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	7.080%	13295.75	9.94
Q9H9M0	tr|Q9H9M0|Q9H9M0_HUMAN cDNA FLJ12662 fis, clone NT2RM4002205, moderately similar to ELONGATION FACTOR G, MITOCHONDRIAL OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	4.170%	16660.15	9.48
Q9NTA6	tr|Q9NTA6|Q9NTA6_HUMAN Uncharacterized protein DKFZp761I2124 (Fragment) OS=Homo sapiens OX=9606 GN=DKFZp761I2124 PE=2 SV=1	DKFZp761I2	1	1	1.010%	69294.44	5.84
Q9NXK9	tr|Q9NXK9|Q9NXK9_HUMAN cDNA FLJ20187 fis, clone COLF0433 OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	3.290%	27831.02	5.47
Q9UES5	tr|Q9UES5|Q9UES5_HUMAN Myosin V (Fragment) OS=Homo sapiens OX=9606 GN=MYO5A PE=1 SV=1	MYO5A	1	1	3.950%	26456.44	5.13
R4GNG6	tr|R4GNG6|R4GNG6_HUMAN Ubiquitin-conjugating enzyme E2 E3 OS=Homo sapiens OX=9606 GN=UBE2E3 PE=1 SV=1	UBE2E3	1	1	5.380%	14140.54	4.99
R9Y4B7	tr|R9Y4B7|R9Y4B7_HUMAN NADH-ubiquinone oxidoreductase chain 5 OS=Homo sapiens OX=9606 GN=ND5 PE=3 SV=1	ND5	1	1	1.000%	64757	8.99
V5L5K8	tr|V5L5K8|V5L5K8_HUMAN MHC class I antigen (Fragment) OS=Homo sapiens OX=9606 GN=HLA-B PE=3 SV=1	HLA-B	1	1	7.590%	8995.85	5.31

V9GY20	tr|V9GY20|V9GY20_HUMAN Transmembrane prolyl 4-hydroxylase (Fragment) OS=Homo sapiens OX=9606 GN=P4HTM PE=1 SV=1	P4HTM	1	1	8.280%	17843.82	4.82
V9HW06	tr|V9HW06|V9HW06_HUMAN Serine hydroxymethyltransferase OS=Homo sapiens OX=9606 GN=HEL-S-51e PE=2 SV=1	HEL-S-51e	1	1	1.190%	55992.33	8.76
V9HW90	tr|V9HW90|V9HW90_HUMAN Glutathione reductase OS=Homo sapiens OX=9606 GN=HEL-75 PE=2 SV=1	HEL-75	1	1	2.300%	56256.4	8.74
V9HWA9	tr|V9HWA9|V9HWA9_HUMAN C3-beta-c OS=Homo sapiens OX=9606 GN=HEL-S-62p PE=2 SV=1	HEL-S-62p	1	1	0.360%	187145.88	6.02
V9P4H4	tr|V9P4H4|V9P4H4_HUMAN Magi1d OS=Homo sapiens OX=9606 PE=2 SV=1		1	1	0.460%	144697.26	7.46
H0YBL3	tr|H0YBL3|H0YBL3_HUMAN Protein MTSS 1 (Fragment) OS=Homo sapiens OX=9606 GN=MTSS1 PE=1 SV=1	MTSS1	5	1	3.800%	20726.63	9.56
A0A5C2GDU5	tr|A0A5C2GDU5|A0A5C2GDU5_HUMAN IG c1004_heavy_IGHV3-15_IGHD2-2_IGHJ5 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		4	1	12.610%	12921.36	9.01
A0A5C2GPP2	tr|A0A5C2GPP2|A0A5C2GPP2_HUMAN IG c833_heavy_IGHV4-39_IGHD2-2_IGHJ2 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		4	1	4.100%	13496.78	5.09
A0A0A0MS14	sp|A0A0A0MS14|HV145_HUMAN Immunoglobulin heavy variable 1-45 OS=Homo sapiens OX=9606 GN=IGHV1-45 PE=3 SV=1	IGHV1-45	3	1	9.400%	13508.21	9.2
A0A075B6Z2	tr|A0A075B6Z2|A0A075B6Z2_HUMAN T cell receptor alpha joining 56 (Fragment) OS=Homo sapiens OX=9606 GN=TRAJ56 PE=4 SV=1	TRAJ56	3	1	38.100%	2110.41	10.29
A2NWW2	tr|A2NWW2|A2NWW2_HUMAN VH-3 family (VH26)D/J protein (Fragment) OS=Homo sapiens OX=9606 GN=VH-3 family (VH26)D/J PE=4 SV=1	VH-3 family (	3	1	13.640%	12195.67	7.79
Q6MZT2	tr|Q6MZT2|Q6MZT2_HUMAN Receptor protein-tyrosine kinase OS=Homo sapiens OX=9606 GN=DKFZp686D1354 PE=2 SV=1	DKFZp686D	3	1	1.050%	96745.25	5.2
A0A024R1R8	tr|A0A024R1R8|A0A024R1R8_HUMAN Coiled-coil domain-containing protein 72 OS=Homo sapiens OX=9606 GN=hCG_2014768 PE=3 SV=1	hCG_20147	2	1	12.500%	7091.31	10

A0A0A0MT67	tr|A0A0A0MT67|A0A0A0MT67_HUMAN Mucin-15 OS=Homo sapiens OX=9606 GN=MUC15 PE=1 SV=1	MUC15	2	1	2.220%	39327.64	5.42
A0A5C2FTW2	tr|A0A5C2FTW2|A0A5C2FTW2_HUMAN IGL c152_light_IGKV1D-13_IGKJ5 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	1	14.950%	11386.59	8.02
A0A5C2GML0	tr|A0A5C2GML0|A0A5C2GML0_HUMAN IG c775_heavy_IGHV3-15_IGHD3-10_IGHJ4 (Fragment) OS=Homo sapiens OX=9606 PE=2 SV=1		2	1	11.810%	13678.37	8.65
C9IZL5	tr|C9IZL5|C9IZL5_HUMAN AP-4 complex subunit mu-1 OS=Homo sapiens OX=9606 GN=AP4M1 PE=1 SV=1	AP4M1	2	1	2.770%	35742.45	8.94
H0YC69	tr|H0YC69|H0YC69_HUMAN Cell cycle and apoptosis regulator protein 2 (Fragment) OS=Homo sapiens OX=9606 GN=CCAR2 PE=1 SV=1	CCAR2	2	1	6.080%	16253.67	10.53
J3QLI9	tr|J3QLI9|J3QLI9_HUMAN Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens OX=9606 GN=SNRPD1 PE=1 SV=1	SNRPD1	2	1	17.330%	8392.64	11.83
K7EPH2	tr|K7EPH2|K7EPH2_HUMAN Phenylalanine--tRNA ligase (Fragment) OS=Homo sapiens OX=9606 GN=FARSA PE=1 SV=8	FARSA	2	1	1.850%	42930.35	6.99
Q5HYC4	tr|Q5HYC4|Q5HYC4_HUMAN Uncharacterized protein DKFZp686J08125 (Fragment) OS=Homo sapiens OX=9606 GN=DKFZp686J08125 PE=4 SV=1	DKFZp686J	2	1	2.950%	38157.2	5.63
S6AWD6	tr|S6AWD6|S6AWD6_HUMAN IgG L chain OS=Homo sapiens OX=9606 PE=2 SV=1		2	1	8.990%	19449.87	8.69
A0A0A6YYK7	sp|A0A0A6YYK7|TVA19_HUMAN T cell receptor alpha variable 19 OS=Homo sapiens OX=9606 GN=TRAV19 PE=2 SV=5	TRAV19	1	1	6.030%	13194.73	4.75
A2RUB6	sp|A2RUB6|CCD66_HUMAN Coiled-coil domain-containing protein 66 OS=Homo sapiens OX=9606 GN=CCDC66 PE=1 SV=4	CCDC66	1	1	0.840%	109410.05	8.47
A6NK02	sp|A6NK02|TRI75_HUMAN Putative tripartite motif-containing protein 75 OS=Homo sapiens OX=9606 GN=TRIM75P PE=5 SV=2	TRIM75P	1	1	1.500%	53677.05	7.79
A6NMB9	sp|A6NMB9|FIGL2_HUMAN Fidgetin-like protein 2 OS=Homo sapiens OX=9606 GN=FIGNL2 PE=2 SV=2	FIGNL2	1	1	1.230%	66602.59	6.3

A6NNT2	sp|A6NNT2|CP096_HUMAN Uncharacterized protein C16orf96 OS=Homo sapiens OX=9606 GN=C16orf96 PE=4 SV=3	C16orf96	1	1	0.700%	125039.98	6.58
D6RGH6	sp|D6RGH6|MCIN_HUMAN Multicilin OS=Homo sapiens OX=9606 GN=MCIDAS PE=1 SV=1	MCIDAS	1	1	2.080%	41719.46	5.62
O00443	sp|O00443|P3C2A_HUMAN Phosphatidylinositol 4-phosphate 3-kinase C2 domain-containing subunit alpha OS=Homo sapiens OX=9606 GN=PIK3C2A PE=1 SV=2	PIK3C2A	1	1	0.650%	190677.29	8.25
O00507	sp|O00507|USP9Y_HUMAN Probable ubiquitin carboxyl-terminal hydrolase FAF-Y OS=Homo sapiens OX=9606 GN=USP9Y PE=2 SV=2	USP9Y	1	1	0.230%	291073.61	5.56
O14526	sp|O14526|FCHO1_HUMAN F-BAR domain only protein 1 OS=Homo sapiens OX=9606 GN=FCHO1 PE=1 SV=2	FCHO1	1	1	0.900%	96859.8	6.51
O14776	sp|O14776|TCRG1_HUMAN Transcription elongation regulator 1 OS=Homo sapiens OX=9606 GN=TCERG1 PE=1 SV=2	TCERG1	1	1	1.000%	123899.61	8.71
O14782	sp|O14782|KIF3C_HUMAN Kinesin-like protein KIF3C OS=Homo sapiens OX=9606 GN=KIF3C PE=1 SV=3	KIF3C	1	1	0.760%	89425.2	8.28
O15230	sp|O15230|LAMA5_HUMAN Laminin subunit alpha-5 OS=Homo sapiens OX=9606 GN=LAMA5 PE=1 SV=8	LAMA5	1	1	0.270%	399733.32	6.66
O15516	sp|O15516|CLOCK_HUMAN Circadian locomoter output cycles protein kaput OS=Homo sapiens OX=9606 GN=CLOCK PE=1 SV=1	CLOCK	1	1	0.830%	95302.69	6.51
O43776	sp|O43776|SYNC_HUMAN Asparagine--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=NARS1 PE=1 SV=1	NARS1	1	1	1.460%	62942.23	5.9
O60287	sp|O60287|NPA1P_HUMAN Nucleolar pre-ribosomal-associated protein 1 OS=Homo sapiens OX=9606 GN=URB1 PE=1 SV=4	URB1	1	1	0.310%	254386.09	6.03
O60293	sp|O60293|ZC3H1_HUMAN Zinc finger C3H1 domain-containing protein OS=Homo sapiens OX=9606 GN=ZFC3H1 PE=1 SV=3	ZFC3H1	1	1	0.500%	226352.95	8.39
O60299	sp|O60299|LZTS3_HUMAN Leucine zipper putative tumor suppressor 3 OS=Homo sapiens OX=9606 GN=LZTS3 PE=2 SV=1	LZTS3	1	1	1.630%	71789.95	7.56

O60403	sp|O60403|O10H2_HUMAN Olfactory receptor 10H2 OS=Homo sapiens OX=9606 GN=OR10H2 PE=2 SV=1	OR10H2	1	1	1.590%	34662.24	8.71
O60673	sp|O60673|REV3L_HUMAN DNA polymerase zeta catalytic subunit OS=Homo sapiens OX=9606 GN=REV3L PE=1 SV=2	REV3L	1	1	0.190%	352771.7	8.72
O60763	sp|O60763|USO1_HUMAN General vesicular transport factor p115 OS=Homo sapiens OX=9606 GN=USO1 PE=1 SV=2	USO1	1	1	0.730%	107894.02	4.85
O60783	sp|O60783|RT14_HUMAN 28S ribosomal protein S14, mitochondrial OS=Homo sapiens OX=9606 GN=MRPS14 PE=1 SV=1	MRPS14	1	1	11.720%	15138.55	11.42
O60869	sp|O60869|EDF1_HUMAN Endothelial differentiation-related factor 1 OS=Homo sapiens OX=9606 GN=EDF1 PE=1 SV=1	EDF1	1	1	4.730%	16368.48	9.95
O75153	sp|O75153|CLU_HUMAN Clustered mitochondria protein homolog OS=Homo sapiens OX=9606 GN=CLUH PE=1 SV=2	CLUH	1	1	0.690%	146668.14	5.75
O75165	sp|O75165|DJC13_HUMAN DnaJ homolog subfamily C member 13 OS=Homo sapiens OX=9606 GN=DNAJC13 PE=1 SV=5	DNAJC13	1	1	0.490%	254411.98	6.31
O75607	sp|O75607|NPM3_HUMAN Nucleoplasmin-3 OS=Homo sapiens OX=9606 GN=NPM3 PE=1 SV=3	NPM3	1	1	8.990%	19343.48	4.55
O75762	sp|O75762|TRPA1_HUMAN Transient receptor potential cation channel subfamily A member 1 OS=Homo sapiens OX=9606 GN=TRPA1 PE=1 SV=3	TRPA1	1	1	0.540%	127499.59	6.69
O94812	sp|O94812|BAIP3_HUMAN BAI1-associated protein 3 OS=Homo sapiens OX=9606 GN=BAIAP3 PE=1 SV=2	BAIAP3	1	1	0.590%	131899.15	5.95
O95071	sp|O95071|UBR5_HUMAN E3 ubiquitin-protein ligase UBR5 OS=Homo sapiens OX=9606 GN=UBR5 PE=1 SV=2	UBR5	1	1	0.290%	309349.01	5.59
O95235	sp|O95235|KI20A_HUMAN Kinesin-like protein KIF20A OS=Homo sapiens OX=9606 GN=KIF20A PE=1 SV=1	KIF20A	1	1	1.570%	100276.82	6.49
P04004	sp|P04004|VTNC_HUMAN Vitronectin OS=Homo sapiens OX=9606 GN=VTN PE=1 SV=1	VTN	1	1	1.050%	54304.97	5.55

P05109	sp|P05109|S10A8_HUMAN Protein S100-A8 OS=Homo sapiens OX=9606 GN=S100A8 PE=1 SV=1	S100A8	1	1	11.830%	10834.38	6.51
P05423	sp|P05423|RPC4_HUMAN DNA-directed RNA polymerase III subunit RPC4 OS=Homo sapiens OX=9606 GN=POLR3D PE=1 SV=2	POLR3D	1	1	1.760%	44395.33	6.51
P06732	sp|P06732|KCRM_HUMAN Creatine kinase M-type OS=Homo sapiens OX=9606 GN=CKM PE=1 SV=2	CKM	1	1	1.570%	43100.62	6.77
P06870	sp|P06870|KLK1_HUMAN Kallikrein-1 OS=Homo sapiens OX=9606 GN=KLK1 PE=1 SV=2	KLK1	1	1	4.960%	28889.31	4.68
P07737	sp|P07737|PROF1_HUMAN Profilin-1 OS=Homo sapiens OX=9606 GN=PFN1 PE=1 SV=2	PFN1	1	1	10.000%	15054.07	8.44
P09543	sp|P09543|CN37_HUMAN 2',3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens OX=9606 GN=CNP PE=1 SV=2	CNP	1	1	2.140%	47578.06	9.17
P09884	sp|P09884|DPOLA_HUMAN DNA polymerase alpha catalytic subunit OS=Homo sapiens OX=9606 GN=POLA1 PE=1 SV=2	POLA1	1	1	0.960%	165910.88	5.61
P0C628	sp|P0C628|O5AC1_HUMAN Olfactory receptor 5AC1 OS=Homo sapiens OX=9606 GN=OR5AC1 PE=3 SV=1	OR5AC1	1	1	2.610%	34762.06	9.22
P0CB33	sp|P0CB33|ZN735_HUMAN Putative zinc finger protein 735 OS=Homo sapiens OX=9606 GN=ZNF735 PE=5 SV=1	ZNF735	1	1	1.700%	47564.98	9.31
P0CB47	sp|P0CB47|UBFL1_HUMAN Upstream-binding factor 1-like protein 1 OS=Homo sapiens OX=9606 GN=UBTFL1 PE=1 SV=1	UBTFL1	1	1	2.800%	46133.85	9.52
P0DPB6	sp|P0DPB6|RPAC2_HUMAN DNA-directed RNA polymerases I and III subunit RPAC2 OS=Homo sapiens OX=9606 GN=POLR1D PE=1 SV=1	POLR1D	1	1	4.510%	15237.05	5.55
P12757	sp|P12757|SKIL_HUMAN Ski-like protein OS=Homo sapiens OX=9606 GN=SKIL PE=1 SV=2	SKIL	1	1	1.170%	76975.15	6.72
P13807	sp|P13807|GYS1_HUMAN Glycogen [starch] synthase, muscle OS=Homo sapiens OX=9606 GN=GYS1 PE=1 SV=2	GYS1	1	1	1.360%	83784.57	5.8

P17980	sp|P17980|PRS6A_HUMAN 26S proteasome regulatory subunit 6A OS=Homo sapiens OX=9606 GN=PSMC3 PE=1 SV=3	PSMC3	1	1	2.280%	49202.99	5.13
P18089	sp|P18089|ADA2B_HUMAN Alpha-2B adrenergic receptor OS=Homo sapiens OX=9606 GN=ADRA2B PE=1 SV=4	ADRA2B	1	1	1.560%	49953.12	8.8
P20742	sp|P20742|PZP_HUMAN Pregnancy zone protein OS=Homo sapiens OX=9606 GN=PZP PE=1 SV=4	PZP	1	1	0.810%	163861.02	5.97
P23470	sp|P23470|PTPRG_HUMAN Receptor-type tyrosine-protein phosphatase gamma OS=Homo sapiens OX=9606 GN=PTPRG PE=1 SV=4	PTPRG	1	1	0.420%	162001.6	5.99
P23588	sp|P23588|IF4B_HUMAN Eukaryotic translation initiation factor 4B OS=Homo sapiens OX=9606 GN=EIF4B PE=1 SV=2	EIF4B	1	1	2.130%	69150.37	5.55
P25789	sp|P25789|PSA4_HUMAN Proteasome subunit alpha type-4 OS=Homo sapiens OX=9606 GN=PSMA4 PE=1 SV=1	PSMA4	1	1	3.830%	29483.47	7.58
P26640	sp|P26640|SYVC_HUMAN Valine--tRNA ligase OS=Homo sapiens OX=9606 GN=VARS1 PE=1 SV=4	VARS1	1	1	0.870%	140474.33	7.53
P28289	sp|P28289|TMOD1_HUMAN Tropomodulin-1 OS=Homo sapiens OX=9606 GN=TMOD1 PE=1 SV=1	TMOD1	1	1	2.510%	40568.69	5.03
P28332	sp|P28332|ADH6_HUMAN Alcohol dehydrogenase 6 OS=Homo sapiens OX=9606 GN=ADH6 PE=1 SV=3	ADH6	1	1	2.170%	39072.18	8.07
P29218	sp|P29218|IMPA1_HUMAN Inositol monophosphatase 1 OS=Homo sapiens OX=9606 GN=IMPA1 PE=1 SV=1	IMPA1	1	1	2.890%	30188.5	5.16
P29374	sp|P29374|ARI4A_HUMAN AT-rich interactive domain-containing protein 4A OS=Homo sapiens OX=9606 GN=ARID4A PE=1 SV=3	ARID4A	1	1	0.560%	142750.06	5.02
P36871	sp|P36871|PGM1_HUMAN Phosphoglucomutase-1 OS=Homo sapiens OX=9606 GN=PGM1 PE=1 SV=3	PGM1	1	1	1.420%	61448.39	6.3
P37288	sp|P37288|V1AR_HUMAN Vasopressin V1a receptor OS=Homo sapiens OX=9606 GN=AVPR1A PE=1 SV=1	AVPR1A	1	1	1.440%	46799.02	9.48

P38432	sp|P38432|COIL_HUMAN Coilin OS=Homo sapiens OX=9606 GN=COIL PE=1 SV=1	COIL	1	1	1.560%	62607.59	9.2
P43686	sp|P43686|PRS6B_HUMAN 26S proteasome regulatory subunit 6B OS=Homo sapiens OX=9606 GN=PSMC4 PE=1 SV=2	PSMC4	1	1	4.310%	47365.69	5.09
P47989	sp|P47989|XDH_HUMAN Xanthine dehydrogenase/oxidase OS=Homo sapiens OX=9606 GN=XDH PE=1 SV=4	XDH	1	1	1.200%	146422.57	7.86
P48736	sp|P48736|PK3CG_HUMAN Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit gamma isoform OS=Homo sapiens OX=9606 GN=PIK3CG PE=1 SV=3	PIK3CG	1	1	0.540%	126452.16	7.23
P50748	sp|P50748|KNTC1_HUMAN Kinetochore-associated protein 1 OS=Homo sapiens OX=9606 GN=KNTC1 PE=1 SV=1	KNTC1	1	1	0.360%	250745.63	5.67
P51149	sp|P51149|RAB7A_HUMAN Ras-related protein Rab-7a OS=Homo sapiens OX=9606 GN=RAB7A PE=1 SV=1	RAB7A	1	1	4.830%	23489.48	6.4
P52948	sp|P52948|NUP98_HUMAN Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens OX=9606 GN=NUP98 PE=1 SV=4	NUP98	1	1	0.440%	197576.98	5.97
P53007	sp|P53007|TXTP_HUMAN Tricarboxylate transport protein, mitochondrial OS=Homo sapiens OX=9606 GN=SLC25A1 PE=1 SV=2	SLC25A1	1	1	2.570%	34012.3	9.91
P61020	sp|P61020|RAB5B_HUMAN Ras-related protein Rab-5B OS=Homo sapiens OX=9606 GN=RAB5B PE=1 SV=1	RAB5B	1	1	2.790%	23706.54	8.29
P62273	sp|P62273|RS29_HUMAN 40S ribosomal protein S29 OS=Homo sapiens OX=9606 GN=RPS29 PE=1 SV=2	RPS29	1	1	19.640%	6676.71	10.16
P62318	sp|P62318|SMD3_HUMAN Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens OX=9606 GN=SNRPD3 PE=1 SV=1	SNRPD3	1	1	7.940%	13916.11	10.33
P98196	sp|P98196|AT11A_HUMAN Phospholipid-transporting ATPase IH OS=Homo sapiens OX=9606 GN=ATP11A PE=1 SV=3	ATP11A	1	1	0.620%	129754.24	6.17
Q00688	sp|Q00688|FKBP3_HUMAN Peptidyl-prolyl cis-trans isomerase FKBP3 OS=Homo sapiens OX=9606 GN=FKBP3 PE=1 SV=1	FKBP3	1	1	3.130%	25176.51	9.29

Q02241	sp|Q02241|KIF23_HUMAN Kinesin-like protein KIF23 OS=Homo sapiens OX=9606 GN=KIF23 PE=1 SV=3	KIF23	1	1	1.250%	110057.6	8.76
Q02413	sp|Q02413|DSG1_HUMAN Desmoglein-1 OS=Homo sapiens OX=9606 GN=DSG1 PE=1 SV=2	DSG1	1	1	0.670%	113746.35	4.9
Q02952	sp|Q02952|AKA12_HUMAN A-kinase anchor protein 12 OS=Homo sapiens OX=9606 GN=AKAP12 PE=1 SV=4	AKAP12	1	1	0.560%	191479.5	4.37
Q05481	sp|Q05481|ZNF91_HUMAN Zinc finger protein 91 OS=Homo sapiens OX=9606 GN=ZNF91 PE=2 SV=2	ZNF91	1	1	0.500%	137215.96	9.45
Q06124	sp|Q06124|PTN11_HUMAN Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens OX=9606 GN=PTPN11 PE=1 SV=3	PTPN11	1	1	2.020%	68010.01	6.87
Q06547	sp|Q06547|GABP1_HUMAN GA-binding protein subunit beta-1 OS=Homo sapiens OX=9606 GN=GABPB1 PE=1 SV=2	GABPB1	1	1	1.520%	42482.17	4.77
Q08426	sp|Q08426|ECHP_HUMAN Peroxisomal bifunctional enzyme OS=Homo sapiens OX=9606 GN=EHHADH PE=1 SV=3	EHHADH	1	1	1.240%	79493.94	9.24
Q12797	sp|Q12797|ASPH_HUMAN Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens OX=9606 GN=ASPH PE=1 SV=3	ASPH	1	1	1.850%	85861.58	4.92
Q13112	sp|Q13112|CAF1B_HUMAN Chromatin assembly factor 1 subunit B OS=Homo sapiens OX=9606 GN=CHAF1B PE=1 SV=1	CHAF1B	1	1	1.970%	61491.79	7.18
Q13206	sp|Q13206|DDX10_HUMAN Probable ATP-dependent RNA helicase DDX10 OS=Homo sapiens OX=9606 GN=DDX10 PE=1 SV=2	DDX10	1	1	1.260%	100886.74	8.72
Q13724	sp|Q13724|MOGS_HUMAN Mannosyl-oligosaccharide glucosidase OS=Homo sapiens OX=9606 GN=MOGS PE=1 SV=5	MOGS	1	1	1.430%	91916.43	8.97
Q14055	sp|Q14055|CO9A2_HUMAN Collagen alpha-2(IX) chain OS=Homo sapiens OX=9606 GN=COL9A2 PE=1 SV=2	COL9A2	1	1	1.020%	65130.17	9.23
Q14166	sp|Q14166|TTL12_HUMAN Tubulin--tyrosine ligase-like protein 12 OS=Homo sapiens OX=9606 GN=TTLL12 PE=1 SV=2	TTLL12	1	1	1.550%	74402.76	5.33

Q14494	sp|Q14494|NF2L1_HUMAN Endoplasmic reticulum membrane sensor NFE2L1 OS=Homo sapiens OX=9606 GN=NFE2L1 PE=1 SV=1	NFE2L1	1	1	0.910%	84702.83	4.52
Q15386	sp|Q15386|UBE3C_HUMAN Ubiquitin-protein ligase E3C OS=Homo sapiens OX=9606 GN=UBE3C PE=1 SV=3	UBE3C	1	1	0.740%	123921.18	6.27
Q15633	sp|Q15633|TRBP2_HUMAN RISC-loading complex subunit TARBP2 OS=Homo sapiens OX=9606 GN=TARBP2 PE=1 SV=3	TARBP2	1	1	1.910%	39038.9	6.11
Q15650	sp|Q15650|TRIP4_HUMAN Activating signal cointegrator 1 OS=Homo sapiens OX=9606 GN=TRIP4 PE=1 SV=4	TRIP4	1	1	1.380%	66145.46	8.05
Q15835	sp|Q15835|GRK1_HUMAN Rhodopsin kinase GRK1 OS=Homo sapiens OX=9606 GN=GRK1 PE=1 SV=1	GRK1	1	1	1.070%	63525.14	5.63
Q16559	sp|Q16559|TAL2_HUMAN T-cell acute lymphocytic leukemia protein 2 OS=Homo sapiens OX=9606 GN=TAL2 PE=1 SV=1	TAL2	1	1	8.330%	12291.07	10.48
Q16625	sp|Q16625|OCLN_HUMAN Occludin OS=Homo sapiens OX=9606 GN=OCLN PE=1 SV=1	OCLN	1	1	1.530%	59143.1	5.77
Q16643	sp|Q16643|DREB_HUMAN Drebrin OS=Homo sapiens OX=9606 GN=DBN1 PE=1 SV=4	DBN1	1	1	3.080%	71428.45	4.41
Q2LD37	sp|Q2LD37|K1109_HUMAN Transmembrane protein KIAA1109 OS=Homo sapiens OX=9606 GN=KIAA1109 PE=1 SV=2	KIAA1109	1	1	0.100%	555475.45	6.12
Q2VIQ3	sp|Q2VIQ3|KIF4B_HUMAN Chromosome-associated kinesin KIF4B OS=Homo sapiens OX=9606 GN=KIF4B PE=2 SV=2	KIF4B	1	1	0.810%	140033.65	5.88
Q3KP66	sp|Q3KP66|INAVA_HUMAN Innate immunity activator protein OS=Homo sapiens OX=9606 GN=INAVA PE=1 SV=2	INAVA	1	1	0.750%	72913.41	9.42
Q3L8U1	sp|Q3L8U1|CHD9_HUMAN Chromodomain-helicase-DNA-binding protein 9 OS=Homo sapiens OX=9606 GN=CHD9 PE=1 SV=2	CHD9	1	1	0.280%	326018.05	6.56
Q3SY52	sp|Q3SY52|ZIK1_HUMAN Zinc finger protein interacting with ribonucleoprotein K OS=Homo sapiens OX=9606 GN=ZIK1 PE=1 SV=1	ZIK1	1	1	1.030%	54785.69	9.1

Q4G0X9	sp|Q4G0X9|CCD40_HUMAN Coiled-coil domain-containing protein 40 OS=Homo sapiens OX=9606 GN=CCDC40 PE=1 SV=2	CCDC40	1	1	0.610%	130111.89	5.21
Q4VC05	sp|Q4VC05|BCL7A_HUMAN B-cell CLL/lymphoma 7 protein family member A OS=Homo sapiens OX=9606 GN=BCL7A PE=1 SV=1	BCL7A	1	1	2.860%	22809.65	5.01
Q58HT5	sp|Q58HT5|AWAT1_HUMAN Acyl-CoA wax alcohol acyltransferase 1 OS=Homo sapiens OX=9606 GN=AWAT1 PE=1 SV=1	AWAT1	1	1	1.520%	37758.6	9.06
Q59EK9	sp|Q59EK9|RUN3A_HUMAN RUN domain-containing protein 3A OS=Homo sapiens OX=9606 GN=RUNDC3A PE=1 SV=2	RUNDC3A	1	1	1.350%	49746.48	5.19
Q5BKZ1	sp|Q5BKZ1|ZN326_HUMAN DBIRD complex subunit ZNF326 OS=Homo sapiens OX=9606 GN=ZNF326 PE=1 SV=2	ZNF326	1	1	1.890%	65653.07	5.08
Q5FYB1	sp|Q5FYB1|ARSI_HUMAN Arylsulfatase I OS=Homo sapiens OX=9606 GN=ARSI PE=1 SV=1	ARSI	1	1	1.050%	64029.5	8.82
Q5JY77	sp|Q5JY77|GASP1_HUMAN G-protein coupled receptor-associated sorting protein 1 OS=Homo sapiens OX=9606 GN=GPRASP1 PE=1 SV=3	GPRASP1	1	1	0.570%	156863.68	4.64
Q5NUL3	sp|Q5NUL3|FFAR4_HUMAN Free fatty acid receptor 4 OS=Homo sapiens OX=9606 GN=FFAR4 PE=1 SV=3	FFAR4	1	1	1.660%	40493.9	9.7
Q5SZK8	sp|Q5SZK8|FREM2_HUMAN FRAS1-related extracellular matrix protein 2 OS=Homo sapiens OX=9606 GN=FREM2 PE=1 SV=2	FREM2	1	1	0.280%	351152.69	4.89
Q5TFE4	sp|Q5TFE4|NT5D1_HUMAN 5'-nucleotidase domain-containing protein 1 OS=Homo sapiens OX=9606 GN=NT5DC1 PE=1 SV=1	NT5DC1	1	1	1.980%	51844.35	5.94
Q5TGL8	sp|Q5TGL8|PXDC1_HUMAN PX domain-containing protein 1 OS=Homo sapiens OX=9606 GN=PXDC1 PE=2 SV=3	PXDC1	1	1	3.030%	26559.6	4.94
Q5THR3	sp|Q5THR3|EFCB6_HUMAN EF-hand calcium-binding domain-containing protein 6 OS=Homo sapiens OX=9606 GN=EFCAB6 PE=1 SV=1	EFCAB6	1	1	0.470%	172927.77	8.67
Q5VT52	sp|Q5VT52|RPRD2_HUMAN Regulation of nuclear pre-mRNA domain-containing protein 2 OS=Homo sapiens OX=9606 GN=RPRD2 PE=1 SV=1	RPRD2	1	1	0.620%	156017.72	6.97

Q5VTB9	sp|Q5VTB9|RN220_HUMAN E3 ubiquitin-protein ligase RNF220 OS=Homo sapiens OX=9606 GN=RNF220 PE=1 SV=1	RNF220	1	1	1.060%	62764.62	5.7
Q5W0B1	sp|Q5W0B1|OBI1_HUMAN ORC ubiquitin ligase 1 OS=Homo sapiens OX=9606 GN=OBI1 PE=1 SV=1	OBI1	1	1	1.240%	81115.58	5.53
Q6IC98	sp|Q6IC98|GRAM4_HUMAN GRAM domain-containing protein 4 OS=Homo sapiens OX=9606 GN=GRAMD4 PE=1 SV=1	GRAMD4	1	1	1.900%	66407.32	8.98
Q6IF00	sp|Q6IF00|OR2T2_HUMAN Olfactory receptor 2T2 OS=Homo sapiens OX=9606 GN=OR2T2 PE=2 SV=1	OR2T2	1	1	2.160%	36227.99	9.03
Q6IPR3	sp|Q6IPR3|TYW3_HUMAN tRNA wybutosine-synthesizing protein 3 homolog OS=Homo sapiens OX=9606 GN=TYW3 PE=1 SV=2	TYW3	1	1	2.320%	29793.81	7.59
Q6JVE5	sp|Q6JVE5|LCN12_HUMAN Epididymal-specific lipocalin-12 OS=Homo sapiens OX=9606 GN=LCN12 PE=2 SV=1	LCN12	1	1	3.130%	21499.3	5.48
Q6PGP7	sp|Q6PGP7|TTC37_HUMAN Tetratricopeptide repeat protein 37 OS=Homo sapiens OX=9606 GN=TTC37 PE=1 SV=1	TTC37	1	1	0.640%	175484.31	7.47
Q6TFL3	sp|Q6TFL3|CC171_HUMAN Coiled-coil domain-containing protein 171 OS=Homo sapiens OX=9606 GN=CCDC171 PE=2 SV=1	CCDC171	1	1	0.450%	152808.23	6.37
Q6UWE0	sp|Q6UWE0|LRSM1_HUMAN E3 ubiquitin-protein ligase LRSAM1 OS=Homo sapiens OX=9606 GN=LRSAM1 PE=1 SV=1	LRSAM1	1	1	0.690%	83592.98	5.7
Q6UWY0	sp|Q6UWY0|ARSK_HUMAN Arylsulfatase K OS=Homo sapiens OX=9606 GN=ARSK PE=1 SV=1	ARSK	1	1	1.120%	61449.72	9.02
Q6WRI0	sp|Q6WRI0|IGS10_HUMAN Immunoglobulin superfamily member 10 OS=Homo sapiens OX=9606 GN=IGSF10 PE=1 SV=1	IGSF10	1	1	0.300%	290834.56	9.25
Q6XZF7	sp|Q6XZF7|DNMBP_HUMAN Dynamin-binding protein OS=Homo sapiens OX=9606 GN=DNMBP PE=1 SV=1	DNMBP	1	1	0.380%	177345.03	5.26
Q6ZRP7	sp|Q6ZRP7|QSOX2_HUMAN Sulfhydryl oxidase 2 OS=Homo sapiens OX=9606 GN=QSOX2 PE=1 SV=3	QSOX2	1	1	0.860%	77527.82	7.64

Q709C8	sp|Q709C8|VP13C_HUMAN Vacuolar protein sorting-associated protein 13C OS=Homo sapiens OX=9606 GN=VPS13C PE=1 SV=1	VPS13C	1	1	0.270%	422385.06	6.38
Q70Z35	sp|Q70Z35|PREX2_HUMAN Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 2 protein OS=Homo sapiens OX=9606 GN=PREX2 PE=1 SV=1	PREX2	1	1	0.560%	182620	7.26
Q719I0	sp|Q719I0|AHSA2_HUMAN Putative activator of 90 kDa heat shock protein ATPase homolog 2 OS=Homo sapiens OX=9606 GN=AHSA2P PE=5 SV=2	AHSA2P	1	1	2.680%	33805.62	6.98
Q7Z404	sp|Q7Z404|TMC4_HUMAN Transmembrane channel-like protein 4 OS=Homo sapiens OX=9606 GN=TMC4 PE=1 SV=3	TMC4	1	1	0.840%	79206.73	9.16
Q86VR8	sp|Q86VR8|FJX1_HUMAN Four-jointed box protein 1 OS=Homo sapiens OX=9606 GN=FJX1 PE=2 SV=1	FJX1	1	1	1.370%	48505.95	10.66
Q86WK6	sp|Q86WK6|AMGO1_HUMAN Amphoterin-induced protein 1 OS=Homo sapiens OX=9606 GN=AMIGO1 PE=1 SV=1	AMIGO1	1	1	2.030%	55238.6	6.22
Q86WS4	sp|Q86WS4|CL040_HUMAN Uncharacterized protein C12orf40 OS=Homo sapiens OX=9606 GN=C12orf40 PE=1 SV=3	C12orf40	1	1	1.230%	74503.75	8.21
Q86XI2	sp|Q86XI2|CNDG2_HUMAN Condensin-2 complex subunit G2 OS=Homo sapiens OX=9606 GN=NCAPG2 PE=1 SV=1	NCAPG2	1	1	0.870%	130958.77	6.43
Q86Y56	sp|Q86Y56|DAAF5_HUMAN Dynein axonemal assembly factor 5 OS=Homo sapiens OX=9606 GN=DNAAF5 PE=1 SV=4	DNAAF5	1	1	1.400%	93520.07	5.98
Q8IU60	sp|Q8IU60|DCP2_HUMAN m7GpppN-mRNA hydrolase OS=Homo sapiens OX=9606 GN=DCP2 PE=1 SV=3	DCP2	1	1	1.670%	48422.58	8.21
Q8IWI9	sp|Q8IWI9|MGAP_HUMAN MAX gene-associated protein OS=Homo sapiens OX=9606 GN=MGA PE=1 SV=4	MGA	1	1	0.330%	336155.56	6.48
Q8IX94	sp|Q8IX94|CTGE4_HUMAN cTAGE family member 4 OS=Homo sapiens OX=9606 GN=CTAGE4 PE=2 SV=3	CTAGE4	1	1	0.640%	87987.88	5.18
Q8IXQ8	sp|Q8IXQ8|PDZD9_HUMAN PDZ domain-containing protein 9 OS=Homo sapiens OX=9606 GN=PDZD9 PE=2 SV=2	PDZD9	1	1	2.270%	29903.61	8.99

Q8IYB3	sp|Q8IYB3|SRRM1_HUMAN Serine/arginine repetitive matrix protein 1 OS=Homo sapiens OX=9606 GN=SRRM1 PE=1 SV=2	SRRM1	1	1	1.330%	102333.88	11.84
Q8IYE0	sp|Q8IYE0|CC146_HUMAN Coiled-coil domain-containing protein 146 OS=Homo sapiens OX=9606 GN=CCDC146 PE=1 SV=2	CCDC146	1	1	0.630%	112805.18	8.59
Q8IYM2	sp|Q8IYM2|SLN12_HUMAN Schlafen family member 12 OS=Homo sapiens OX=9606 GN=SLFN12 PE=1 SV=2	SLFN12	1	1	1.210%	66971.77	8.84
Q8IZC6	sp|Q8IZC6|CORA1_HUMAN Collagen alpha-1(XXVII) chain OS=Homo sapiens OX=9606 GN=COL27A1 PE=1 SV=1	COL27A1	1	1	0.540%	186890.15	9.83
Q8IZF6	sp|Q8IZF6|AGRG4_HUMAN Adhesion G-protein coupled receptor G4 OS=Homo sapiens OX=9606 GN=ADGRG4 PE=2 SV=2	ADGRG4	1	1	0.190%	333364.23	5.82
Q8IZH2	sp|Q8IZH2|XRN1_HUMAN 5'-3' exoribonuclease 1 OS=Homo sapiens OX=9606 GN=XRN1 PE=1 SV=1	XRN1	1	1	0.470%	194105	6.78
Q8N158	sp|Q8N158|GPC2_HUMAN Glypican-2 OS=Homo sapiens OX=9606 GN=GPC2 PE=1 SV=1	GPC2	1	1	1.040%	62828.9	8.33
Q8N3C0	sp|Q8N3C0|ASCC3_HUMAN Activating signal cointegrator 1 complex subunit 3 OS=Homo sapiens OX=9606 GN=ASCC3 PE=1 SV=3	ASCC3	1	1	0.450%	251457.36	6.64
Q8N456	sp|Q8N456|LRC18_HUMAN Leucine-rich repeat-containing protein 18 OS=Homo sapiens OX=9606 GN=LRRC18 PE=1 SV=2	LRRC18	1	1	2.300%	29736.5	9.83
Q8N999	sp|Q8N999|CL029_HUMAN Uncharacterized protein C12orf29 OS=Homo sapiens OX=9606 GN=C12orf29 PE=1 SV=2	C12orf29	1	1	3.080%	37489.59	6.6
Q8N9F0	sp|Q8N9F0|NAT8L_HUMAN N-acetylaspartate synthetase OS=Homo sapiens OX=9606 GN=NAT8L PE=1 SV=3	NAT8L	1	1	2.980%	32836.86	9.05
Q8NB90	sp|Q8NB90|AFG2H_HUMAN ATPase family protein 2 homolog OS=Homo sapiens OX=9606 GN=SPATA5 PE=1 SV=3	SPATA5	1	1	1.340%	97903.29	5.5
Q8NDB2	sp|Q8NDB2|BANK1_HUMAN B-cell scaffold protein with ankyrin repeats OS=Homo sapiens OX=9606 GN=BANK1 PE=1 SV=3	BANK1	1	1	1.270%	89280.86	5.28

Q8NEJ9	sp|Q8NEJ9|NGDN_HUMAN Neuroguidin OS=Homo sapiens OX=9606 GN=NGDN PE=1 SV=1	NGDN	1	1	5.710%	35893.68	9.57
Q8NEP3	sp|Q8NEP3|DAAF1_HUMAN Dynein axonemal assembly factor 1 OS=Homo sapiens OX=9606 GN=DNAAF1 PE=1 SV=5	DNAAF1	1	1	1.100%	80025.22	4.57
Q8NEZ4	sp|Q8NEZ4|KMT2C_HUMAN Histone-lysine N-methyltransferase 2C OS=Homo sapiens OX=9606 GN=KMT2C PE=1 SV=3	KMT2C	1	1	0.140%	541363.8	6.07
Q8NFW9	sp|Q8NFW9|MYRIP_HUMAN Rab effector MyRIP OS=Homo sapiens OX=9606 GN=MYRIP PE=1 SV=2	MYRIP	1	1	1.750%	95705.17	5.44
Q8NFZ8	sp|Q8NFZ8|CADM4_HUMAN Cell adhesion molecule 4 OS=Homo sapiens OX=9606 GN=CADM4 PE=1 SV=1	CADM4	1	1	3.610%	42784.82	5.92
Q8TAT5	sp|Q8TAT5|NEIL3_HUMAN Endonuclease 8-like 3 OS=Homo sapiens OX=9606 GN=NEIL3 PE=1 SV=3	NEIL3	1	1	2.150%	67768.38	9.23
Q8TAT6	sp|Q8TAT6|NPL4_HUMAN Nuclear protein localization protein 4 homolog OS=Homo sapiens OX=9606 GN=NPLOC4 PE=1 SV=3	NPLOC4	1	1	1.320%	68119.46	5.94
Q8TC07	sp|Q8TC07|TBC15_HUMAN TBC1 domain family member 15 OS=Homo sapiens OX=9606 GN=TBC1D15 PE=1 SV=2	TBC1D15	1	1	1.740%	79489.78	5.44
Q8TCG1	sp|Q8TCG1|CIP2A_HUMAN Protein CIP2A OS=Homo sapiens OX=9606 GN=CIP2A PE=1 SV=2	CIP2A	1	1	0.880%	102183.83	5.85
Q8TDW7	sp|Q8TDW7|FAT3_HUMAN Protocadherin Fat 3 OS=Homo sapiens OX=9606 GN=FAT3 PE=2 SV=3	FAT3	1	1	0.200%	501972.22	4.72
Q8TEC5	sp|Q8TEC5|SH3R2_HUMAN E3 ubiquitin-protein ligase SH3RF2 OS=Homo sapiens OX=9606 GN=SH3RF2 PE=1 SV=3	SH3RF2	1	1	0.820%	79318.8	9.96
Q8TEQ6	sp|Q8TEQ6|GEMI5_HUMAN Gem-associated protein 5 OS=Homo sapiens OX=9606 GN=GEMIN5 PE=1 SV=3	GEMIN5	1	1	0.600%	168587.45	6.17
Q8WU90	sp|Q8WU90|ZC3HF_HUMAN Zinc finger CCCH domain-containing protein 15 OS=Homo sapiens OX=9606 GN=ZC3H15 PE=1 SV=1	ZC3H15	1	1	3.990%	48601.91	5.22