Supporting Table 1A. List of Proteins Detected in the Human Tip49a/b Dataset.
pages 2-6

Supporting Table 1B. Detailed List of Proteins and Peptides Detected in the Combined Human TIP49a/b Dataset.
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Supporting Table 1C. List of Proteins after contaminant extraction and SVD ranking.
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Supporting Table 1A. List of Proteins Detected in the Human TIP49a/b Dataset.

The number of peptides (column header ends with _P), number of spectra (_S), sequence coverage (_SC), and normalized spectral abundance factor (_NSAF) are specified for each run (i.e. each run is represented by 4 columns of numbers).
Proteins are grouped by: "proteins detected in *n* runs", proteins detected in (*n* -1) runs, and proteins unique to each run.

Contrast_Rank	Locus	Description	ALL_P	ALL_S	ALL_SC	ALL_NSAF	ARP5_P	ARP5_S	ARP5_SC
1	gi|Flag_peptid	[FLAG peptide]	1	26	100	0.018	1	3	100
8	gi|89067014|r	PREDICTED: similar to RuvB-like pro	6	587	89.09	0.061	4	16	61.82
9	gi|31542680|r	ARP5 actin-related protein 5 homolog	34	643	66.72	0.006	31	417	58.81
10	gi|5730023|re	RuvB-like 2 [Homo sapiens]	55	4389	89.85	0.054	24	73	55.29
11	gi|4506753|re	TATA binding protein interacting prot	41	5441	85.09	0.068	17	50	51.1
12	gi|42822884|r	hypothetical protein LOC125476 [Hor	14	148	75.52	0.004	6	26	40.1
13	gi|39812115|r	actin-related protein 8 [Homo sapiens	49	1098	75.48	0.01	17	32	33.01
14	gi|5453603|re	chaperonin containing TCP1, subunit	30	245	70.84	0.003	10	16	31.78
15	gi|24307939|r	chaperonin containing TCP1, subunit	18	153	49.91	0.002	9	31	28.84
16	gi|4757718|re	actin-like 6A isoform 1 [Homo sapiens	18	513	49.42	0.007	7	16	25.87
17	gi|58761486|r	chaperonin containing TCP1, subunit	24	109	56.8	0.001	8	16	25.55
19	gi|6005814|re	serine/threonine kinase 38 [Homo sa	27	1059	61.94	0.013	9	23	24.3
20	gi|4501885|re	beta actin [Homo sapiens]	18	925	62.93	0.014	5	13	21.6
22	gi|4885431|re	heat shock 70kDa protein 1B [Homo s	37	1356	72.54	0.012	12	29	21.22
23	gi|5453607|re	chaperonin containing TCP1, subunit	20	183	52.3	0.002	6	19	20.99
24	gi|13775202|r	high mobility group AT-hook 1-like 4	12	108	58.02	0.002	3	9	20.99
25	gi|27734727|r	hypothetical protein LOC283899 [Hor	8	381	51.23	0.009	3	8	19.67
26	gi|48762932|r	chaperonin containing TCP1, subunit	33	135	69.34	0.001	6	15	17.88
27	gi|33469139|r	yeast INO80-like protein [Homo sapie	46	330	38.24	0.001	20	43	17.61
29	gi|23346420|r	nuclear factor related to kappaB bind	63	402	60.42	0.002	18	39	16.31
30	gi|5729877|re	heat shock 70kDa protein 8 isoform 1	28	647	60.06	0.006	8	22	15.63
31	gi|29788768|r	tubulin, beta polypeptide paralog [Ho	21	622	57.98	0.008	4	6	14.38
32	gi|5174735|re	tubulin, beta, 2 [Homo sapiens]	25	691	67.64	0.009	4	6	14.38
33	gi|29788785|r	tubulin, beta polypeptide [Homo sapie	27	839	71.62	0.011	4	6	14.41
34	gi|4502643|re	chaperonin containing TCP1, subunit	19	135	53.86	0.001	6	19	13.56
35	gi|4885375|re	H1 histone family, member 2 [Homo s	14	225	39.91	0.006	3	6	13.62
36	gi|4885379|re	H1 histone family, member 4 [Homo s	12	223	34.7	0.006	3	6	13.24
37	gi|4505813|re	cytoplasmic dynein light polypeptide	4	20	64.04	0.001	1	2	13.48
38	gi|4501881|re	alpha 1 actin precursor [Homo sapien	12	443	36.6	0.007	4	11	13
40	gi|21626466|r	matrin 3 [Homo sapiens]	28	432	44.27	0.003	6	13	12.75
42	gi|89058472|r	PREDICTED: similar to Ig kappa cha	1	183	12.26	0.01	1	4	12.26
46	gi|29893564|r	microspherule protein 1 isoform 1 [Ho	17	177	46.32	0.002	4	7	12.12
48	gi|4507955|re	YY1 transcription factor [Homo sapie	8	38	22.95	5E-04	4	5	12.08
49	gi|10835063|r	nucleophosmin 1 isoform 1 [Homo sa	9	138	42.52	0.003	3	12	11.9
51	gi|11036646|r	H2B histone family, member S [Homo	8	142	57.14	0.006	1	2	11.9
52	gi|20336754|r	H2B histone family, member R [Hom	7	116	57.14	0.005	1	2	11.9
54	gi|7706753|re	ubiquitin C-terminal hydrolase UCH37	13	62	55.62	0.001	3	4	11.25
55	gi|4504255|re	H2A histone family, member Z [Homo	5	185	53.91	0.008	1	2	10.94
56	gi|50053795|r	eukaryotic translation initiation factor	14	98	31.59	9E-04	3	6	10.47
57	gi|38488718|r	hypothetical protein LOC54891 [Hom	13	39	20.62	3E-04	5	10	10.14
58	gi|57863257|r	T-complex protein 1 isoform a [Homo	26	159	64.75	0.002	3	8	9.71
59	gi|34932414|r	non-POU domain containing, octame	16	225	44.8	0.003	3	7	9.55
60	gi|38455427|r	chaperonin containing TCP1, subunit	21	152	62.34	0.002	4	13	9.46
61	gi|14210536|r	tubulin, beta 6 [Homo sapiens]	11	213	35.87	0.003	3	5	8.74
63	gi|6857818|re	nucleophosmin/nucleoplasmin 3 [Hor	1	3	8.43	1E-04	1	1	8.43
64	gi|7661958|re	BCL2-associated transcription factor	27	219	33.59	0.001	5	11	7.93
65	gi|7019371|re	TCF3 (E2A) fusion partner (in childho	15	376	58.5	0.008	1	13	7.91
66	gi|4758302|re	enhancer of rudimentary homolog [Ho	4	75	34.62	0.004	1	4	7.69
67	gi|20127479|r	RNA binding motif protein 10 isoform	29	314	40.97	0.002	3	8	7.63
68	gi|23111018|r	RNA binding motif protein 10 isoform	26	295	40.49	0.002	3	8	8.33
69	gi|40254869|r	pre-mRNA processing factor 31 hom	15	187	45.09	0.002	2	7	7.62
70	gi|5174449|re	H1 histone family, member X [Homo s	8	76	28.64	0.002	1	1	7.51
71	gi|11321591|r	high-mobility group box 2 [Homo sapi	3	6	12.92	2E-04	1	2	7.18
72	gi|4826998|re	splicing factor proline/glutamine rich (	18	203	30.27	0.002	3	5	7.07
73	gi|52632383|r	heterogeneous nuclear ribonucleopro	22	146	66.21	0.001	2	3	7.13
74	gi|5730065|re	spindlin [Homo sapiens]	12	58	56.68	0.001	1	2	6.88
75	gi|89061489|r	PREDICTED: similar to Bcl-2-associa	22	205	32.57	0.001	4	9	6.67
76	gi|14043070|r	heterogeneous nuclear ribonucleopro	17	160	43.55	0.002	2	2	6.72
78	gi|13676857|r	heat shock 70kDa protein 2 [Homo sa	9	176	13.46	0.002	3	8	6.57
79	gi|4501955|re	poly (ADP-ribose) polymerase family,	33	253	42.31	0.001	4	7	6.51
80	gi|31542947|r	chaperonin [Homo sapiens]	20	130	54.1	0.001	2	4	6.46
82	gi|27735029|r	MOB1, Mps One Binder kinase activa	2	3	12.04	8E-05	1	2	6.48
84	gi|4827040|re	thyroid hormone receptor associated	29	182	34.76	0.001	5	11	6.39
85	gi|34419635|r	heat shock 70kDa protein 6 (HSP70B	8	269	15.24	0.002	3	11	6.38
86	gi|27436929|r	heat shock 70kDa protein 1-like [Hom	9	487	21.53	0.004	3	5	6.24
87	gi|4504511|re	DnaJ (Hsp40) homolog, subfamily A,	4	30	21.16	4E-04	1	2	6.05
88	gi|12056465|r	fibrillarin [Homo sapiens]	7	81	31.78	0.001	1	4	5.92
89	gi|5031753|re	heterogeneous nuclear ribonucleopro	13	276	50.11	0.003	2	4	5.79
91	gi|74099697|r	heterogeneous nuclear ribonucleopro	7	175	26.28	0.002	2	4	5.79
92	gi|50592996|r	tubulin, beta, 4 [Homo sapiens]	14	365	29.56	0.005	2	4	5.56
93	gi|47271443|r	splicing factor, arginine/serine-rich 2	3	15	13.12	4E-04	1	2	4.98
94	gi|14389309|r	tubulin alpha 6 [Homo sapiens]	19	503	66.82	0.006	1	2	4.68
95	gi|9507215|re	tubulin, alpha 8 [Homo sapiens]	10	335	31.18	0.004	1	2	4.68
96	gi|57013276|r	tubulin, alpha, ubiquitous [Homo sapi	20	591	70.73	0.007	1	2	4.66
97	gi|17986283|r	tubulin, alpha 3 [Homo sapiens]	21	507	74.28	0.006	1	2	4.66
98	gi|17921989|r	tubulin, alpha 1 [Homo sapiens]	14	460	44.42	0.006	1	2	4.69
99	gi|39930523|r	hypothetical protein LOC144097 [Hor	7	42	34.38	6E-04	1	1	4.72
100	gi|88983853|r	PREDICTED: similar to Heterogeneo	8	38	27.3	8E-04	1	1	4.26
111	gi|5174525|re	microtubule-associated protein 1B iso	73	448	46.84	0.001	7	13	4.13
112	gi|14165435|r	heterogeneous nuclear ribonucleopro	21	411	53.56	0.005	1	3	3.67
115	gi|57863301|r	CLIP-associating protein 2 [Homo sa	24	118	23.57	4E-04	4	7	3.52
116	gi|5032087|re	splicing factor 3a, subunit 1, 120kDa	9	59	19.04	4E-04	1	1	3.53
117	gi|7706254|re	nucleolar protein NOP5/NOP58 [Hom	17	112	44.42	0.001	1	1	3.4
118	gi|4758560|re	WD repeat domain 57 (U5 snRNP sp	9	37	47.62	6E-04	1	2	3.36
119	gi|14043072|r	heterogeneous nuclear ribonucleopro	15	184	49.86	0.003	1	1	3.4
121	gi|4758860|re	nucleolar and coiled-body phosphopr	8	85	13.3	7E-04	1	2	3.29
122	gi|13514813|r	DEAD/H (Asp-Glu-Ala-Asp/His) box p	13	94	27.49	8E-04	1	2	3.32
124	gi|21359884|r	calcium homeostasis endoplasmic re	7	12	16.29	8E-05	2	2	3.17
125	gi|19923653|r	PC4 and SFRS1 interacting protein 1	6	27	16.04	3E-04	1	1	3.21
126	gi|5730027|re	KH domain containing, RNA binding,	7	53	15.12	7E-04	1	1	3.16
127	gi|4503471|re	eukaryotic translation elongation facto	15	319	48.7	0.004	1	1	3.03
128	gi|4503475|re	eukaryotic translation elongation facto	11	170	35.21	0.002	1	1	3.02
129	gi|62414289|r	vimentin [Homo sapiens]	10	55	30.69	7E-04	1	1	2.79
130	gi|56243583|r	WD repeat domain 18 [Homo sapiens	3	10	8.56	1E-04	1	1	2.78
131	gi|13699824|r	kinesin family member 11 [Homo sap	44	472	51.89	0.003	2	3	2.56
132	gi|12025678|r	actinin, alpha 4 [Homo sapiens]	18	72	28.98	4E-04	2	2	2.52
133	gi|4501891|re	actinin, alpha 1 [Homo sapiens]	7	31	9.64	2E-04	2	2	2.58
134	gi|29789090|r	RCC1-like [Homo sapiens]	7	19	22.41	2E-04	1	1	2.49
135	gi|44955910|r	E2F transcription factor 7 [Homo sapi	7	24	11.64	1E-04	1	3	2.41
136	gi|4758138|re	DEAD (Asp-Glu-Ala-Asp) box polype	19	94	41.37	9E-04	2	3	2.44
137	gi|24307971|r	serine/threonine kinase 38 like [Homo	13	176	36.64	0.002	1	2	2.37
138	gi|4826760|re	heterogeneous nuclear ribonucleopro	10	218	46.75	0.003	1	2	2.41
139	gi|4503483|re	eukaryotic translation elongation facto	15	65	27.74	4E-04	1	1	2.33
141	gi|16507237|r	heat shock 70kDa protein 5 (glucose-	24	218	44.8	0.002	1	1	2.14
142	gi|50659095|r	DEAD (Asp-Glu-Ala-Asp) box polype	21	102	33.72	7E-04	1	1	1.79
143	gi|4503745|re	filamin 1 (actin-binding protein-280) [	74	357	47.45	8E-04	3	6	1.7
144	gi|21237802|r	SWI/SNF-related matrix-associated a	7	42	9.41	2E-04	1	1	1.72
145	gi|74136883|r	heterogeneous nuclear ribonucleopro	30	153	43.03	0.001	1	4	1.58
146	gi|38201710|r	DEAD box polypeptide 17 isoform p8	16	100	24.83	8E-04	1	1	1.65
147	gi|56676335|r	RAP1 interacting factor 1 [Homo sapi	33	111	22.29	3E-04	2	3	1.46
148	gi|30581135|r	SMC1 structural maintenance of chro	17	38	19.06	2E-04	1	1	1.14
149	gi|51492636|r	PREDICTED: U2-associated SR140	15	82	22.12	4E-04	1	1	1.11
151	gi|4503297|re	DEAH (Asp-Glu-Ala-His) box polypep	44	637	47.15	0.003	1	1	1.02
152	gi|4507195|re	spectrin, beta, non-erythrocytic 1 isof	40	148	26.44	4E-04	1	1	0.72
153	gi|51599156|r	chromodomain helicase DNA binding	15	43	14.96	1E-04	1	1	0.63
156	gi|52630322|r	chromodomain helicase DNA binding	7	25	6.1	7E-05	1	1	0.61
157	gi|19923466|r	splicing coactivator subunit SRm300	30	144	17.59	3E-04	1	1	0.51
158	gi|13654237|r	protein kinase, DNA-activated, cataly	110	711	40.43	1E-03	1	1	0.34
159	gi|4506671|re	ribosomal protein P2 [Homo sapiens]	6	45	70.43	0.002	X	X	X
160	gi|30795231|r	brain abundant, membrane attached	8	20	63.44	5E-04	X	X	X
161	gi|4507129|re	small nuclear ribonucleoprotein polyp	3	36	52.17	0.002	X	X	X
162	gi|4506669|re	ribosomal protein P1 isoform 1 [Hom	2	29	51.75	0.001	X	X	X
163	gi|29294624|r	small nuclear ribonucleoprotein polyp	7	72	55.93	0.003	X	X	X
165	gi|4504041|re	guanine nucleotide binding protein (G	12	37	47.32	6E-04	X	X	X
166	gi|50593002|r	small nuclear ribonucleoprotein polyp	10	121	65.1	0.003	X	X	X
167	gi|4506687|re	ribosomal protein S15 [Homo sapiens	6	76	62.07	0.003	X	X	X
168	gi|4506693|re	ribosomal protein S17 [Homo sapiens	7	123	57.04	0.005	X	X	X
169	gi|5902102|re	small nuclear ribonucleoprotein D1 p	4	175	54.62	0.008	X	X	X
170	gi|11321585|r	guanine nucleotide-binding protein, b	10	27	45.29	5E-04	X	X	X
171	gi|20357529|r	guanine nucleotide-binding protein, b	10	19	45.29	3E-04	X	X	X
172	gi|16933546|r	ribosomal protein P0 [Homo sapiens]	11	54	53.63	1E-03	X	X	X
174	gi|11415030|r	H4 histone family, member E [Homo s	10	93	61.17	0.005	X	X	X
191	gi|5803225|re	tyrosine 3/tryptophan 5 -monooxygen	10	78	54.51	0.002	X	X	X
192	gi|4506605|re	ribosomal protein L23 [Homo sapiens	6	56	40.71	0.002	X	X	X
193	gi|10863977|r	LSM2 homolog, U6 small nuclear RN	2	7	40	4E-04	X	X	X
194	gi|24234688|r	heat shock 70kDa protein 9B precurs	23	121	45.21	0.001	X	X	X
195	gi|4506613|re	ribosomal protein L22 proprotein [Ho	3	15	39.06	7E-04	X	X	X
196	gi|5032051|re	ribosomal protein S14 [Homo sapiens	6	46	65.56	0.002	X	X	X
199	gi|5803076|re	chromobox homolog 1 (HP1 beta hor	6	23	46.49	7E-04	X	X	X
200	gi|4506681|re	ribosomal protein S11 [Homo sapiens	5	34	36.71	0.001	X	X	X
201	gi|14211889|r	dpy-30-like protein [Homo sapiens]	2	67	36.36	0.004	X	X	X
202	gi|15718687|r	ribosomal protein S3 [Homo sapiens]	11	143	53.91	0.003	X	X	X
203	gi|4506597|re	ribosomal protein L12 [Homo sapiens	6	27	54.55	9E-04	X	X	X
204	gi|4502549|re	calmodulin 2 [Homo sapiens]	4	13	35.57	5E-04	X	X	X
207	gi|4506455|re	reticulocalbin 1 precursor [Homo sapi	6	23	35.05	4E-04	X	X	X
208	gi|4506701|re	ribosomal protein S23 [Homo sapiens	5	16	48.25	6E-04	X	X	X
209	gi|5031699|re	flotillin 1 [Homo sapiens]	10	30	34.66	4E-04	X	X	X
210	gi|51036603|r	G-protein gamma-12 subunit [Homo s	2	2	34.72	2E-04	X	X	X
211	gi|5729850|re	guanine nucleotide binding protein (G	7	24	34.18	4E-04	X	X	X
212	gi|17986258|r	smooth muscle and non-muscle myos	4	27	33.77	0.001	X	X	X
216	gi|7669492|re	glyceraldehyde-3-phosphate dehydro	19	152	65.67	0.003	X	X	X
217	gi|4506643|re	ribosomal protein L37a [Homo sapier	4	7	51.09	4E-04	X	X	X
218	gi|4502491|re	complement component 1, q subcom	4	42	32.27	8E-04	X	X	X
219	gi|38372923|r	basigin isoform 4 [Homo sapiens]	3	4	31.71	1E-04	X	X	X
220	gi|4826860|re	NHP2 non-histone chromosome prote	4	30	31.25	0.001	X	X	X
222	gi|4506691|re	ribosomal protein S16 [Homo sapiens	5	59	32.19	0.002	X	X	X
223	gi|32483377|r	peroxiredoxin 3 isoform b [Homo sap	4	17	30.67	4E-04	X	X	X
225	gi|4757834|re	BCL2-associated athanogene 2 [Hom	4	11	30.33	3E-04	X	X	X
226	gi|10835067|r	autoantigen La [Homo sapiens]	10	65	29.66	9E-04	X	X	X
227	gi|4506457|re	reticulocalbin 2, EF-hand calcium bin	7	31	46.06	6E-04	X	X	X
228	gi|15431301|r	ribosomal protein L7 [Homo sapiens]	8	35	38.31	8E-04	X	X	X
229	gi|14916501|r	ribosomal protein S24 isoform a [Hor	4	27	34.62	0.001	X	X	X
231	gi|13904870|r	ribosomal protein S5 [Homo sapiens]	7	184	37.75	0.005	X	X	X
232	gi|14591909|r	ribosomal protein L5 [Homo sapiens]	11	86	52.19	0.002	X	X	X
233	gi|11968057|r	ARP6 actin-related protein 6 homolog	24	340	67.17	0.005	X	X	X
234	gi|15809016|r	myosin regulatory light chain MRCL2	4	15	28.49	5E-04	X	X	X
236	gi|34147630|r	Tu translation elongation factor, mitoc	12	49	38.46	6E-04	X	X	X
237	gi|4502551|re	calumenin precursor [Homo sapiens]	5	10	27.94	2E-04	X	X	X
238	gi|20070220|r	SKB1 homolog [Homo sapiens]	21	224	53.06	0.002	X	X	X
239	gi|4506725|re	ribosomal protein S4, X-linked X isofo	6	21	27.38	5E-04	X	X	X
240	gi|13129110|r	methylosome protein 50 [Homo sapie	10	117	50.58	0.002	X	X	X
241	gi|4503571|re	enolase 1 [Homo sapiens]	13	106	45.62	0.001	X	X	X
242	gi|14277700|r	ribosomal protein S12 [Homo sapiens	5	37	40.91	0.002	X	X	X
245	gi|16579885|r	ribosomal protein L4 [Homo sapiens]	14	60	32.08	8E-04	X	X	X
246	gi|16753227|r	ribosomal protein L6 [Homo sapiens]	9	65	33.68	0.001	X	X	X
248	gi|4504253|re	H2A histone family, member X [Homo	4	58	52.45	0.002	X	X	X
249	gi|41406064|r	myosin, heavy polypeptide 10, non-m	51	139	36.84	4E-04	X	X	X
250	gi|4506743|re	ribosomal protein S8 [Homo sapiens]	6	38	32.69	0.001	X	X	X
251	gi|4505343|re	nuclear cap binding protein subunit 1	13	51	25.44	4E-04	X	X	X
252	gi|10800130|r	histone 1, H2ad [Homo sapiens]	4	89	54.62	0.004	X	X	X
258	gi|24638446|r	H2A histone family, member Q [Hom	4	92	55.04	0.004	X	X	X
262	gi|4758012|re	clathrin heavy chain 1 [Homo sapiens	36	139	34.69	5E-04	X	X	X
263	gi|4506685|re	ribosomal protein S13 [Homo sapiens	5	24	30.46	9E-04	X	X	X
264	gi|4757810|re	ATP synthase, H+ transporting, mitoc	8	32	24.77	3E-04	X	X	X
267	gi|4759160|re	small nuclear ribonucleoprotein polyp	3	41	31.75	0.002	X	X	X
268	gi|30474871|r	serine palmitoyltransferase subunit 1	2	3	24.48	1E-04	X	X	X
270	gi|14141152|r	heterogeneous nuclear ribonucleopro	15	121	30.41	9E-04	X	X	X
271	gi|33946324|r	guanine nucleotide binding protein (G	7	20	23.73	3E-04	X	X	X
272	gi|7019485|re	programmed cell death 6 [Homo sapi	6	24	38.74	7E-04	X	X	X
273	gi|55770900|r	BRIX [Homo sapiens]	4	14	23.51	2E-04	X	X	X
274	gi|34098946|r	nuclease sensitive element binding p	7	23	35.19	4E-04	X	X	X
275	gi|10440560|r	H3 histone family, member I [Homo s	2	32	30.15	0.001	X	X	X
283	gi|31742503|r	H3 histone family, member M [Homo	2	25	30.15	0.001	X	X	X
286	gi|4504279|re	H3 histone, family 3A [Homo sapiens	2	46	30.15	0.002	X	X	X
289	gi|14165464|r	polypyrimidine tract-binding protein 1	15	259	47.64	0.003	X	X	X
292	gi|4507879|re	voltage-dependent anion channel 1 [H	4	9	23.32	2E-04	X	X	X
293	gi|4758394|re	flotillin 2 [Homo sapiens]	6	16	23.22	2E-04	X	X	X
294	gi|25453472|r	eukaryotic translation elongation facto	9	38	43.77	8E-04	X	X	X
296	gi|4506723|re	ribosomal protein S3a [Homo sapiens	5	39	23.11	8E-04	X	X	X
297	gi|5729875|re	progesterone receptor membrane co	2	6	23.08	2E-04	X	X	X
298	gi|4758504|re	hydroxyacyl-Coenzyme A dehydroge	4	9	32.95	2E-04	X	X	X
299	gi|15431288|r	ribosomal protein L10a [Homo sapier	5	25	29.49	7E-04	X	X	X
300	gi|15431293|r	ribosomal protein L15 [Homo sapiens	5	28	27.45	8E-04	X	X	X
310	gi|13514822|r	DEAH (Asp-Glu-Ala-His) box polypep	11	115	47.23	0.003	X	X	X
311	gi|55956788|r	nucleolin [Homo sapiens]	23	504	28.03	0.004	X	X	X
312	gi|17158044|r	ribosomal protein S6 [Homo sapiens]	5	9	26.1	2E-04	X	X	X
313	gi|89038911|r	PREDICTED: similar to ribosomal pro	4	30	22.48	8E-04	X	X	X
317	gi|5453597|re	F-actin capping protein alpha-1 subur	8	26	52.45	5E-04	X	X	X
318	gi|41151097|r	PREDICTED: similar to ribosomal pro	4	8	28.04	2E-04	X	X	X
323	gi|4507231|re	single-stranded DNA binding protein	2	4	22.3	2E-04	X	X	X
324	gi|7705425|r	mitochondrial ribosomal protein S17 [	1	5	22.31	2E-04	X	X	X
325	gi|5902076|re	splicing factor, arginine/serine-rich 1 (	12	76	43.95	0.002	X	X	X
326	gi|4506649|re	ribosomal protein L3 isoform a [Homo	10	47	27.3	7E-04	X	X	X
328	gi|88947729|r	PREDICTED: similar to ribosomal pro	8	92	29.45	0.002	X	X	X
331	gi|4503481|re	eukaryotic translation elongation facto	14	80	42.11	0.001	X	X	X
332	gi|4506617|re	ribosomal protein L17 [Homo sapiens	4	25	27.17	8E-04	X	X	X
350	gi|14150100|r	hypothetical protein LOC84284 [Hom	4	9	28.42	3E-04	X	X	X
351	gi|12667788|r	myosin, heavy polypeptide 9, non-mu	40	132	29.8	4E-04	X	X	X
352	gi|12056468|r	junction plakoglobin [Homo sapiens]	10	31	21.21	2E-04	X	X	X
354	gi|46195723|r	ribosomal L1 domain containing 1 [Ho	13	87	33.67	0.001	X	X	X
355	gi|18104948|r	ribosomal protein L21 [Homo sapiens	3	22	27.5	8E-04	X	X	X
362	gi|4506713|re	ubiquitin and ribosomal protein S27a	2	13	20.51	5E-04	X	X	X
365	gi|4504733|re	insulin receptor substrate 4 [Homo sa	17	52	22.51	2E-04	X	X	X
366	gi|4504431|re	high mobility group AT-hook 2 isoforr	1	4	20.18	2E-04	X	X	X
369	gi|4506901|re	splicing factor, arginine/serine-rich 3	7	63	40.85	0.002	X	X	X
370	gi|40254861|r	ubiquitin associated protein 2-like [Ho	15	72	22.26	4E-04	X	X	X
371	gi|57242798|r	acid sphingomyelinase-like phosphod	5	12	19.56	2E-04	X	X	X
373	gi|21536286|r	brain creatine kinase [Homo sapiens]	7	23	29.66	3E-04	X	X	X
374	gi|57242777|r	c-myc binding protein [Homo sapiens	2	33	35.92	0.002	X	X	X
375	gi|5803111|re	EBNA1 binding protein 2 [Homo sapi	5	11	19.28	2E-04	X	X	X
376	gi|13027644|r	small nuclear ribonucleoprotein polyp	6	42	19.17	1E-03	X	X	X
383	gi|6678271|re	TAR DNA binding protein [Homo sap	11	93	46.86	0.001	X	X	X
384	gi|4506607|re	ribosomal protein L18 [Homo sapiens	6	17	36.7	5E-04	X	X	X
385	gi|11968182|r	ribosomal protein S18 [Homo sapiens	9	20	43.42	7E-04	X	X	X
386	gi|20336746|r	H2A histone family, member Y isoforr	5	18	24.93	3E-04	X	X	X
389	gi|5031863|re	galectin 3 binding protein [Homo sapi	8	40	22.22	4E-04	X	X	X
390	gi|4506003|re	protein phosphatase 1, catalytic subu	12	137	50.91	0.002	X	X	X
391	gi|10835165|r	CD59 antigen p18-20 [Homo sapiens	2	9	18.75	4E-04	X	X	X
395	gi|46367787|r	poly(A) binding protein, cytoplasmic 1	8	33	18.71	3E-04	X	X	X
396	gi|5031877|re	lamin B1 [Homo sapiens]	10	19	22.35	2E-04	X	X	X
397	gi|4506661|re	ribosomal protein L7a [Homo sapiens	10	64	34.59	0.001	X	X	X
398	gi|4502303|re	mitochondrial ATP synthase, O subur	2	4	18.31	1E-04	X	X	X
399	gi|19913428|r	ATPase, H+ transporting, lysosomal 5	5	8	18.2	9E-05	X	X	X
400	gi|88954948|r	PREDICTED: similar to ribosomal pro	8	72	30.72	0.001	X	X	X
404	gi|14141166|r	poly(rC)-binding protein 2 isoform b [	9	45	44.2	7E-04	X	X	X
406	gi|15431290|r	ribosomal protein L11 [Homo sapiens	3	18	23.03	6E-04	X	X	X
407	gi|46430642|r	myosin IC [Homo sapiens]	16	29	24.03	2E-04	X	X	X
408	gi|4506633|re	ribosomal protein L31 [Homo sapiens	4	16	25.6	7E-04	X	X	X
409	gi|4506715|re	ribosomal protein S28 [Homo sapiens	2	27	30.43	0.002	X	X	X
415	gi|66392203|r	NME1-NME2 protein [Homo sapiens]	6	11	30.34	2E-04	X	X	X
416	gi|4507133|re	small nuclear ribonucleoprotein polyp	2	19	26.32	0.001	X	X	X
417	gi|4506635|re	ribosomal protein L32 [Homo sapiens	2	7	17.04	3E-04	X	X	X
423	gi|14110428|r	heterogeneous nuclear ribonucleopro	4	23	16.83	4E-04	X	X	X
425	gi|4506711|re	ribosomal protein S27 [Homo sapiens	2	8	16.67	5E-04	X	X	X
433	gi|4506675|re	ribophorin I precursor [Homo sapiens	6	13	19.11	1E-04	X	X	X
434	gi|15431295|r	ribosomal protein L13 [Homo sapiens	4	27	16.59	7E-04	X	X	X
436	gi|4826659|re	F-actin capping protein beta subunit [	6	16	36.03	3E-04	X	X	X
437	gi|15055539|r	ribosomal protein S2 [Homo sapiens]	8	82	29.69	0.002	X	X	X
438	gi|7657649|re	tropomodulin 3 (ubiquitous) [Homo sa	6	21	35.23	3E-04	X	X	X
439	gi|5453549|re	thioredoxin peroxidase [Homo sapien	4	11	24.72	2E-04	X	X	X
440	gi|5032007|re	purine-rich element binding protein A	4	18	27.02	3E-04	X	X	X
441	gi|14110414|r	heterogeneous nuclear ribonucleopro	10	47	35.62	9E-04	X	X	X
443	gi|41872577|r	raft-linking protein [Homo sapiens]	5	8	15.57	8E-05	X	X	X
444	gi|4506005|re	protein phosphatase 1, catalytic subu	11	117	44.65	0.002	X	X	X
446	gi|4506007|re	protein phosphatase 1, catalytic subu	12	126	48.92	0.002	X	X	X
447	gi|4503545|re	eukaryotic translation initiation factor	4	12	38.96	4E-04	X	X	X
448	gi|46276893|r	elongin B isoform b [Homo sapiens]	1	5	15.53	2E-04	X	X	X
450	gi|4506625|re	ribosomal protein L27a [Homo sapier	4	7	28.38	3E-04	X	X	X

453	gi|4506031|re	palmitoyl-protein thioesterase 1 (cero	3	4	15.36	7E-05	X	X	X	X
454	gi|21464101|r	tyrosine 3-monooxygenase/tryptopha	4	16	29.96	4E-04	X	X	X	X
455	gi|89031528|r	PREDICTED: similar to ribosomal pro	4	30	19.54	7E-04	X	X	X	X
457	gi|11415026|r	ribosomal protein L18a [Homo sapien	3	10	15.34	3E-04	X	X	X	X
462	gi|56118234|r	proline rich 6 [Homo sapiens]	2	4	15.07	8E-05	X	X	X	X
463	gi|38201714|r	ELAV-like 1 [Homo sapiens]	9	58	40.8	0.001	X	X	X	X
464	gi|22208967|r	high mobility group AT-hook 1 isoform	2	16	23.36	9E-04	X	X	X	X
467	gi|4885661|re	viral oncogene yes-1 homolog 1 [Hom	4	7	14.92	7E-05	X	X	X	X
468	gi|19424130|r	CD109 [Homo sapiens]	14	27	14.67	1E-04	X	X	X	X
469	gi|7661806|re	mitochondrial ribosomal protein L15 [	3	5	14.53	1E-04	X	X	X	X
470	gi|4506679|re	ribosomal protein S10 [Homo sapiens	5	75	36.97	0.003	X	X	X	X
471	gi|16117791|r	ribosomal protein L35a [Homo sapien	2	8	14.55	4E-04	X	X	X	X
472	gi|27436904|r	mitochondrial ribosomal protein L23 [	1	3	14.38	1E-04	X	X	X	X
473	gi|4502281|re	Na+/K+ -ATPase beta 3 subunit [Hom	3	4	14.34	8E-05	X	X	X	X
474	gi|4506645|re	ribosomal protein L38 [Homo sapiens	2	10	32.86	8E-04	X	X	X	X
475	gi|19913432|r	ATPase, H+ transporting, lysosomal,	2	3	13.96	5E-05	X	X	X	X
476	gi|51460917|r	PREDICTED: similar to 60S acidic rib	2	19	32.46	9E-04	X	X	X	X
478	gi|5032179|re	tripartite motif-containing 28 protein [	10	17	30.06	1E-04	X	X	X	X
479	gi|31742498|r	unc-84 homolog B [Homo sapiens]	9	20	19.53	2E-04	X	X	X	X
480	gi|4506695|re	ribosomal protein S19 [Homo sapiens	7	36	43.45	0.001	X	X	X	X
481	gi|4504715|re	poly A binding protein, cytoplasmic 4	6	13	13.66	1E-04	X	X	X	X
482	gi|6005942|re	valosin-containing protein [Homo sap	18	56	36.6	4E-04	X	X	X	X
483	gi|48526509|r	translocase of inner mitochondrial me	4	14	13.6	2E-04	X	X	X	X
484	gi|51100974|r	myosin ID [Homo sapiens]	11	22	16.3	1E-04	X	X	X	X
485	gi|5453854|re	poly(rC) binding protein 1 [Homo sap	8	58	42.42	9E-04	X	X	X	X
486	gi|35493811|r	RNA-binding region containing protei	9	62	30	7E-04	X	X	X	X
491	gi|5031741|re	DnaJ subfamily A member 2 [Homo s	7	32	28.16	4E-04	X	X	X	X
492	gi|4557032|re	lactate dehydrogenase B [Homo sapi	5	6	20.06	1E-04	X	X	X	X
493	gi|18105007|r	carbamoylphosphate synthetase 2/as	21	55	18.43	1E-04	X	X	X	X
494	gi|13904866|r	ribosomal protein L28 [Homo sapiens	2	8	13.14	3E-04	X	X	X	X
495	gi|33286418|r	pyruvate kinase 3 isoform 1 [Homo sa	16	46	42.94	5E-04	X	X	X	X
496	gi|21328448|r	tyrosine 3-monooxygenase/tryptopha	5	21	25.61	5E-04	X	X	X	X
498	gi|72534660|r	splicing factor, arginine/serine-rich 7,	5	54	23.11	0.001	X	X	X	X
499	gi|63029937|r	heat shock protein 90kDa alpha (cyto	16	90	25.41	6E-04	X	X	X	X
500	gi|5803227|re	tyrosine 3/tryptophan 5 -monooxygen	5	16	27.35	4E-04	X	X	X	X
501	gi|21735625|r	tyrosine 3/tryptophan 5 -monooxygen	5	26	29.8	6E-04	X	X	X	X
503	gi|15082258|r	chromobox homolog 3 [Homo sapiens	6	40	45.9	0.001	X	X	X	X
506	gi|51479152|r	ATP synthase, H+ transporting, mitoc	1	2	12.41	8E-05	X	X	X	X
508	gi|48762920|r	liver phosphofructokinase isoform b [	5	10	12.31	7E-05	X	X	X	X
510	gi|32189394|r	ATP synthase, H+ transporting, mitoc	6	11	22.31	1E-04	X	X	X	X
511	gi|4503841|re	ATP-dependent DNA helicase II, 70 k	15	75	34.15	7E-04	X	X	X	X
512	gi|40217790|r	zinc finger protein 512 [Homo sapiens	7	19	21.16	2E-04	X	X	X	X
513	gi|17105394|r	ribosomal protein L23a [Homo sapien	4	19	28.85	7E-04	X	X	X	X
516	gi|44889481|r	myosin IB [Homo sapiens]	12	31	17.07	2E-04	X	X	X	X
517	gi|21735621|r	mitochondrial malate dehydrogenase	4	17	19.23	3E-04	X	X	X	X
518	gi|6912292|re	chromobox homolog 5 (HP1 alpha ho	2	29	12.04	9E-04	X	X	X	X
519	gi|7661920|re	DEAD (Asp-Glu-Ala-Asp) box polype	5	21	15.57	3E-04	X	X	X	X
520	gi|25777711|r	S-phase kinase-associated protein 1A	1	4	11.88	1E-04	X	X	X	X
522	gi|4507191|re	spectrin, alpha, non-erythrocytic 1 (al	35	156	21.32	4E-04	X	X	X	X
523	gi|56181387|r	STIP1 homology and U-box containin	3	3	11.55	6E-05	X	X	X	X
524	gi|42476281|r	voltage-dependent anion channel 2 [H	3	6	18.03	1E-04	X	X	X	X
527	gi|27436901|r	mitochondrial ribosomal protein L12 [	2	5	11.62	1E-04	X	X	X	X
528	gi|4502313|re	ATPase, H+ transporting, lysosomal,	1	2	11.61	7E-05	X	X	X	X
530	gi|22202629|r	programmed cell death 8 isoform 2 [H	5	11	13.96	1E-04	X	X	X	X
532	gi|4885281|re	glutamate dehydrogenase 1 [Homo sa	4	11	11.47	1E-04	X	X	X	X
533	gi|13375656|r	UL16 binding protein 3 [Homo sapien	2	2	11.48	5E-05	X	X	X	X
534	gi|16117794|r	ribosomal protein L36 [Homo sapiens	3	5	20	3E-04	X	X	X	X
536	gi|4885371|re	H1 histone family, member 0 [Homo s	3	19	16.49	6E-04	X	X	X	X
537	gi|4507127|re	small nuclear ribonucleoprotein polyp	2	12	18.87	4E-04	X	X	X	X
538	gi|5174559|re	melanoma-associated antigen p97 iso	5	8	11.25	6E-05	X	X	X	X
539	gi|5902078|re	splicing factor, arginine/serine-rich 5 [	1	3	11.21	2E-04	X	X	X	X
540	gi|16753225|r	ribosomal protein L14 [Homo sapiens	4	32	19.91	8E-04	X	X	X	X
541	gi|89036402|r	PREDICTED: similar to ubiquitin C is	3	189	14.85	0.005	X	X	X	X
547	gi|14150124|r	hypothetical protein LOC84298 [Hom	2	11	23.26	5E-04	X	X	X	X
550	gi|4506697|re	ribosomal protein S20 [Homo sapiens	3	32	20.17	0.002	X	X	X	X
551	gi|34577110|r	aldolase A [Homo sapiens]	20	73	74.73	0.001	X	X	X	X
554	gi|12707570|r	mitochondrial short-chain enoyl-coen	4	7	23.79	1E-04	X	X	X	X
555	gi|22547136|r	mitochondrial ribosomal protein L4 is	2	4	10.61	7E-05	X	X	X	X
557	gi|21265084|r	mitochondrial ribosomal protein L1 [H	2	2	10.56	4E-05	X	X	X	X
558	gi|4506631|re	ribosomal protein L30 [Homo sapiens	2	7	24.35	3E-04	X	X	X	X
559	gi|5031635|re	cofilin 1 (non-muscle) [Homo sapiens	4	10	27.11	3E-04	X	X	X	X
560	gi|54112390|r	calcium channel, voltage-dependent,	6	14	10.08	7E-05	X	X	X	X
561	gi|13899231|r	mitochondrial ribosomal protein L9 [H	2	3	10.11	6E-05	X	X	X	X
562	gi|4758410|re	fragile X mental retardation syndrome	6	18	12.93	2E-04	X	X	X	X
563	gi|4503765|re	fragile X mental retardation 1 [Homo s	5	14	12.18	1E-04	X	X	X	X
564	gi|61835148|r	fragile X mental retardation-related pr	6	29	11.43	3E-04	X	X	X	X
567	gi|24308085|r	monooxygenase, DBH-like 1 isoform	3	7	9.91	7E-05	X	X	X	X
569	gi|24308009|r	methionyl aminopeptidase 1 [Homo sa	2	3	9.93	6E-05	X	X	X	X
570	gi|37544743|r	PREDICTED: similar to 60S ribosoma	1	2	9.9	1E-04	X	X	X	X
575	gi|21361181|r	Na+/K+ -ATPase alpha 1 subunit isof	8	13	9.78	7E-05	X	X	X	X
576	gi|8922789|re	paraspeckle protein 1 [Homo sapiens	4	32	17.37	5E-04	X	X	X	X
577	gi|11321601|r	phosphofructokinase, platelet [Homo	6	14	12.37	1E-04	X	X	X	X
578	gi|6005854|re	prohibitin 2 [Homo sapiens]	3	5	16.05	1E-04	X	X	X	X
579	gi|27482992|r	PREDICTED: similar to 60S ribosoma	1	13	9.68	5E-04	X	X	X	X
587	gi|56676330|r	HP1-BP74 [Homo sapiens]	6	44	17.18	5E-04	X	X	X	X
588	gi|24430155|r	proteasome 26S ATPase subunit 4 is	4	7	20.41	1E-04	X	X	X	X
590	gi|66529294|r	paraoxonase 2 isoform 1 [Homo sapi	2	3	9.6	5E-05	X	X	X	X
592	gi|7705855|re	steroid dehydrogenase homolog [Hor	2	4	9.62	7E-05	X	X	X	X
593	gi|38045913|r	non-metastatic cells 1, protein (NM23	3	6	23.16	2E-04	X	X	X	X
595	gi|46249412|r	latent transforming growth factor beta	12	38	15.4	2E-04	X	X	X	X
597	gi|40254924|r	hypothetical protein LOC55379 [Hom	2	3	9.45	6E-05	X	X	X	X
598	gi|28557709|r	phosphoribosyl pyrophosphate synthe	3	9	14.47	2E-04	X	X	X	X
600	gi|24432016|r	pre-mRNA cleavage factor I, 59 kDa s	2	16	9.34	2E-04	X	X	X	X
601	gi|14141193|r	ribosomal protein S9 [Homo sapiens]	4	10	14.43	3E-04	X	X	X	X
602	gi|5453706|re	SPFH domain family, member 1 [Hom	2	3	9.25	5E-05	X	X	X	X
603	gi|59859885|r	ribosomal protein SA [Homo sapiens]	7	59	39.66	0.001	X	X	X	X
605	gi|89036252|r	PREDICTED: similar to 40S ribosoma	6	58	28.47	0.001	X	X	X	X
606	gi|4506609|re	ribosomal protein L19 [Homo sapiens	4	18	18.37	5E-04	X	X	X	X
607	gi|19923142|r	karyopherin beta 1 [Homo sapiens]	8	23	15.64	1E-04	X	X	X	X
608	gi|20149594|r	heat shock 90kDa protein 1, beta [Ho	14	48	24.86	4E-04	X	X	X	X
609	gi|4504183|re	glutathione transferase [Homo sapien	2	4	16.67	1E-04	X	X	X	X
610	gi|42544159|r	heat shock 105kD [Homo sapiens]	6	18	9.79	1E-04	X	X	X	X
611	gi|4503403|re	desmoglein 2 preproprotein [Homo sa	5	7	8.77	4E-05	X	X	X	X
612	gi|16554609|r	mitochondrial ribosomal protein S11 i	2	6	14.43	2E-04	X	X	X	X
613	gi|4503337|re	dyskerin [Homo sapiens]	5	22	12.65	2E-04	X	X	X	X
614	gi|20070160|r	cold shock domain protein A [Homo s	4	17	17.74	3E-04	X	X	X	X
615	gi|54112121|r	splicing factor 3b, subunit 3 [Homo sa	15	82	20.13	4E-04	X	X	X	X
616	gi|16117787|r	ribosomal protein L34 [Homo sapiens	1	2	8.55	1E-04	X	X	X	X
620	gi|54112117|r	splicing factor 3b, subunit 1 isoform 1	30	126	37.35	5E-04	X	X	X	X
621	gi|5031973|re	protein disulfide isomerase-associate	6	15	24.32	2E-04	X	X	X	X
622	gi|32454741|r	serine (or cysteine) proteinase inhibit	5	6	19.14	8E-05	X	X	X	X
623	gi|38149981|r	small nuclear ribonucleoprotein polyp	5	27	28	7E-04	X	X	X	X
625	gi|18104971|r	protein tyrosine phosphatase type IVA	1	4	8.38	1E-04	X	X	X	X
643	gi|4506619|re	ribosomal protein L24 [Homo sapiens	2	13	14.01	5E-04	X	X	X	X
644	gi|68509926|r	DEAH (Asp-Glu-Ala-His) box polypep	8	20	15.22	1E-04	X	X	X	X
645	gi|32483374|r	nucleolar protein 5A [Homo sapiens]	10	47	22.05	5E-04	X	X	X	X
646	gi|6005926|re	U2 (RNU2) small nuclear RNA auxilia	9	52	38.95	6E-04	X	X	X	X
648	gi|4507677|re	tumor rejection antigen (gp96) 1 [Hon	12	43	19.68	3E-04	X	X	X	X
649	gi|11321581|r	succinate-CoA ligase, GDP-forming, a	2	10	8.11	2E-04	X	X	X	X
650	gi|4506623|re	ribosomal protein L27 [Homo sapiens	2	6	14.71	3E-04	X	X	X	X
651	gi|5032013|re	kinesin family member 20A [Homo sa	3	4	7.87	3E-05	X	X	X	X
652	gi|19913424|r	ATPase, H+ transporting, lysosomal 7	3	6	7.94	6E-05	X	X	X	X
653	gi|4758958|re	cAMP-dependent protein kinase, regu	2	4	7.92	6E-05	X	X	X	X
654	gi|56118310|r	nuclear ubiquitous casein kinase and	2	3	8.23	7E-05	X	X	X	X
655	gi|7705437|re	60S ribosome subunit biogenesis pro	1	2	7.78	6E-05	X	X	X	X
656	gi|62865879|r	Bcl-2 inhibitor of transcription isoform	1	2	7.78	6E-05	X	X	X	X
658	gi|7661606|re	nucleolar complex associated 2 homo	5	8	14.42	6E-05	X	X	X	X
659	gi|24234747|r	interleukin enhancer binding factor 2	8	71	32.82	0.001	X	X	X	X
660	gi|34740329|r	heterogeneous nuclear ribonucleopro	8	31	27.25	5E-04	X	X	X	X
661	gi|4885079|re	ATP synthase, H+ transporting, mitoc	2	3	7.74	6E-05	X	X	X	X
663	gi|27597059|r	DnaJ homolog, subfamily C, member	1	2	7.69	4E-05	X	X	X	X
664	gi|19920317|r	cytoskeleton-associated protein 4 [Ho	3	5	7.64	5E-05	X	X	X	X
665	gi|5174447|re	guanine nucleotide binding protein (G	16	214	77.6	0.004	X	X	X	X
666	gi|88953190|r	PREDICTED: similar to ribosomal pro	2	13	18.94	6E-04	X	X	X	X
668	gi|50582540|r	myosin VI [Homo sapiens]	6	11	7.47	5E-05	X	X	X	X
669	gi|5454064|re	RNA binding motif protein 14 [Homo s	12	26	31.39	2E-04	X	X	X	X
670	gi|4505775|re	solute carrier family 25 member 3 iso	1	13	7.48	2E-04	X	X	X	X
672	gi|5803207|re	U2 small nuclear RNA auxillary factor	3	23	17.08	5E-04	X	X	X	X
673	gi|8923579|re	hypothetical protein LOC55004 [Hom	1	3	7.45	1E-04	X	X	X	X
674	gi|38202257|r	alpha glucosidase II alpha subunit iso	6	19	8.37	1E-04	X	X	X	X
676	gi|35493916|r	ribophorin II precursor [Homo sapiens	3	7	7.45	6E-05	X	X	X	X
677	gi|4503521|re	murine mammary tumor integration s	2	6	7.42	8E-05	X	X	X	X
678	gi|4885063|re	fructose-bisphosphate aldolase C [Ho	4	16	18.41	3E-04	X	X	X	X
679	gi|56711248|r	hypothetical protein LOC23167 [Hom	3	4	7.26	3E-05	X	X	X	X
680	gi|5453539|re	phosphoribosylaminoimidazole carbo	4	6	18.35	8E-05	X	X	X	X
681	gi|8922498|re	pyridoxine 5'-phosphate oxidase [Hor	2	2	15.33	4E-05	X	X	X	X
682	gi|22547114|r	mitochondrial ribosomal protein L10 i	1	4	7.28	9E-05	X	X	X	X
684	gi|42657272|r	PREDICTED: similar to 40S ribosoma	3	7	23.39	3E-04	X	X	X	X
687	gi|4506903|re	splicing factor, arginine/serine-rich 9 [	2	3	12.67	8E-05	X	X	X	X
688	gi|5453634|re	dynein, cytoplasmic, light intermediat	4	9	17.48	1E-04	X	X	X	X
689	gi|38327552|r	Ras-GTPase-activating protein SH3-c	10	23	36.48	3E-04	X	X	X	X
691	gi|25188179|r	voltage-dependent anion channel 3 [	1	3	7.07	6E-05	X	X	X	X
692	gi|10863945|r	ATP-dependent DNA helicase II [Hon	12	41	25.68	3E-04	X	X	X	X
693	gi|20070197|r	dolichyl-diphosphooligosaccharide-pr	2	2	7.02	2E-05	X	X	X	X
694	gi|20127499|r	arginine/serine-rich splicing factor 6 [	2	5	6.98	8E-05	X	X	X	X
695	gi|27764863|r	solute carrier family 25, member A6 [	4	10	11.07	2E-04	X	X	X	X
697	gi|41872631|r	fatty acid synthase [Homo sapiens]	13	28	9.04	6E-05	X	X	X	X
698	gi|27436946|r	lamin A/C isoform 1 precursor [Homo	24	64	40.96	5E-04	X	X	X	X
699	gi|14028877|r	mitochondrial ribosomal protein S25 [	2	4	18.5	1E-04	X	X	X	X
700	gi|76150623|r	nucleolar protein 1, 120kDa [Homo sa	4	7	8.66	5E-05	X	X	X	X
702	gi|11136628|r	eukaryotic translation elongation facto	7	27	45.78	7E-04	X	X	X	X
704	gi|6453818|re	kinesin family member 22 [Homo sap	3	5	6.62	4E-05	X	X	X	X
705	gi|15431306|r	ribosomal protein L8 [Homo sapiens]	4	28	22.96	6E-04	X	X	X	X
707	gi|5729838|re	glioma-amplified sequence-41 [Homo	15	178	61.67	0.004	X	X	X	X
708	gi|21536320|r	E1B-55kDa-associated protein 5 isofo	9	28	21.16	2E-04	X	X	X	X
711	gi|10801345|r	eukaryotic translation initiation factor	1	2	6.42	5E-05	X	X	X	X
712	gi|17105400|r	phosphatidylinositol 4-kinase, catalyti	7	13	6.26	4E-05	X	X	X	X
713	gi|27477134|r	nucleoporin 210 [Homo sapiens]	7	9	6.2	3E-05	X	X	X	X
714	gi|4502317|re	ATPase, H+ transporting, lysosomal 3	1	2	6.19	5E-05	X	X	X	X
715	gi|4506741|re	ribosomal protein S7 [Homo sapiens]	2	27	17.53	8E-04	X	X	X	X
716	gi|5032093|re	solute carrier family 1 (neutral amino	2	4	6.1	4E-05	X	X	X	X
717	gi|50811883|r	decreased expression in renal and pr	2	2	6.11	2E-05	X	X	X	X
719	gi|4503607|re	electron transfer flavoprotein, alpha p	2	3	12.91	5E-05	X	X	X	X
720	gi|4758950|re	peptidylprolyl isomerase B precursor	2	2	12.04	5E-05	X	X	X	X
721	gi|5031931|re	nascent-polypeptide-associated comp	2	7	13.02	2E-04	X	X	X	X
722	gi|15011916|r	nucleolar protein family A, member 1	2	2	14.29	5E-05	X	X	X	X
724	gi|21614525|r	glypican 4 [Homo sapiens]	2	5	5.94	5E-05	X	X	X	X
725	gi|20070125|r	prolyl 4-hydroxylase, beta subunit [Ho	4	12	13.98	1E-04	X	X	X	X
726	gi|6005721|re	SPFH domain family, member 2 isofo	1	3	5.9	5E-05	X	X	X	X
727	gi|19913418|r	ATPase, H+ transporting, lysosomal V	3	8	5.78	5E-05	X	X	X	X
728	gi|5454158|re	valyl-tRNA synthetase [Homo sapiens	4	12	6.96	5E-05	X	X	X	X
729	gi|21327701|r	TBP-associated factor 15 isoform 1 [H	5	23	14.7	2E-04	X	X	X	X
731	gi|22095347|r	immunoglobulin superfamily, member	1	2	5.66	3E-05	X	X	X	X
732	gi|11125772|r	myristoylated alanine-rich protein kina	1	4	5.72	7E-05	X	X	X	X
733	gi|15431303|r	ribosomal protein L9 [Homo sapiens]	1	2	5.73	6E-05	X	X	X	X
737	gi|31543164|r	WD repeat domain 58 [Homo sapiens	4	15	21.99	3E-04	X	X	X	X
738	gi|7705373|re	epithelial protein lost in neoplasm bet	4	9	6.98	7E-05	X	X	X	X
739	gi|38044290|r	zinc finger, CCHC domain containing	2	2	5.52	2E-05	X	X	X	X
740	gi|18426915|r	drebrin 1 isoform a [Homo sapiens]	8	10	22.8	9E-05	X	X	X	X
741	gi|31881687|r	replication factor C 4 [Homo sapiens]	4	11	20.11	2E-04	X	X	X	X
743	gi|4505753|re	phosphoglycerate mutase 1 (brain) [H	3	4	10.24	9E-05	X	X	X	X
750	gi|63003897|r	transcription factor NRF [Homo sapie	2	3	5.36	2E-05	X	X	X	X
751	gi|27734917|r	hypothetical protein LOC196463 [Hor	2	2	5.43	2E-05	X	X	X	X
752	gi|22035692|r	GDNF family receptor alpha 1 isoform	2	2	5.43	2E-05	X	X	X	X
753	gi|29731731|r	PREDICTED: similar to eukaryotic tra	2	21	9.42	3E-04	X	X	X	X
760	gi|22538431|r	cathepsin B preproprotein [Homo sap	2	6	9.44	1E-04	X	X	X	X
765	gi|HsSRCAP	current presumptive full-length huma	87	961	37	0.002	X	X	X	X
766	gi|15149476|r	arginyl-tRNA synthetase [Homo sapie	2	3	5.15	3E-05	X	X	X	X
767	gi|45505163|r	LISCH protein isoform 1 [Homo sapie	2	2	5.24	2E-05	X	X	X	X
770	gi|14719402|r	homolog of yeast ribosome biogenes	2	2	7.4	3E-05	X	X	X	X
771	gi|70166852|r	adenosine deaminase, RNA-specific	6	11	8.24	5E-05	X	X	X	X
775	gi|56237027|r	insulin-like growth factor 2 mRNA bin	5	8	13.17	8E-05	X	X	X	X
776	gi|16905526|r	death-associated protein 3 [Homo sa	3	17	11.56	2E-04	X	X	X	X
778	gi|5174429|re	acetyl-coenzyme A acyltransferase 2	1	2	5.04	3E-05	X	X	X	X
779	gi|8922388|re	RNA binding motif protein 28 [Homo s	2	4	4.87	3E-05	X	X	X	X
780	gi|21361282|r	splicing factor, arginine/serine-rich 4 [	4	11	9.72	1E-04	X	X	X	X
781	gi|38016127|r	RNA binding motif protein 34 [Homo s	2	6	9.18	8E-05	X	X	X	X
782	gi|20149592|r	serine/threonine kinase receptor asso	1	2	4.86	3E-05	X	X	X	X
783	gi|14141157|r	heterogeneous nuclear ribonucleopro	2	7	12.43	1E-04	X	X	X	X
785	gi|4759098|re	splicing factor, arginine/serine-rich 10	3	11	17.71	2E-04	X	X	X	X
786	gi|4758788|re	NADH dehydrogenase (ubiquinone) F	2	2	10.61	4E-05	X	X	X	X
787	gi|9506689|re	exosome component 4 [Homo sapien	1	5	4.9	1E-04	X	X	X	X
788	gi|13124875|r	smooth muscle myosin heavy chain 1	7	24	5.83	7E-05	X	X	X	X
790	gi|4557761|re	mutS homolog 2 [Homo sapiens]	5	32	8.57	2E-04	X	X	X	X
791	gi|7657381|re	PRP19/PSO4 pre-mRNA processing	11	66	42.46	7E-04	X	X	X	X
792	gi|5031573|re	ARP3 actin-related protein 3 homolog	3	12	20.81	2E-04	X	X	X	X
793	gi|19923521|r	cytoskeleton associated protein 2 [Ho	2	4	4.69	3E-05	X	X	X	X
794	gi|61744475|r	solute carrier family 3 (activators of d	2	4	4.69	3E-05	X	X	X	X
800	gi|33350932|r	dynein, cytoplasmic, heavy polypepti	37	124	13.67	2E-04	X	X	X	X
801	gi|31621305|r	leucine-rich PPR motif-containing pro	5	9	5.38	4E-05	X	X	X	X
802	gi|13435359|r	damage-specific DNA binding protein	5	11	8.42	5E-05	X	X	X	X
805	gi|10716563|r	calnexin precursor [Homo sapiens]	3	5	7.26	5E-05	X	X	X	X
807	gi|19923748|r	dihydrolipoamide S-succinyltransferas	2	6	7.51	8E-05	X	X	X	X
808	gi|38195084|r	HMT1 hnRNP methyltransferase-like	3	7	12.39	1E-04	X	X	X	X
811	gi|5902060|re	XRP2 protein [Homo sapiens]	1	2	4.57	3E-05	X	X	X	X
812	gi|41152056|r	U5 snRNP-specific protein, 116 kD [H	40	265	57.3	0.002	X	X	X	X
813	gi|13899354|r	RNA binding motif protein 4B [Homo	1	2	4.46	3E-05	X	X	X	X
818	gi|29826335|r	eukaryotic translation initiation factor	1	3	4.5	5E-05	X	X	X	X
819	gi|5031857|re	lactate dehydrogenase A [Homo sapi	8	16	31.63	3E-04	X	X	X	X
820	gi|32455264|r	peroxiredoxin 1 [Homo sapiens]	8	17	40.2	5E-04	X	X	X	X
823	gi|45643123|r	nuclear VCP-like isoform 1 [Homo sa	3	12	6.43	8E-05	X	X	X	X
825	gi|5453994|re	RAD21 homolog [Homo sapiens]	6	14	13.95	1E-04	X	X	X	X
826	gi|45593130|r	guanine nucleotide binding protein-lik	2	6	8.74	6E-05	X	X	X	X
829	gi|5174715|re	transcription factor-like 1 [Homo sapi	13	191	45.05	0.003	X	X	X	X
830	gi|49472822|r	eukaryotic translation initiation factor	2	3	12.19	5E-05	X	X	X	X
831	gi|62241042|r	glutamyl-prolyl tRNA synthetase [Hor	6	10	6.48	4E-05	X	X	X	X
832	gi|6631095|re	minichromosome maintenance protei	3	4	5.45	3E-05	X	X	X	X
833	gi|4503971|re	GDP dissociation inhibitor 1 [Homo sa	1	8	4.25	1E-04	X	X	X	X
835	gi|21361144|r	proteasome 26S ATPase subunit 3 [H	1	2	4.33	3E-05	X	X	X	X
836	gi|5031569|re	ARP1 actin-related protein 1 homolog	2	7	7.18	1E-04	X	X	X	X
837	gi|17511255|r	poly(A) binding protein interacting pro	1	2	4.18	2E-05	X	X	X	X
842	gi|14249678|r	RNA binding motif protein 17 [Homo s	4	13	14.21	2E-04	X	X	X	X
843	gi|55956919|r	heterogeneous nuclear ribonucleopro	8	44	23.8	8E-04	X	X	X	X
845	gi|24638454|r	ATPase, Ca++ transporting, cardiac m	3	5	4.13	3E-05	X	X	X	X
847	gi|17017991|r	FtsJ homolog 3 [Homo sapiens]	6	19	14.76	1E-04	X	X	X	X
848	gi|21361454|r	pyrroline-5-carboxylate reductase fan	2	2	9.69	4E-05	X	X	X	X
849	gi|21361875|r	hypothetical protein LOC84946 [Hom	1	2	4	2E-05	X	X	X	X
850	gi|5031631|re	scavenger receptor class B, member	1	3	3.97	4E-05	X	X	X	X
851	gi|14861834|r	cat eye syndrome chromosome regio	1	4	4.02	5E-05	X	X	X	X
853	gi|5032069|re	splicing factor 3b, subunit 4 [Homo sa	3	22	14.15	3E-04	X	X	X	X
854	gi|4507659|re	translocated promoter region (to activ	11	41	8.51	1E-04	X	X	X	X
855	gi|40217847|r	activating signal cointegrator 1 compl	57	254	39.42	7E-04	X	X	X	X
856	gi|4503529|re	eukaryotic translation initiation factor	12	32	47.04	4E-04	X	X	X	X
857	gi|4503531|re	eukaryotic translation initiation factor	7	19	21.13	3E-04	X	X	X	X
858	gi|14211540|r	Mov10, Moloney leukemia virus 10, h	4	6	7.08	3E-05	X	X	X	X
859	gi|38327039|r	heat shock 70kDa protein 4 isoform a	3	6	4.76	4E-05	X	X	X	X
860	gi|42544123|r	splicing factor 1 isoform 3 [Homo sap	6	21	18.07	2E-04	X	X	X	X
863	gi|7669501|re	lysosomal-associated membrane pro	1	2	3.85	3E-05	X	X	X	X
864	gi|58761500|r	GTP-binding protein PTD004 isoform	1	5	3.79	7E-05	X	X	X	X
865	gi|4507555|re	thymopoietin isoform alpha [Homo sa	17	74	41.64	6E-04	X	X	X	X
866	gi|73760405|r	thymopoietin isoform beta [Homo sap	9	52	29.96	7E-04	X	X	X	X
867	gi|4505895|re	pleiotropic regulator 1 (PRL1 homolo	6	16	20.62	2E-04	X	X	X	X
868	gi|66933016|r	inosine monophosphate dehydrogena	6	10	16.15	1E-04	X	X	X	X
869	gi|19923485|r	cisplatin resistance-associated overe	3	8	11.11	1E-04	X	X	X	X
871	gi|21361376|r	splicing factor 3a, subunit 2 [Homo sa	1	6	3.66	7E-05	X	X	X	X
872	gi|31377603|r	HIV-1 rev binding protein 2 [Homo sa	4	15	15.22	2E-04	X	X	X	X
873	gi|25777615|r	proteasome 26S non-ATPase subuni	2	3	6.48	5E-05	X	X	X	X
874	gi|4504555|re	isoleucine-tRNA synthetase [Homo sa	3	5	3.57	2E-05	X	X	X	X
876	gi|25777602|r	proteasome 26S non-ATPase subuni	6	18	10.9	1E-04	X	X	X	X
877	gi|21264355|r	SWI/SNF-related matrix-associated a	3	6	11.19	8E-05	X	X	X	X
878	gi|31541941|r	heat shock 70kDa protein 4-like [Hom	2	6	3.46	4E-05	X	X	X	X
879	gi|4557641|re	histone deacetylase 2 [Homo sapiens	7	21	23.16	2E-04	X	X	X	X
880	gi|5453599|re	capping protein (actin filament) musc	3	9	16.43	2E-04	X	X	X	X
881	gi|47174861|r	peter pan homolog [Homo sapiens]	2	6	11.21	7E-05	X	X	X	X
882	gi|5453629|re	dynactin 2 [Homo sapiens]	2	12	8.13	2E-04	X	X	X	X
883	gi|17999537|r	U5 snRNP-specific protein [Homo sa	43	178	27.75	4E-04	X	X	X	X
884	gi|4507457|re	transferrin receptor [Homo sapiens]	5	6	8.55	4E-05	X	X	X	X
885	gi|55769546|r	PAK1 interacting protein 1 [Homo sap	1	2	3.32	3E-05	X	X	X	X
886	gi|23238211|r	actin related protein 2/3 complex sub	2	2	13	4E-05	X	X	X	X
888	gi|23510338|r	ubiquitin-activating enzyme E1 [Hom	4	8	7.37	4E-05	X	X	X	X
890	gi|19923272|r	xenotropic and polytropic retrovirus re	1	2	3.16	2E-05	X	X	X	X
891	gi|26667180|r	calcium/calmodulin-dependent protei	1	2	3.21	2E-05	X	X	X	X
895	gi|7657351|re	MYB binding protein 1a [Homo sapien	36	236	39.31	0.001	X	X	X	X
896	gi|4758304|re	protein disulfide isomerase-associate	3	3	8.53	3E-05	X	X	X	X
897	gi|4885399|re	chondroitin sulfate proteoglycan 6 (ba	11	27	12.9	1E-04	X	X	X	X
898	gi|24432106|r	p30 DBC protein [Homo sapiens]	7	22	12.78	1E-04	X	X	X	X
900	gi|21361361|r	ilvB (bacterial acetolactate synthase)-	4	7	11.71	6E-05	X	X	X	X
901	gi|18201905|r	glucose phosphate isomerase [Homo	4	10	10.39	1E-04	X	X	X	X
902	gi|17298690|r	fuse-binding protein-interacting repres	5	18	19.74	2E-04	X	X	X	X
904	gi|23308577|r	phosphoglycerate dehydrogenase [He	3	5	10.69	5E-05	X	X	X	X

905	gi|20806097|r	nucleolar complex associated 3 homo	2	7	4.88	5E-05	X	X	X	X	X	X	X	X	X	800	92548	9.2	N
906	gi|40254978|r	FIP1-like 1 [Homo sapiens]	4	11	13.8	1E-04	X	X	X	X	X	X	X	X	X	594	66526	5.6	N
907	gi|25777730|r	aldehyde dehydrogenase 1B1 precur	1	3	2.9	3E-05	X	X	X	X	X	X	X	X	X	517	57249	7	N
908	gi|5454096|re	serine/threonine kinase 4 [Homo sapi	2	3	5.54	4E-05	X	X	X	X	X	X	X	X	X	487	55630	5.1	N
909	gi|4759100|re	splicing factor p54 [Homo sapiens]	3	13	10.74	2E-04	X	X	X	X	X	X	X	X	X	484	53542	10.5	N
910	gi|4504897|re	karyopherin alpha 2 [Homo sapiens]	9	53	34.97	6E-04	X	X	X	X	X	X	X	X	X	529	57862	5.4	N
913	gi|71979932|r	solute carrier family 7 (cationic amino	1	2	2.76	2E-05	X	X	X	X	X	X	X	X	X	507	55010	7.7	N
914	gi|4506439|re	retinoblastoma binding protein 7 [Hor	12	43	54.82	6E-04	X	X	X	X	X	X	X	X	X	425	47820	5	N
915	gi|54112392|r	calcium channel, voltage-dependent,	2	3	2.71	1E-05	X	X	X	X	X	X	X	X	X	1145	129269	5.7	N
917	gi|22027516|r	serine carboxypeptidase vitellogenic-	2	9	6.3	1E-04	X	X	X	X	X	X	X	X	X	476	54192	5.6	N
919	gi|24497603|r	nucleoporin 62kDa [Homo sapiens]	1	3	2.68	3E-05	X	X	X	X	X	X	X	X	X	522	53255	5.3	N
923	gi|31543831|r	tubulin, gamma 1 [Homo sapiens]	4	7	20.18	9E-05	X	X	X	X	X	X	X	X	X	451	51170	6.1	N
924	gi|33620775|r	kinectin 1 [Homo sapiens]	2	3	2.58	1E-05	X	X	X	X	X	X	X	X	X	1357	156275	5.6	N
925	gi|4503131|re	catenin (cadherin-associated protein)	2	3	2.56	2E-05	X	X	X	X	X	X	X	X	X	781	85497	5.9	N
933	gi|40217805|r	hypothetical protein LOC79707 [Hom	5	11	14.81	9E-05	X	X	X	X	X	X	X	X	X	702	79277	9.2	N
934	gi|5803167|re	splicing factor 3a, subunit 3 [Homo sa	8	30	26.95	3E-04	X	X	X	X	X	X	X	X	X	501	58849	5.4	N
935	gi|4758786|re	NADH dehydrogenase (ubiquinone) F	1	3	2.59	4E-05	X	X	X	X	X	X	X	X	X	463	52546	7.6	N
936	gi|55741641|r	kinase D-interacting substance of 220	2	4	2.48	1E-05	X	X	X	X	X	X	X	X	X	1771	196541	6.6	N
937	gi|32490572|r	erythrocyte membrane protein band 4	2	3	2.48	2E-05	X	X	X	X	X	X	X	X	X	1087	120677	5.2	N
938	gi|61676188|r	HECT, UBA and WWE domain conta	5	8	2.4	1E-05	X	X	X	X	X	X	X	X	X	4374	481896	5.2	N
939	gi|51493127|r	PREDICTED: YLP motif containing 1	5	21	4.49	6E-05	X	X	X	X	X	X	X	X	X	2140	240735	6.6	N
951	gi|5453660|re	spindle pole body protein [Homo sapi	1	7	2.43	4E-05	X	X	X	X	X	X	X	X	X	907	103571	8.1	N
952	gi|33356547|r	minichromosome maintenance protei	1	4	2.43	3E-05	X	X	X	X	X	X	X	X	X	904	101896	5.5	N
953	gi|45439306|r	aspartyl-tRNA synthetase [Homo sap	1	2	2.4	2E-05	X	X	X	X	X	X	X	X	X	501	57136	6.5	N
954	gi|28373117|r	contactin 1 isoform 1 precursor [Hom	1	2	2.26	1E-05	X	X	X	X	X	X	X	X	X	1018	113320	5.9	N
956	gi|4758024|re	coilin [Homo sapiens]	2	4	5.21	4E-05	X	X	X	X	X	X	X	X	X	576	62608	9.1	N
957	gi|4507947|re	tyrosyl-tRNA synthetase [Homo sapie	2	3	5.68	3E-05	X	X	X	X	X	X	X	X	X	528	59144	7	N
958	gi|4506787|re	IQ motif containing GTPase activating	2	3	2.17	1E-05	X	X	X	X	X	X	X	X	X	1657	189251	6.5	N
959	gi|7706501|re	WW domain binding protein 11 [Hom	2	4	4.52	4E-05	X	X	X	X	X	X	X	X	X	641	69998	8.4	N
960	gi|50658082|r	centrosomal protein 70 kDa [Homo sa	1	2	2.18	2E-05	X	X	X	X	X	X	X	X	X	597	69752	5.7	N
961	gi|30795212|r	insulin-like growth factor 2 mRNA bin	2	3	5.7	3E-05	X	X	X	X	X	X	X	X	X	579	63705	8.9	N
962	gi|4557525|re	dihydrolipoamide dehydrogenase pre	1	2	2.16	2E-05	X	X	X	X	X	X	X	X	X	509	54150	7.7	N
963	gi|51873036|r	oxoglutarate (alpha-ketoglutarate) de	2	2	3.81	1E-05	X	X	X	X	X	X	X	X	X	1023	115935	6.9	N
964	gi|42741679|r	ATPase, H+ transporting, lysosomal V	1	2	2.1	1E-05	X	X	X	X	X	X	X	X	X	856	98082	6.6	N
965	gi|19743813|r	integrin beta 1 isoform 1A precursor [	1	2	2.13	1E-05	X	X	X	X	X	X	X	X	X	798	88415	5.4	N
971	gi|13376259|r	nucleoporin 85 [Homo sapiens]	1	2	2.13	2E-05	X	X	X	X	X	X	X	X	X	656	75019	5.6	N
972	gi|4505055|re	v-yes-1 Yamaguchi sarcoma viral rela	1	2	2.15	2E-05	X	X	X	X	X	X	X	X	X	512	58574	7.1	N
973	gi|9910242|re	hypothetical protein LOC57003 [Hom	2	2	5.8	2E-05	X	X	X	X	X	X	X	X	X	483	55816	4.9	N
974	gi|54859722|r	nucleoporin 160kDa [Homo sapiens]	2	2	2.02	8E-06	X	X	X	X	X	X	X	X	X	1436	162121	5.5	N
975	gi|58761546|r	amine oxidase (flavin containing) don	5	14	8.57	9E-05	X	X	X	X	X	X	X	X	X	852	92903	6.5	N
976	gi|11067747|r	CDC5-like [Homo sapiens]	18	60	33.79	4E-04	X	X	X	X	X	X	X	X	X	802	92251	8.2	N
977	gi|29826319|r	adducin 1 (alpha) isoform a [Homo sa	2	3	4.34	2E-05	X	X	X	X	X	X	X	X	X	737	80955	5.8	N
981	gi|7662128|re	zinc finger and BTB domain containin	2	4	4.59	3E-05	X	X	X	X	X	X	X	X	X	697	78292	7.6	N
982	gi|4504957|re	lysosomal-associated membrane prot	1	2	1.95	3E-05	X	X	X	X	X	X	X	X	X	410	44961	5.6	N
984	gi|33946327|r	nucleoporin 214kDa [Homo sapiens]	4	11	4.26	3E-05	X	X	X	X	X	X	X	X	X	2090	213618	7.5	N
985	gi|31377595|r	conserved nuclear protein NHN1 [Ho	6	18	11.54	1E-04	X	X	X	X	X	X	X	X	X	953	106359	8.2	N
986	gi|28372493|r	cullin 4B [Homo sapiens]	1	2	1.86	1E-05	X	X	X	X	X	X	X	X	X	913	103982	7.4	N
987	gi|11559929|r	coatomer protein complex, subunit ga	5	7	11.1	5E-05	X	X	X	X	X	X	X	X	X	874	97718	5.5	N
988	gi|7427519|re	minichromosome maintenance protei	3	4	5.97	3E-05	X	X	X	X	X	X	X	X	X	821	92889	5.4	N
989	gi|38683855|r	hypothetical protein LOC55037 [Hom	3	5	5.37	4E-05	X	X	X	X	X	X	X	X	X	689	78550	6.4	N
990	gi|4506411|re	Ran GTPase activating protein 1 [Ho	5	8	16.7	8E-05	X	X	X	X	X	X	X	X	X	587	63542	4.7	N
991	gi|4504327|re	hydroxyacyl dehydrogenase, subunit	1	2	1.9	2E-05	X	X	X	X	X	X	X	X	X	474	51294	9.4	N
992	gi|38490531|r	splicing factor, arginine/serine-rich 14	4	6	11	3E-05	X	X	X	X	X	X	X	X	X	1082	120237	7.3	N
994	gi|18497286|r	DEAH (Asp-Glu-Ala-His) box polypep	1	2	1.79	1E-05	X	X	X	X	X	X	X	X	X	1008	114776	7.7	N
995	gi|14043022|r	methionine-tRNA synthetase [Homo s	1	2	1.78	1E-05	X	X	X	X	X	X	X	X	X	900	101116	6.2	N
996	gi|24234750|r	interleukin enhancer binding factor 3	13	28	28.64	2E-04	X	X	X	X	X	X	X	X	X	894	95339	8.8	N
997	gi|33356174|r	pinin, desmosome associated protein	2	7	4.18	6E-05	X	X	X	X	X	X	X	X	X	717	81614	7.2	N
998	gi|7706485|re	TNF receptor-associated protein 1 [H	2	2	5.97	2E-05	X	X	X	X	X	X	X	X	X	704	80011	8	N
999	gi|33563340|r	myosin, heavy polypeptide 14 [Homo	4	5	2.71	1E-05	X	X	X	X	X	X	X	X	X	1995	228000	5.9	N
1000	gi|47933339|r	RNA binding motif protein 15 [Homo s	3	7	5.22	4E-05	X	X	X	X	X	X	X	X	X	977	107188	10.1	N
1001	gi|25777600|r	proteasome 26S non-ATPase subuni	3	5	7.76	3E-05	X	X	X	X	X	X	X	X	X	953	105836	5.4	N
1002	gi|55749531|r	splicing factor 3B subunit 2 [Homo sa	10	30	14.19	2E-04	X	X	X	X	X	X	X	X	X	895	100228	5.7	N
1003	gi|4503165|re	cullin 3 [Homo sapiens]	1	3	1.69	2E-05	X	X	X	X	X	X	X	X	X	768	88930	8.5	N
1004	gi|71361682|r	nuclear mitotic apparatus protein 1 [H	22	84	17.4	2E-04	X	X	X	X	X	X	X	X	X	2115	238257	5.8	N
1005	gi|18375673|r	regulator of nonsense transcripts 1 [H	1	2	1.61	1E-05	X	X	X	X	X	X	X	X	X	1118	123036	6.7	N
1006	gi|14670350|r	general transcription factor II, i isofor	16	47	25.45	3E-04	X	X	X	X	X	X	X	X	X	998	112416	6.4	N
1010	gi|18860916|r	5'-3' exoribonuclease 2 [Homo sapier	5	8	7.37	5E-05	X	X	X	X	X	X	X	X	X	950	108583	7.5	N
1011	gi|21264343|r	scaffold attachment factor B [Homo s	3	5	5.9	3E-05	X	X	X	X	X	X	X	X	X	915	102642	5.5	N
1014	gi|89047143|r	PREDICTED: myosin VB isoform 1 [H	2	2	1.52	6E-06	X	X	X	X	X	X	X	X	X	1848	213671	7.2	N
1016	gi|89040264|r	PREDICTED: zinc finger protein 629	1	2	1.5	1E-05	X	X	X	X	X	X	X	X	X	869	96620	7.9	N
1018	gi|10834990|r	neural cell adhesion molecule 1 isofo	1	2	1.53	1E-05	X	X	X	X	X	X	X	X	X	848	93361	4.9	N
1020	gi|21040314|r	SON DNA-binding protein isoform B [	2	3	1.43	7E-06	X	X	X	X	X	X	X	X	X	2303	250386	5.6	N
1026	gi|32698750|r	serine arginine-rich pre-mRNA splicin	3	12	5.26	5E-05	X	X	X	X	X	X	X	X	X	1312	139265	9.2	N
1027	gi|26051235|r	nucleoporin 133kDa [Homo sapiens]	1	2	1.38	1E-05	X	X	X	X	X	X	X	X	X	1156	128979	5.1	N
1028	gi|7662310|re	FERM, RhoGEF and pleckstrin doma	1	2	1.42	1E-05	X	X	X	X	X	X	X	X	X	1054	119888	8.8	N
1029	gi|55770844|r	catenin, alpha 1 [Homo sapiens]	1	2	1.43	1E-05	X	X	X	X	X	X	X	X	X	906	100071	6.3	N
1031	gi|55769587|r	hypothetical protein LOC8602 [Homo	1	4	1.4	3E-05	X	X	X	X	X	X	X	X	X	857	97668	7.6	N
1032	gi|54607053|r	GCN1 general control of amino-acid s	21	86	12.13	2E-04	X	X	X	X	X	X	X	X	X	2671	292708	7.4	N
1033	gi|4503747|re	filamin B, beta (actin binding protein 2	16	42	10.3	9E-05	X	X	X	X	X	X	X	X	X	2602	278193	5.7	N
1034	gi|4503509|re	eukaryotic translation initiation factor	9	19	8.83	8E-05	X	X	X	X	X	X	X	X	X	1382	166569	6.8	N
1035	gi|56676371|r	cleavage and polyadenylation specifi	8	12	9.56	5E-05	X	X	X	X	X	X	X	X	X	1443	160883	6.4	N
1036	gi|15559211|r	RE1-silencing transcription factor [Ho	1	2	1.28	1E-05	X	X	X	X	X	X	X	X	X	1097	121888	6.7	N
1037	gi|39725634|r	la related protein isoform 1 [Homo sa	2	2	3.14	1E-05	X	X	X	X	X	X	X	X	X	1019	116465	9.1	N
1039	gi|42542379|r	serine/arginine repetitive matrix 1 [Ho	1	9	1.33	6E-05	X	X	X	X	X	X	X	X	X	904	102335	11.8	N
1040	gi|7661686|re	polymerase (RNA) I polypeptide A, 19	12	35	13.74	1E-04	X	X	X	X	X	X	X	X	X	1717	194190	7.2	N
1041	gi|31543299|r	neuropathy target esterase [Homo sa	1	2	1.21	9E-06	X	X	X	X	X	X	X	X	X	1327	146269	7.8	N
1042	gi|31563531|r	stromal antigen 2 [Homo sapiens]	4	11	5.44	5E-05	X	X	X	X	X	X	X	X	X	1231	141326	5.4	N
1043	gi|4758030|re	coatomer protein complex, subunit al	15	34	23.28	2E-04	X	X	X	X	X	X	X	X	X	1224	138331	7.7	N
1044	gi|33239445|r	eukaryotic translation initiation factor	4	16	8.11	1E-04	X	X	X	X	X	X	X	X	X	814	92482	5	N
1045	gi|88953910|r	PREDICTED: hypothetical protein LO	3	3	3.1	7E-06	X	X	X	X	X	X	X	X	X	2354	265615	6.2	N
1047	gi|42734339|r	hypothetical protein LOC55215 [Hom	4	9	8.17	6E-05	X	X	X	X	X	X	X	X	X	906	102387	6.8	N
1048	gi|4753161|re	general transcription factor IIIC, polyp	3	6	2.84	2E-05	X	X	X	X	X	X	X	X	X	2109	238417	7.4	N
1049	gi|19923790|r	rab3 GTPase-activating protein, non-	1	4	1.01	2E-05	X	X	X	X	X	X	X	X	X	1393	155984	5.6	N
1050	gi|21327715|r	transcription elongation regulator 1 [H	4	7	4.64	4E-05	X	X	X	X	X	X	X	X	X	1098	123901	8.6	N
1051	gi|33695086|r	nicotinamide nucleotide transhydroge	1	2	1.01	1E-05	X	X	X	X	X	X	X	X	X	1086	113923	8	N
1052	gi|57634534|r	nucleoporin 205kDa [Homo sapiens]	1	2	0.89	6E-06	X	X	X	X	X	X	X	X	X	2012	227918	6.2	N
1053	gi|62955803|r	nucleoporin 188kDa [Homo sapiens]	2	3	1.94	1E-05	X	X	X	X	X	X	X	X	X	1749	196041	6.7	N
1054	gi|7662238|re	apoptotic chromatin condensation ind	7	28	8.28	1E-04	X	X	X	X	X	X	X	X	X	1341	151887	6.4	N
1055	gi|89028962|r	PREDICTED: similar to epiplakin 1 [H	1	2	0.85	4E-06	X	X	X	X	X	X	X	X	X	2951	322607	5.8	N
1056	gi|21626468|r	zinc finger protein 638 [Homo sapiens	2	4	1.62	1E-05	X	X	X	X	X	X	X	X	X	1978	220623	6.4	N
1058	gi|4885403|re	host cell factor C1 (VP16-accessory p	19	45	16.2	1E-04	X	X	X	X	X	X	X	X	X	1938	198471	7.3	N
1059	gi|21071056|r	SWI/SNF-related matrix-associated a	10	20	9.29	7E-05	X	X	X	X	X	X	X	X	X	1647	184644	7.9	N
1061	gi|48255898|r	SWI/SNF-related matrix-associated a	4	11	3.63	4E-05	X	X	X	X	X	X	X	X	X	1572	179280	7.3	N
1062	gi|24430139|r	RNA polymerase II associated protei	1	2	0.79	8E-06	X	X	X	X	X	X	X	X	X	1393	152754	6.4	N
1063	gi|33620716|r	retinoblastoma-binding protein 6 isofo	2	10	1.54	3E-05	X	X	X	X	X	X	X	X	X	1758	197286	9.6	N
1065	gi|24415404|r	MDN1, midasin homolog [Homo sapie	10	20	2.98	2E-05	X	X	X	X	X	X	X	X	X	5596	632827	5.7	N
1066	gi|15147337|r	E3 ubiquitin protein ligase, HECT dor	19	43	11.97	9E-05	X	X	X	X	X	X	X	X	X	2799	309352	5.8	N
1067	gi|21361116|r	chondroitin sulfate proteoglycan 2 (ve	1	2	0.5	3E-06	X	X	X	X	X	X	X	X	X	3396	372821	4.5	N
1068	gi|14790190|r	spen homolog, transcriptional regulat	5	7	2.57	1E-05	X	X	X	X	X	X	X	X	X	3664	402251	7.6	N
1069	gi|61743954|r	AHNAK nucleoprotein isoform 1 [Hon	5	16	1.58	2E-05	X	X	X	X	X	X	X	X	X	5890	629114	6.1	N
1070	gi|13123776|r	DNA methyltransferase 1-associated	30	431	60.81	0.005	X	X	X	X	0.019	X	X	X	X	467	52993	9.5	N
1071	gi|88970681|r	PREDICTED: similar to heterogeneou	4	6	30.37	3E-04	X	X	X	X	X	X	X	X	X	135	14926	8.2	N
1072	gi|5901926|re	cleavage and polyadenylation specifi	8	36	59.47	9E-04	X	X	X	X	X	X	X	X	X	227	26227	8.8	N
1073	gi|16905517|r	FUS interacting protein (serine-argini	1	7	6.11	2E-04	X	X	X	X	X	X	X	X	X	262	31301	11.3	N
1083	gi|41327764|r	aldo-keto reductase family 7, membe	2	4	9.47	6E-05	X	X	X	X	X	X	X	X	X	359	39589	7.2	N
1084	gi|18379334|r	RNA-binding protein S1, serine-rich d	1	4	4.92	7E-05	X	X	X	X	X	X	X	X	X	305	34208	11.8	N
1086	gi|8922712|re	septin 11 [Homo sapiens]	3	4	12.12	5E-05	X	X	X	X	X	X	X	X	X	429	49398	6.8	N
1087	gi|88953744|r	PREDICTED: formin binding protein 1	2	5	7.69	7E-05	X	X	X	X	X	X	X	X	X	429	50740	8.7	N
1091	gi|4506145|re	protease, serine, 1 preproprotein [Ho	1	6	4.05	1E-04	X	X	X	X	X	X	X	X	X	247	26558	6.5	N
1092	gi|40807496|r	OTU domain containing 4 protein isof	7	15	12.12	8E-05	X	X	X	X	X	X	X	X	X	1048	116954	6.7	N
1093	gi|24307879|r	dynein, cytoplasmic, intermediate pol	2	5	7.52	4E-05	X	X	X	X	X	X	X	X	X	638	71457	5.2	N
1094	gi|7657013|re	apoptosis antagonizing transcription f	1	6	3.21	6E-05	X	X	X	X	X	X	X	X	X	560	63133	4.9	N
1095	gi|4757790|re	ash2 (absent, small, or homeotic)-like	4	5	10.35	5E-05	X	X	X	X	X	X	X	X	X	628	68683	5.7	N
1096	gi|4885225|re	Ewing sarcoma breakpoint region 1 is	2	7	5.03	6E-05	X	X	X	X	X	X	X	X	X	656	68478	9.3	N
1098	gi|4557493|re	cleavage stimulation factor subunit 2	4	15	13.17	1E-04	X	X	X	X	X	X	X	X	X	577	60959	6.8	N
1099	gi|4826734|re	fusion (involved in t(12;16) in maligna	8	27	22.43	3E-04	X	X	X	X	X	X	X	X	X	526	53426	9.4	N
1100	gi|4502027|re	albumin precursor [Homo sapiens]	17	49	36.45	5E-04	X	X	X	X	X	X	X	X	X	609	69367	6.3	N
1101	gi|24308033|r	formin binding protein 4 [Homo sapie	1	3	1.97	2E-05	X	X	X	X	X	X	X	X	X	1015	110064	4.7	N
1102	gi|21237805|r	SWI/SNF-related matrix-associated a	11	49	13.43	2E-04	X	X	X	X	X	X	X	X	X	1214	132879	5.7	N
1104	gi|55741709|r	RNA binding motif protein 25 [Homo s	6	15	12.46	1E-04	X	X	X	X	X	X	X	X	X	843	100186	6.3	N
1105	gi|52486999|r	THO complex 2 [Homo sapiens]	8	22	9.54	8E-05	X	X	X	X	X	X	X	X	X	1478	169581	8.7	N
1106	gi|57164942|r	colonic and hepatic tumor over-expre	11	27	8.02	8E-05	X	X	X	X	X	X	X	X	X	2032	225493	7.8	N
1108	gi|5032189|re	tumor protein p53 binding protein, 1 [	5	7	5.63	2E-05	X	X	X	X	X	X	X	X	X	1972	213573	4.7	N
1109	gi|89052285|r	PREDICTED: hypothetical protein LO	10	14	15.18	6E-05	X	X	X	X	X	X	X	X	X	1278	138244	8.4	N
1111	gi|19923217|r	antigen identified by monoclonal antib	23	56	12.62	1E-04	X	X	X	X	X	X	X	X	X	3256	358747	9.4	N
1112	gi|57164975|r	Treacher Collins-Franceschetti syndro	18	52	15.66	2E-04	X	X	X	X	X	X	X	X	X	1411	144314	9	N
1113	gi|6382079|re	RAN binding protein 2 [Homo sapiens	11	28	5.37	5E-05	X	X	X	X	X	X	X	X	X	3224	358173	6.2	N
1114	gi|89038196|r	PREDICTED: MAX dimerization prote	22	65	13.42	1E-04	X	X	X	X	X	X	X	X	X	2855	315119	6.8	N
1118	gi|7706326|re	splicing factor 3B, 14 kDa subunit [Ho	4	8	40.8	4E-04	X	X	X	X	X	X	X	X	X	125	14585	9.4	N
1119	gi|4507131|re	small nuclear ribonucleoprotein polyp	1	3	16.28	2E-04	X	X	X	X	X	X	X	X	X	86	9725	4.7	N
1120	gi|18702323|r	dynein, cytoplasmic, light polypeptide	1	2	12.5	1E-04	X	X	X	X	X	X	X	X	X	96	10855	7.5	N
1123	gi|4504983|re	galectin 3 [Homo sapiens]	4	9	21.2	2E-04	X	X	X	X	X	X	X	X	X	250	26188	8.5	N
1124	gi|7705320|re	hepatoma-derived growth factor, relat	2	6	16.26	2E-04	X	X	X	X	X	X	X	X	X	203	22620	8	N
1125	gi|21704261|r	MAX protein isoform a [Homo sapiens	2	3	20	1E-04	X	X	X	X	X	X	X	X	X	160	18275	6.3	N
1127	gi|20149629|r	DEAD (Asp-Glu-Ala-Asp) box polypep	3	8	9.23	1E-04	X	X	X	X	X	X	X	X	X	455	50647	9.1	N
1129	gi|13376840|r	WD repeat domain 61 [Homo sapiens	4	16	28.52	3E-04	X	X	X	X	X	X	X	X	X	305	33581	5.5	N
1130	gi|40556376|r	cytokine-like nuclear factor n-pac [Ho	2	17	6.51	2E-04	X	X	X	X	X	X	X	X	X	553	60547	9.2	N
1131	gi|40018640|r	parafibromin [Homo sapiens]	2	5	6.4	5E-05	X	X	X	X	X	X	X	X	X	531	60577	9.6	N
1132	gi|46852388|r	cell-cycle and apoptosis regulatory pr	7	53	9.57	3E-04	X	X	X	X	X	X	X	X	X	1150	132821	5.8	N
1133	gi|41327771|r	DEAD (Asp-Glu-Ala-Asp) box polypep	8	18	17.56	1E-04	X	X	X	X	X	3	4	6.34	5E-04	820	95583	9.6	N
1134	gi|24234690|r	meiotic recombination 11 homolog A	3	4	5.88	3E-05	X	X	X	X	X	X	X	X	X	680	77642	5.8	N
1136	gi|5031653|re	breast carcinoma amplified sequence	6	24	36.89	6E-04	X	X	X	X	X	X	X	X	X	225	26131	5.6	N
1137	gi|5803036|re	heterogeneous nuclear ribonucleopro	3	12	16.72	2E-04	X	X	X	X	X	X	X	X	X	305	30841	9.3	N
1138	gi|14702171|r	PolII_Rpb3 {DNA directed RNA polym	3	9	20.73	2E-04	X	X	X	X	X	X	X	X	X	275	31441	4.9	N
1140	gi|11034845|r	hypothetical protein LOC58490 [Hom	2	3	9.51	5E-05	X	X	X	X	X	X	X	X	X	326	36900	6	N
1141	gi|89044285|r	PREDICTED: structural maintenance	16	36	14.06	1E-04	X	X	X	X	X	X	X	X	X	1949	220240	7.7	N
1143	gi|5901928|re	cleavage and polyadenylation specifi	5	53	15.06	5E-04	X	X	X	X	X	X	X	X	X	551	59209	7.4	N
1144	gi|5031755|re	heterogeneous nuclear ribonucleopro	11	41	21.33	4E-04	X	X	X	X	X	X	X	X	X	633	70943	8.1	N
1145	gi|13376204|r	Cas-Br-M (murine) ecotropic retrovira	1	4	4.07	5E-05	X	X	X	X	X	X	X	X	X	491	54503	8.3	N
1146	gi|27545326|r	SWI/SNF related, matrix associated,	3	4	13.77	6E-05	X	X	X	X	X	X	X	X	X	385	44141	6.2	N
1148	gi|56699409|r	RNA binding motif protein, X-linked [H	3	5	7.67	7E-05	X	X	X	X	X	X	X	X	X	391	42332	10.1	N
1149	gi|33946282|r	hypothetical protein LOC25962 isofor	5	6	3.53	2E-05	X	X	X	X	X	X	X	X	X	1812	202023	5	N
1150	gi|23397429|r	B5 receptor [Homo sapiens]	3	5	10.7	8E-05	X	X	X	X	X	X	X	X	X	374	42503	5.6	N
1151	gi|51479192|r	ring finger protein 1 [Homo sapiens]	3	5	10.59	7E-05	X	X	X	X	X	X	X	X	X	406	42429	5.6	N
1152	gi|6005747|re	ring finger protein 2 [Homo sapiens]	2	4	8.33	7E-05	X	X	X	X	X	X	X	X	X	336	37655	6.8	N
1153	gi|4503525|re	eukaryotic translation initiation factor	2	6	3.29	4E-05	X	X	X	X	X	X	X	X	X	913	105344	5.7	N
1160	gi|50959085|r	Fms-interacting protein [Homo sapier	2	5	4.69	4E-05	X	X	X	X	X	X	X	X	X	683	78508	6.9	N
1164	gi|4503249|re	DEK oncogene (DNA binding) [Homo	7	18	19.47	3E-04	X	X	X	X	X	X	X	X	X	375	42674	8.6	N
1165	gi|5174409|re	CD2 antigen (cytoplasmic tail) binding	4	7	23.75	1E-04	X	X	X	X	X	3	6	20.53	0.002	341	37646	4.6	N
1166	gi|5032027|re	retinoblastoma binding protein 4 [Hor	12	69	60.71	9E-04	X	X	X	X	X	X	X	X	X	425	47656	4.9	N
1167	gi|14150171|r	THO complex 3 [Homo sapiens]	1	4	3.13	6E-05	X	X	X	X	X	X	X	X	X	351	38772	6.1	N
1169	gi|33383233|r	arsenate resistance protein ARS2 iso	11	21	23.37	2E-04	X	X	X	X	X	X	X	X	X	796	90251	5.7	N
1171	gi|19924129|r	RAD50 homolog isoform 1 [Homo sap	7	21	8.46	9E-05	X	X	X	X	X	X	X	X	X	1312	153892	6.9	N
1172	gi|5454172|re	X-ray repair cross complementing pro	5	8	8.85	7E-05	X	X	X	X	X	X	X	X	X	633	69526	6.4	N
1173	gi|40807485|r	U5 snRNP-associated 102 kDa prote	10	18	13.28	1E-04	X	X	X	X	X	5	6	5.63	7E-04	941	106925	8.3	N
1174	gi|38569503|r	ATP-dependent RNA helicase ROK1	6	16	20.16	2E-04	X	X	X	X	X	X	X	X	X	491	55217	9.7	N
1176	gi|13129068|r	nucleolar complex associated 4 homo	2	3	4.84	3E-05	X	X	X	X	X	X	X	X	X	516	58468	7.5	N
1178	gi|13128860|r	histone deacetylase 1 [Homo sapiens	8	16	21.78	2E-04	X	X	X	X	X	X	X	X	X	482	55103	5.5	N
1179	gi|22094121|r	SCC-112 protein [Homo sapiens]	7	11	8.79	5E-05	X	X	X	X	X	X	X	X	X	1297	146610	8.1	N
1180	gi|39930353|r	superkiller viralicidic activity 2-like 2 [	4	4	5.09	2E-05	X	X	X	X	X	X	X	X	X	1042	117761	6.7	N
1181	gi|4557495|re	cleavage stimulation factor subunit 3	3	10	6.69	8E-05	X	X	X	X	X	X	X	X	X	717	82922	8.1	N
1182	gi|23397427|r	synaptotagmin binding, cytoplasmic R	10	35	22.63	3E-04	X	X	X	X	X	X	X	X	X	623	69633	8.6	N
1183	gi|29568103|r	U1 small nuclear ribonucleoprotein 70	5	8	15.1	1E-04	X	X	X	X	X	X	X	X	X	437	51557	9.9	N
1184	gi|44888822|r	hypothetical protein LOC23248 [Hom	2	4	2.04	2E-05	X	X	X	X	X	X	X	X	X	1424	152587	7.3	N
1185	gi|8922679|re	smu-1 suppressor of mec-8 and unc-	2	2	5.26	2E-05	X	X	X	X	X	X	X	X	X	513	57528	7.2	N
1186	gi|14110407|r	heterogeneous nuclear ribonucleopro	5	10	16.9	1E-04	X	X	X	X	X	X	X	X	X	420	46437	9.6	N
1188	gi|56550051|r	ubiquitin specific protease 39 [Homo	5	9	14.87	9E-05	X	X	X	X	X	X	X	X	X	565	65381	8.9	N
1189	gi|34101288|r	cleavage and polyadenylation specifi	1	5	1.66	4E-05	X	X	X	X	X	X	X	X	X	782	88487	5.1	N
1190	gi|11225260|r	DNA topoisomerase I [Homo sapiens	7	21	12.81	2E-04	X	X	X	X	X	X	X	X	X	765	90726	9.3	N
1191	gi|19913408|r	DNA topoisomerase II, beta isozyme	16	36	13.26	1E-04	X	X	X	X	X	X	X	X	X	1621	182661	8.1	N
1192	gi|4759196|re	symplekin [Homo sapiens]	5	14	11.82	7E-05	X	X	X	X	X	X	X	X	X	1142	126500	6.4	N
1193	gi|24308177|r	hypothetical protein LOC55677 [Hom	1	2	1.47	1E-05	X	X	X	X	X	X	X	X	X	819	91969	4.7	N
1194	gi|10863889|r	squamous cell carcinoma antigen rec	7	13	15.13	9E-05	X	X	X	X	X	X	X	X	X	800	90255	6.1	N
1195	gi|8923269|re	testis expressed sequence 10 [Homo	7	29	11.95	2E-04	X	X	X	X	X	X	X	X	X	929	105693	9.4	N
1196	gi|45446743|r	DEAD box polypeptide 42 protein [Ho	7	20	16.52	1E-04	X	X	X	X	X	X	X	X	X	938	102975	7	N
1198	gi|4504865|re	KH-type splicing regulatory protein (F	10	35	18.99	3E-04	X	X	X	X	X	X	X	X	X	711	73161	7.3	N
1199	gi|42734325|r	KIAA0261 [Homo sapiens]	4	7	5.63	3E-05	X	X	X	X	X	X	X	X	X	1190	132945	5.4	N
1200	gi|13470086|r	retinoic acid induced 14 [Homo sapie	1	3	1.33	2E-05	X	X	X	X	X	X	X	X	X	980	110042	6.2	N
1201	gi|41281483|r	BMS1-like, ribosome assembly protei	1	4	1.17	2E-05	X	X	X	X	X	X	X	X	X	1282	145821	6.4	N
1202	gi|15987121|r	hypothetical protein LOC23223 [Hom	3	11	4.01	5E-05	X	X	X	X	X	X	X	X	X	1297	143732	8.8	N
1203	gi|24496789|r	leucyl-tRNA synthetase [Homo sapie	2	2	2.55	1E-05	X	X	X	X	X	X	X	X	X	1176	134411	7.2	N
1204	gi|24415383|r	proline-, glutamic acid-, leucine-rich p	10	27	13.36	1E-04	X	X	X	X	X	X	X	X	X	1130	119624	4.3	N
1205	gi|17999535|r	serine/threonine-protein kinase PRP4	3	5	4.17	3E-05	X	X	X	X	X	X	X	X	X	1007	116973	10.3	N
1207	gi|4504191|re	mutS homolog 6 [Homo sapiens]	11	30	13.53	1E-04	X	X	X	X	X	X	X	X	X	1360	152785	6.9	N
1208	gi|21361794|r	TIP120 protein [Homo sapiens]	5	11	7.48	5E-05	X	X	X	X	X	X	X	X	X	1230	136375	5.8	N
1209	gi|23097292|r	processing of precursor 1, ribonuclea	3	3	4.59	2E-05	X	X	X	X	X	X	X	X	X	1024	114681	9.2	N
1210	gi|19913406|r	DNA topoisomerase II, alpha isozyme	19	67	19.73	2E-04	X	X	X	X	X	X	X	X	X	1531	174384	8.7	N
1211	gi|21361861|r	Fanconi anemia complementation gro	3	3	4.83	1E-05	X	X	X	X	X	X	X	X	X	1471	166461	6.2	N
1213	gi|38201619|r	eukaryotic translation initiation factor	3	7	2.92	3E-05	X	X	X	X	X	X	X	X	X	1403	154804	5.2	N
1218	gi|56243590|r	WD repeat domain 33 isoform 1 [Hon	2	3	1.72	1E-05	X	X	X	X	X	X	X	X	X	1336	145891	9.2	N
1219	gi|40789229|r	splicing factor, arginine/serine-rich 15	3	9	4.27	4E-05	X	X	X	X	X	X	X	X	X	1147	125869	9.6	N
1220	gi|30794372|r	polybromo 1 isoform 1 [Homo sapien	5	6	5.18	2E-05	X	X	X	X	X	X	X	X	X	1602	183689	6.7	N
1222	gi|7706549|re	CDC2-related protein kinase 7 [Homo	2	4	3.15	2E-05	X	X	X	X	X	X	X	X	X	1490	164154	9.5	N
1223	gi|23397666|r	transcriptional co-repressor Sin3A [H	9	21	14.85	9E-05	X	X	X	X	X	X	X	X	X	1273	145175	7.3	N
1224	gi|27597090|r	suppressor of Ty 6 homolog [Homo s	8	12	10.37	4E-05	X	X	X	X	X	X	X	X	X	1726	199071	4.9	N
1225	gi|7661966|re	mediator of DNA damage checkpoint	12	23	11.3	6E-05	X	X	X	X	X	X	X	X	X	2089	226690	5.5	N
1226	gi|4505939|re	PolII_Rpb1 {DNA directed RNA polym	19	58	17.11	2E-04	X	X	X	X	X	X	X	X	X	1970	217204	7.4	N
1227	gi|88953403|r	PREDICTED: similar to RAN-binding	3	5	2.28	2E-05	X	X	X	X	X	X	X	X	X	1758	197486	6.3	N
1232	gi|70980549|r	programmed cell death 11 [Homo sap	9	17	7.75	5E-05	X	X	X	X	X	X	X	X	X	1871	208699	8.9	N
1233	gi|4557809|re	ornithine aminotransferase precursor	4	13	12.98	2E-04	X	X	X	X	X	X	X	X	X	439	48535	7	N
1234	gi|40786394|r	hypothetical protein DKFZp434N062	1	2	7.96	4E-05	X	X	X	X	X	X	X	X	X	314	34613	7.8	N
1236	gi|7705608|re	fumarylacetoacetate hydrolase doma	2	3	8.28	5E-05	X	X	X	X	X	X	X	X	X	314	34582	8.2	N
1237	gi|29029559|r	CSE1 chromosome segregation 1-like	2	5	4.84	3E-05	X	X	X	X	X	X	X	X	X	971	110417	5.8	N
1238	gi|24308444|r	hypothetical protein LOC116143 [Hor	22	659	75.91	0.011	X	X	X	X	X	6	21	27.73	0.006	357	39740	8.1	N
1239	gi|7657162|re	HLA class II region expressed gene K	8	234	62.02	0.01	X	X	X	X	X	2	2	25.58	0.002	129	14583	8.9	N
1240	gi|8923598|re	hypothetical protein LOC55011 [Hom	15	980	72.07	0.019	X	X	X	X	X	5	11	32.07	0.004	290	32363	5.1	N
1241	gi|19924159|r	RPB5-mediating protein isoform a [H	25	631	55.7	0.007	X	X	X	X	X	8	24	26.73	0.005	535	59832	5	N
1243	gi|24041018|r	ubiquitously-expressed transcript isof	8	105	51.48	0.004	X	X	X	X	X	1	2	8.28	0.001	169	19597	7.1	N
1245	gi|18079254|r	p53 and DNA damage-regulated prot	8	314	60.15	0.013	X	X	X	X	X	1	1	12.03	8E-04	133	15511	6	N
1246	gi|14589951|r	PolII_Rpb5 {DNA directed RNA polym	9	223	60.95	0.006	X	X	X	X	X	3	10	19.05	0.005	210	24611	6	N
1247	gi|13375809|r	hypothetical protein LOC79657 [Hom	47	958	63.76	0.008	X	X	X	X	X	14	25	28.42	0.004	665	75703	7.1	N
1248	gi|12408675|r	prefoldin 2 [Homo sapiens]	9	289	62.34	0.011	X	X	X	X	X	3	7	29.22	0.005	154	16648	6.6	N
1249	gi|8923900|re	cytidine 5'-monophosphate N-acetylne	3	14	10.37	2E-04	X	X	X	X	X	X	X	X	X	434	48379	7.9	N
1250	gi|13376202|r	hypothetical protein LOC79871 [Hom	3	23	8.33	2E-04	X	X	X	X	X	X	X	X	X	612	69449	7.8	N
1251	gi|6912618|re	glutaminyl-peptide cyclotransferase p	4	9	16.9	1E-04	X	X	X	X	X	X	X	X	X	361	40877	6.6	N
1252	gi|29837655|r	DNA polymerase delta interacting pro	7	11	25.65	1E-04	X	X	X	X	X	X	X	X	X	421	46089	10	N
1253	gi|7705369|re	coatomer protein complex, subunit be	3	7	6.09	4E-05	X	X	X	X	X	X	X	X	X	953	107142	6	N
1254	gi|39725938|r	polymerase (RNA) III (DNA directed)	37	173	39.21	7E-04	X	X	X	X	X	6	11	6.12	8E-04	1390	155641	8.5	N
1255	gi|39930355|r	DPCD protein [Homo sapiens]	8	67	51.72	0.002	X	X	X	X	X	X	X	X	X	203	23240	9	N
1256	gi|18375623|r	HLA-B associated transcript 1 [Homo	16	126	48.6	0.002	X	X	X	X	X	X	X	X	X	428	48991	5.7	N
1258	gi|21040371|r	DEAD (Asp-Glu-Ala-Asp) box polype	12	70	41.45	9E-04	X	X	X	X	X	X	X	X	X	427	49130	5.7	N
1259	gi|7657611|re	DnaJ (Hsp40) homolog, subfamily C,	2	7	11.36	2E-04	X	X	X	X	X	X	X	X	X	264	30987	9.2	N
1260	gi|45643135|r	MORF-related gene 15 isoform 2 [Ho	33	457	84.25	0.007	X	X	X	X	X	X	X	X	X	362	41474	9.3	N
1261	gi|5803102|re	MORF-related gene 15 isoform 1 [Ho	34	510	86.69	0.009	X	X	X	X	X	X	X	X	X	323	37231	9.2	N
1262	gi|47604944|r	SCY1-like 2 protein [Homo sapiens]	17	73	30.89	4E-04	X	X	X	X	X	X	X	X	X	929	103709	8.2	N
1263	gi|25470886|r	DAZ associated protein 1 isoform b [	2	10	7.86	1E-04	X	X	X	X	X	X	X	X	X	407	43383	8.6	N
1265	gi|21359951|r	hypothetical protein LOC79171 [Hom	2	2	6.67	2E-05	X	X	X	X	X	X	X	X	X	480	50414	9.6	N
1266	gi|4504205|re	general transcription factor IIIC, polyp	2	2	5.71	1E-05	X	X	X	X	X	X	X	X	X	911	100680	7.3	N
1267	gi|5729730|re	apoptosis inhibitor 5 [Homo sapiens]	4	21	15.08	2E-04	X	X	X	X	X	X	X	X	X	504	56770	5.9	N
1268	gi|38327634|r	DEAD (Asp-Glu-Ala-Asp) box polype	8	33	18.66	3E-04	X	X	X	X	X	X	X	X	X	670	75407	9.5	N
1269	gi|5031579|re	A-kinase anchor protein 8 [Homo sap	4	8	11.85	7E-05	X	X	X	X	X	X	X	X	X	692	76108	5.1	N
1270	gi|41146847|r	PREDICTED: hypothetical protein LO	2	2	5.68	2E-05	X	X	X	X	X	X	X	X	X	581	62543	9.4	N
1274	gi|15150805|r	transducin beta-like 1Y [Homo sapien	1	3	2.49	3E-05	X	X	X	X	X	X	X	X	X	522	56688	5.6	N
1279	gi|32967603|r	bromodomain adjacent to zinc finger	3	3	3.79	1E-05	X	X	X	X	X	X	X	X	X	1556	178702	6.6	N
1280	gi|4826882|re	nuclear matrix protein p84 [Homo sap	4	7	7.31	6E-05	X	X	X	X	X	X	X	X	X	657	75627	5	N
1281	gi|77404397|r	staphylococcal nuclease domain cont	7	19	15.93	1E-04	X	X	X	X	X	X	X	X	X	910	101997	7.2	N
1282	gi|9966805|re	DEAD (Asp-Glu-Ala-Asp) box polype	9	21	17.58	1E-04	X	X	X	X	X	X	X	X	X	859	96332	9.1	N
1283	gi|20149698|r	l(3)mbt-like 2 isoform a [Homo sapien	2	7	3.4	6E-05	X	X	X	X	X	X	X	X	X	705	79110	6.9	N
1284	gi|25777671|r	protein phosphatase 1, regulatory sub	4	10	8.62	6E-05	X	X	X	X	X	X	X	X	X	940	99058	9.2	N
1285	gi|32528306|r	replication factor C large subunit [Hor	4	4	5.93	2E-05	X	X	X	X	X	X	X	X	X	1147	128183	9.4	N
1286	gi|11321634|r	CD2-associated protein [Homo sapie	24	59	50.08	5E-04	X	X	X	X	X	X	X	X	X	639	71451	6.4	N
1287	gi|33636750|r	likely ortholog of mouse ubiquitin-con	23	44	31.42	2E-04	X	X	X	X	X	X	X	X	X	1292	141383	5.1	N
1288	gi|46367785|r	hypothetical protein LOC54934 [Hom	12	79	39.49	0.001	X	X	X	X	X	X	X	X	X	390	43483	5.3	N
1289	gi|23503295|r	casein kinase 2, beta polypeptide [Ho	4	15	28.84	4E-04	X	X	X	X	X	X	X	X	X	215	24942	5.6	N
1290	gi|29570791|r	casein kinase II alpha 1 subunit isofo	6	18	21.74	3E-04	X	X	X	X	X	X	X	X	X	391	45144	7.7	N
1292	gi|13540586|r	hypothetical protein LOC81556 [Hom	4	5	15.06	5E-05	X	X	X	X	X	X	X	X	X	518	57341	5.2	N
1293	gi|4502891|re	chloride channel, nucleotide-sensitive	2	12	23.63	3E-04	X	X	X	X	X	X	X	X	X	237	26215	4.1	N
1294	gi|55770864|r	THO complex 4 [Homo sapiens]	4	15	21.79	3E-04	X	X	X	X	X	X	X	X	X	257	26888	11.2	N
1295	gi|4503097|re	casein kinase 2, alpha prime polypep	2	5	8.57	8E-05	X	X	X	X	X	X	X	X	X	350	41213	8.6	N
1296	gi|23308579|r	unactive progesterone receptor, 23 kl	2	2	15.63	7E-05	X	X	X	X	X	X	X	X	X	160	18697	4.5	N
1299	gi|45333883|r	kelch repeat and BTB (POZ) domain-	4	4	7.42	3E-05	X	X	X	X	X	X	X	X	X	674	76138	6.1	N
1300	gi|4506185|re	proteasome alpha 4 subunit [Homo sa	3	6	21.84	1E-04	X	X	X	X	X	X	X	X	X	261	29484	7.7	N
1301	gi|24475847|r	influenza virus NS1A binding protein	2	3	6.54	3E-05	X	X	X	X	X	X	X	X	X	642	71729	5.5	N
1303	gi|6912478|re	karyopherin alpha 6 [Homo sapiens]	4	6	11.01	6E-05	X	X	X	X	X	X	X	X	X	536	60030	5	N
1304	gi|4504895|re	karyopherin alpha 1 [Homo sapiens]	5	11	17.1	1E-04	X	X	X	X	X	X	X	X	X	538	60307	5	N
1305	gi|58535459|r	cell division cycle 10 isoform 1 [Homo	4	10	14.83	1E-04	X	X	X	X	X	X	X	X	X	418	48758	8.6	N
1307	gi|22538465|r	proteasome beta 3 subunit [Homo sa	1	4	4.88	1E-04	X	X	X	X	X	X	X	X	X	205	22949	6.5	N
1308	gi|11024686|r	hypothetical protein LOC55726 [Hom	3	4	6.66	3E-05	X	X	X	X	X	X	X	X	X	706	80103	6.8	N
1309	gi|4503513|re	eukaryotic translation initiation factor	3	4	13.23	7E-05	X	X	X	X	X	X	X	X	X	325	36502	5.6	N
1310	gi|5453842|re	proliferation-associated 2G4, 38kDa [	4	9	20.81	1E-04	X	X	X	X	X	X	X	X	X	394	43813	6.6	N
1311	gi|32307148|r	O-linked GlcNAc transferase isoform	4	7	6.31	4E-05	X	X	X	X	X	X	X	X	X	1046	116924	6.7	N
1313	gi|5031815|re	lysyl-tRNA synthetase [Homo sapiens	2	2	7.37	2E-05	X	X	X	X	X	X	X	X	X	597	68048	6.4	N
1314	gi|53759103|r	importin 8 [Homo sapiens]	1	2	2.22	1E-05	X	X	X	X	X	X	X	X	X	1037	119938	5.2	N
1315	gi|50233868|r	hypothetical protein LOC22897 [Hom	2	4	2.05	2E-05	X	X	X	X	X	X	X	X	X	1460	164341	5.4	N
1316	gi|14702169|r	plasminogen activator, tissue type iso	2	4	5.23	4E-05	X	X	X	X	X	X	X	X	X	516	57371	7.5	N
1318	gi|7705433|re	eukaryotic translation initiation factor	3	3	7.09	3E-05	X	X	X	X	X	X	X	X	X	564	66727	6.3	N
1319	gi|20127460|r	xeroderma pigmentosum, complemer	3	5	4.79	3E-05	X	X	X	X	X	X	X	X	X	940	105953	8.9	N
1320	gi|29171734|r	eukaryotic translation initiation factor	3	3	4.19	2E-05	X	X	X	X	X	X	X	X	X	859	97208	9.2	N
1321	gi|4507943|re	exportin 1 [Homo sapiens]	6	10	9.8	5E-05	X	X	X	X	X	X	X	X	X	1071	123386	6.1	N
1322	gi|50658063|r	SMC4 structural maintenance of chro	3	10	2.87	4E-05	X	X	X	X	X	X	X	X	X	1288	147182	6.8	N

1325	gi|24797086|r	RAN binding protein 5 [Homo sapiens	3	4	3.68	2E-05
1327	gi|4506769|re	S100 calcium-binding protein A7 [Ho	2	5	31.68	3E-04
1328	gi|46852398|r	biogenesis of lysosome-related orga	1	2	19.01	8E-05
1330	gi|7706322|re	chromosome 14 open reading frame	3	6	20.49	1E-04
1331	gi|22208973|r	high mobility group AT-hook 1 isofor	1	2	14.58	1E-04
1335	gi|5031749|re	high-mobility group nucleosomal bind	3	10	36.67	6E-04
1336	gi|5730085|re	t-complex-associated-testis-expresse	2	3	30.09	2E-04
1337	gi|4758356|re	flap structure-specific endonuclease	2	2	12.11	3E-05
1338	gi|5453595|re	adenylyl cyclase-associated protein [	4	7	15.79	8E-05
1339	gi|4826898|re	profilin 1 [Homo sapiens]	1	10	11.43	4E-04
1340	gi|5729842|re	glyoxalase I [Homo sapiens]	1	2	10.87	6E-05
1341	gi|4507349|re	TBP-associated factor 4 [Homo sapie	8	16	14.22	8E-05
1342	gi|4507793|re	ubiquitin-conjugating enzyme E2N [H	2	3	23.03	1E-04
1343	gi|5803092|re	methionyl aminopeptidase 2 [Homo s	3	3	9.41	4E-05
1344	gi|4758140|re	DEAD (Asp-Glu-Ala-Asp) box polype	3	6	13.35	7E-05
1345	gi|9506651|re	potassium channel tetramerisation do	3	7	21.37	2E-04
1346	gi|4507791|re	ubiquitin-conjugating enzyme E2M [H	2	3	25.68	9E-05
1347	gi|10863927|r	peptidylprolyl isomerase A isoform 1	4	18	39.39	6E-04
1351	gi|4507645|re	triosephosphate isomerase 1 [Homo	6	10	34.54	2E-04
1352	gi|4826686|re	DEAD (Asp-Glu-Ala-Asp) box polype	4	27	10	2E-04
1353	gi|51092299|r	adenylate kinase 3-like 2 [Homo sapi	1	2	7.62	5E-05
1359	gi|4504425|re	high-mobility group box 1 [Homo sapi	5	9	25.12	2E-04
1360	gi|4507357|re	transgelin 2 [Homo sapiens]	2	11	16.08	3E-04
1361	gi|13899265|r	Ras association (RalGDS/AF-6) dom	2	4	6.92	6E-05
1364	gi|18375501|r	APEX nuclease [Homo sapiens]	5	12	26.73	2E-04
1367	gi|6912494|re	microtubule-associated protein, RP/E	3	7	21.27	1E-04
1368	gi|11863154|r	archain [Homo sapiens]	1	6	6.26	7E-05
1369	gi|5453555|re	ras-related nuclear protein [Homo sa	2	5	12.5	1E-04
1370	gi|21361368|r	pyrroline-5-carboxylate synthetase is	5	9	10.44	6E-05
1372	gi|10863997|r	polypyrimidine tract binding protein 2	3	6	16.38	6E-05
1373	gi|21614499|r	villin 2 [Homo sapiens]	6	14	10.92	1E-04
1374	gi|28882049|r	replication factor C 2 (40kD) isoform	5	8	29.06	1E-04
1376	gi|7657269|re	androgen-induced prostate proliferati	4	8	6.29	3E-05
1378	gi|13399322|r	N-acetyltransferase-like protein [Hom	2	3	5.07	2E-05
1379	gi|17402900|r	far upstream element-binding protein	6	13	15.37	1E-04
1380	gi|4506891|re	SET translocation (myeloid leukemia-	2	7	16.61	1E-04
1381	gi|4757756|re	annexin A2 isoform 2 [Homo sapiens]	13	36	52.8	6E-04
1384	gi|13540531|r	integrin-linked kinase-associated prot	1	2	4.85	3E-05
1385	gi|24308207|r	leucine rich repeat containing 47 [Ho	4	7	13.38	7E-05
1386	gi|51477359|r	PREDICTED: similar to Transcription	1	2	4.4	3E-05
1391	gi|4505763|re	phosphoglycerate kinase 1 [Homo sa	7	29	26.38	4E-04
1392	gi|29727992|r	PREDICTED: similar to CG17293-PA	1	2	4.13	4E-05
1394	gi|5454052|re	stratifin [Homo sapiens]	2	3	12.9	7E-05
1395	gi|4826806|re	bromodomain containing protein 2 [H	4	7	7.74	5E-05
1396	gi|32483367|r	origin recognition complex, subunit 3	3	4	6.05	3E-05
1398	gi|11496978|r	nuclear transcription factor Y, gamma	1	2	3.88	3E-05
1399	gi|38569466|r	ROD1 regulator of differentiation 1 [H	2	2	7.43	2E-05
1400	gi|4507903|re	vaccinia related kinase 1 [Homo sapi	2	3	7.32	4E-05
1401	gi|7706310|re	LUC7-like 2 [Homo sapiens]	2	2	5.97	3E-05
1402	gi|8923040|re	collaborates/cooperates with ARF (al	1	3	3.62	3E-05
1403	gi|7705853|re	dynein light chain-A [Homo sapiens]	1	8	3.63	9E-05
1404	gi|7705765|re	WD repeat domain 50 [Homo sapiens	1	2	3.45	2E-05
1405	gi|4508017|re	zinc finger protein 207 isoform a [Hor	2	4	7.53	5E-05
1407	gi|4506583|re	replication protein A1, 70kDa [Homo s	2	5	5.68	5E-05
1408	gi|13399296|r	MYC-associated zinc finger protein [H	2	2	5.63	2E-05
1409	gi|89030025|r	PREDICTED: far upstream element (	4	6	16.05	7E-05
1413	gi|73747829|r	ligase III, DNA, ATP-dependent isofo	3	6	4.36	3E-05
1415	gi|29789006|r	pleckstrin homology domain containin	1	2	2.79	2E-05
1416	gi|39995084|r	hypothetical protein LOC65123 [Hom	3	6	6.14	3E-05
1417	gi|30181238|r	N2,N2-dimethylguanosine tRNA meth	1	2	2.73	2E-05
1418	gi|7705284|re	anaphase-promoting complex subuni	3	6	10.09	6E-05
1419	gi|6005757|re	chromatin-specific transcription elong	5	8	9.17	4E-05
1420	gi|21361397|r	Rac GTPase activating protein 1 [Ho	1	2	2.53	2E-05
1421	gi|21361657|r	protein disulfide isomerase-associate	7	14	21.78	2E-04
1422	gi|14149627|r	ubiquitin specific protease 15 [Homo	2	3	5.36	2E-05
1423	gi|7657671|re	upstream binding transcription factor,	5	8	7.85	6E-05
1424	gi|4503735|re	forkhead box C1 [Homo sapiens]	2	2	6.33	2E-05
1425	gi|4758032|re	coatomer protein complex, subunit be	3	7	7.84	4E-05
1426	gi|24497620|r	signal recognition particle 68kDa [Ho	2	2	5.58	2E-05
1427	gi|17999541|r	vacuolar protein sorting 35 [Homo sa	1	2	2.01	1E-05
1429	gi|41327773|r	DEAD (Asp-Glu-Ala-Asp) box polype	3	5	4.56	3E-05
1430	gi|4826960|re	glutaminyl-tRNA synthetase [Homo s	1	2	1.94	1E-05
1431	gi|11079228|r	N-ethylmaleimide-sensitive factor [Ho	1	2	1.88	2E-05
1433	gi|34101286|r	zinc finger RNA binding protein [Hom	4	8	7.17	4E-05
1434	gi|50428935|r	BPY2 interacting protein 1 [Homo sap	4	5	7.27	3E-05
1435	gi|10947135|r	ATP-binding cassette, sub-family F, r	1	2	1.61	1E-05
1437	gi|4507241|re	structure specific recognition protein	6	9	14.81	7E-05
1438	gi|42475941|r	zinc finger protein 261 [Homo sapiens	3	9	4.6	4E-05
1440	gi|4505933|re	polymerase (DNA directed), delta 1, c	2	2	2.71	1E-05
1441	gi|47519639|r	microtubule-associated protein 4 isof	4	5	5.9	2E-05
1442	gi|7662142|re	centrosomal protein 170kDa [Homo s	1	2	1.26	7E-06
1444	gi|15451892|r	translation initiation factor IF2 [Homo	2	5	2.62	2E-05
1445	gi|20149524|r	suppressor of Ty 5 homolog [Homo s	3	3	3.77	2E-05
1446	gi|73695475|r	protein BAP28 [Homo sapiens]	3	4	4.29	1E-05
1447	gi|31982941|r	KIAA0853 [Homo sapiens]	1	2	1.15	7E-06
1448	gi|14589953|r	PolII_Rpb8 (RNA polymerase II, poly	3	5	21.33	2E-04
1449	gi|39930469|r	brix domain containing 1 [Homo sapie	2	2	11.11	4E-05
1450	gi|16554627|r	WD repeat domain 5 [Homo sapiens]	3	7	15.57	1E-04
1452	gi|21361734|r	hypothetical protein LOC55683 [Hom	4	14	9.99	1E-04
1453	gi|20270371|r	hypothetical protein LOC134147 [Hor	2	4	13.88	9E-05
1454	gi|4506331|re	6-pyruvoyltetrahydropterin synthase [	1	5	6.21	2E-04
1455	gi|32698714|r	hypothetical protein LOC284058 [Hor	4	7	5.88	4E-05
1456	gi|31563334|r	forkhead box K2 isoform 2 [Homo sap	2	2	8.14	2E-05
1461	gi|5454106|re	TBP-related factor 10 [Homo sapiens	1	2	11.47	5E-05
1462	gi|5032173|re	nuclear receptor subfamily 2, group F	1	2	9.22	3E-05
1463	gi|6912398|re	general transcription factor IIIC, polyp	3	3	5.64	2E-05
1464	gi|57863269|r	hypothetical protein LOC23076 [Hom	2	3	4.75	2E-05
1465	gi|4758084|re	chondroitin sulfate proteoglycan 3 (ne	1	2	1.67	9E-06
1466	gi|13569879|r	acidic (leucine-rich) nuclear phospho	8	107	51.49	0.002
1467	gi|36287069|r	HIV-1 Tat interactive protein, 60kDa i	24	129	57.51	0.001
1468	gi|47824889|r	hypothetical protein LOC388272 [Hor	4	9	25.97	3E-04
1469	gi|4506773|re	S100 calcium-binding protein A9 [Ho	2	7	24.56	3E-04
1470	gi|29826282|r	protein phosphatase 1G [Homo sapie	8	13	24.18	1E-04
1472	gi|5453617|re	zinc finger, HIT domain containing 1 [	8	44	42.86	0.002
1473	gi|24308261|r	mesoderm induction early response 1	7	15	20.9	2E-04
1474	gi|56549696|r	E1A binding protein p400 [Homo sap	94	853	47.66	0.002
1475	gi|74136549|r	AT rich interactive domain 5B (MRF1	16	29	19.11	1E-04
1476	gi|40255020|r	hypothetical protein LOC64769 [Hom	8	58	36.82	0.002
1477	gi|8393159|re	calmodulin-like skin protein [Homo sa	1	3	15.75	1E-04
1478	gi|4507691|re	transformation/transcription domain-a	141	848	46.92	0.001
1479	gi|21361489|r	enhancer of polycomb homolog 2 [Ho	18	96	32.37	7E-04
1480	gi|8922764|re	MRG-binding protein [Homo sapiens]	18	224	87.75	0.006
1481	gi|13654270|r	LAS1-like [Homo sapiens]	4	7	12.4	5E-05
1482	gi|4502847|re	cold inducible RNA binding protein [H	1	4	12.21	1E-04
1483	gi|5453880|re	acidic (leucine-rich) nuclear phospho	2	4	11.65	9E-05
1484	gi|34452705|r	bromodomain containing 8 isoform 1	39	326	48.79	0.002
1485	gi|6912448|re	MORF-related gene X [Homo sapiens	24	399	65.63	0.008
1486	gi|16751921|r	dermcidin precursor [Homo sapiens]	1	2	10	1E-04
1487	gi|25777617|r	chromodomain protein, Y chromosom	3	5	9.2	5E-05
1489	gi|21359860|r	prothymosin, alpha (gene sequence 2	1	2	9.09	1E-04
1494	gi|21361659|r	importin 9 [Homo sapiens]	6	23	8.65	1E-04
1495	gi|4505185|re	macrophage migration inhibitory facto	1	2	7.83	1E-04
1496	gi|21327708|r	nucleosome assembly protein 1-like 1	3	9	17.65	1E-04
1498	gi|4502171|re	adenine phosphoribosyltransferase is	1	2	7.22	6E-05
1499	gi|5453567|re	craniofacial development protein 1 [H	1	2	7.02	4E-05
1500	gi|13376810|r	enhancer of polycomb 1 [Homo sapie	22	95	38.16	6E-04
1501	gi|29789415|r	juxtaposed with another zinc finger ge	1	5	6.58	1E-04
1502	gi|38201655|r	inhibitor of growth family, member 3 i	7	50	26.56	7E-04
1503	gi|8923059|re	mbt domain containing 1 [Homo sapie	8	22	24.15	3E-04
1504	gi|40255127|r	hypothetical protein LOC166968 [Hor	2	3	5.75	3E-05
1505	gi|21361499|r	SUMO1/sentrin/SMT3 specific protea	3	4	5.57	4E-05
1506	gi|7661952|re	squamous cell carcinoma antigen rec	3	4	6.96	2E-05
1507	gi|4506387|re	UV excision repair protein RAD23 ho	1	4	4.65	6E-05
1508	gi|4507521|re	transketolase [Homo sapiens]	5	5	17.34	5E-05
1509	gi|55769550|r	PHD finger protein 14 isoform 1 [Hom	2	3	4.11	2E-05
1510	gi|46358364|r	beta 3-glycosyltransferase-like [Homo	1	2	2.21	2E-05
1511	gi|41281573|r	bromo adjacent homology domain co	1	2	2.05	1E-05
1512	gi|6912752|re	zinc finger protein 281 [Homo sapiens	4	8	7.26	5E-05
1513	gi|40807477|r	retinoic acid induced 1 [Homo sapien	2	2	3.1	6E-06
1514	gi|32483416|r	neurofilament, heavy polypeptide 200	1	2	0.88	1E-05
1515	gi|4504345|re	alpha 2 globin [Homo sapiens]	4	17	36.62	7E-04
1517	gi|21702733|r	trinucleotide repeat containing 6A iso	1	2	1.07	6E-06
1519	gi|67782328|r	trinucleotide repeat containing 6B iso	2	3	2.96	1E-05
1520	gi|50592994|r	thioredoxin [Homo sapiens]	1	6	12.38	3E-04
1521	gi|17388799|r	DnaJ (Hsp40) homolog, subfamily B,	2	3	9.82	5E-05
1523	gi|41149143|r	PREDICTED: similar to ribosomal pro	1	3	3.94	8E-05
1542	gi|89030033|r	PREDICTED: hypothetical protein LC	13	95	35.52	0.001
1544	gi|89030031|r	PREDICTED: hypothetical protein LC	13	98	7.13	3E-04
1549	gi|32189392|r	peroxiredoxin 2 isoform a [Homo sap	2	4	14.65	1E-04
1551	gi|4758638|re	peroxiredoxin 6 [Homo sapiens]	2	4	11.61	1E-04
1552	gi|18375626|r	HLA-B associated transcript-2 isoforr	4	6	2.78	2E-05
1554	gi|4505293|re	MYB-related protein B [Homo sapiens	25	54	62	4E-04
1555	gi|4758486|re	general transcription factor IIA, 2 (12k	1	2	32.11	1E-04
1556	gi|67003578|r	hypothetical protein LOC91750 [Hom	2	6	31.03	3E-04
1557	gi|28144916|r	hypothetical protein LOC55957 [Hom	5	18	30.08	4E-04
1558	gi|32996737|r	lin-9 homolog [Homo sapiens]	10	51	29.75	5E-04
1559	gi|35493987|r	ubiquitin-conjugating enzyme E2I [Ho	3	6	34.18	2E-04
1563	gi|5803137|re	RNA binding motif protein 3 isoform a	2	9	31.85	3E-04
1565	gi|48928058|r	small ubiquitin-like modifier protein 3	2	3	18.45	2E-04
1573	gi|13775200|r	SF3b10 [Homo sapiens]	1	4	15.12	3E-04
1574	gi|14249398|r	PHD-finger 5A [Homo sapiens]	1	2	14.55	1E-04
1575	gi|4757880|re	BUB3 budding uninhibited by benzim	2	5	14.33	9E-05
1577	gi|5031957|re	polyglutamine binding protein 1 isofor	1	3	12.45	6E-05
1583	gi|8923444|re	nucleolar protein family A, member 2	1	4	12.42	1E-04
1584	gi|4503727|re	FK506-binding protein 3 [Homo sapie	4	9	31.25	2E-04
1585	gi|5031571|re	actin-related protein 2 isoform b [Hor	2	6	11.93	9E-05
1587	gi|21450832|r	hypothetical protein LOC220134 [Hor	1	3	11.76	7E-05
1588	gi|41281398|r	soc-2 suppressor of clear homolog [H	3	3	11.68	3E-05
1589	gi|8400738|re	tumor protein p53 [Homo sapiens]	3	5	16.54	7E-05
1590	gi|56549119|r	dynamin 2 isoform 3 [Homo sapiens]	6	12	10.51	8E-05
1592	gi|5032067|re	Sin3A-associated protein, 18kDa [Ho	1	2	10.46	7E-05
1593	gi|7657647|re	tropomodulin 2 (neuronal) [Homo sap	1	3	10.26	5E-05
1594	gi|6677723|re	replication factor C 5 isoform 1 [Hom	3	4	16.18	7E-05
1595	gi|33457332|r	RAVER1 [Homo sapiens]	2	3	10.07	3E-05
1596	gi|4758158|re	septin 2 [Homo sapiens]	5	11	24.1	2E-04
1600	gi|31563378|r	integrin beta 4 binding protein isoform	2	3	17.14	7E-05
1602	gi|4557491|re	cleavage stimulation factor subunit 1	3	6	19.95	8E-05
1605	gi|16306492|r	cell division cycle 2 protein isoform 2	2	10	16.67	2E-04
1607	gi|21264351|r	SWI/SNF-related matrix-associated a	3	5	10.74	6E-05
1608	gi|45505149|r	nuclear factor I/C isoform 1 [Homo sa	1	2	7.48	3E-05
1610	gi|4759156|re	small nuclear ribonucleoprotein polyp	5	8	30.85	2E-04
1611	gi|31542319|r	epsilon subunit of coatomer protein c	3	8	19.81	1E-04
1613	gi|7656991|re	coronin, actin binding protein, 1C [Ho	2	7	10.34	8E-05
1614	gi|42560246|r	RNA polymerase I subunit isoform 1 [	1	4	6.07	7E-05
1616	gi|41148718|r	PREDICTED: v-myb myeloblastosis v	2	3	5.98	2E-05
1622	gi|34485722|r	karyopherin alpha 3 [Homo sapiens]	1	2	5.57	2E-05
1623	gi|57863281|r	Meis1, myeloid ecotropic viral integra	1	3	5.23	4E-05
1624	gi|14211927|r	protein phosphatase 1, regulatory sul	2	2	4.9	1E-05
1625	gi|45331215|r	leucine zipper, putative tumor suppre	1	2	4.93	2E-05
1626	gi|20149709|r	heterogeneous nuclear ribonucleopro	3	4	7.75	4E-05
1627	gi|4507499|re	TIA-1 related protein isoform 1 [Homo	2	2	8.27	3E-05
1628	gi|8922358|re	PRP38 pre-mRNA processing factor	2	2	8.06	2E-05
1629	gi|5729939|re	cleavage and polyadenylation specifi	1	2	4.46	4E-05
1630	gi|88942850|r	PREDICTED: similar to 40S ribosoma	4	23	21.43	4E-04
1641	gi|21040255|r	splicing factor, arginine/serine-rich 12	2	5	7.28	6E-05
1642	gi|41393554|r	LUC7-like isoform b [Homo sapiens]	1	3	4.31	5E-05
1644	gi|21218438|r	GATA zinc finger domain containing	4	10	11.64	1E-04
1645	gi|5902034|re	periodic tryptophan protein 1 [Homo s	1	3	4.19	3E-05
1646	gi|52630449|r	ubiquitin specific protease 48 isoform	2	2	3.86	1E-05
1647	gi|50980301|r	myosin phosphatase-Rho interacting	2	3	3.71	2E-05
1649	gi|4505317|re	protein phosphatase 1, regulatory (in	5	11	10	6E-05
1650	gi|5032169|re	telomeric repeat binding factor 2 [Hor	2	2	6.8	2E-05
1651	gi|12746590|r	C-terminal binding protein 2 isoform 2	1	2	3.35	1E-05
1653	gi|22027651|r	adaptor-related protein complex 1 be	2	3	4.32	2E-05
1655	gi|21361399|r	alpha isoform of regulatory subunit A,	2	2	6.62	2E-05
1656	gi|66346679|r	SERPINE1 mRNA binding protein 1 i	6	9	18.87	1E-04
1660	gi|5453591|re	structural maintenance of chromosom	3	3	3.68	1E-05
1661	gi|68303639|r	CUG triplet repeat, RNA binding prote	2	2	5.7	2E-05
1664	gi|30410720|r	Sec3 isoform 1 [Homo sapiens]	1	4	2.46	3E-05
1666	gi|21071058|r	SWI/SNF-related matrix-associated a	2	5	2.38	3E-05
1667	gi|11415036|r	zinc finger protein 148 (pHZ-52) [Hor	2	3	3.4	2E-05
1668	gi|62244004|r	modulator of estrogen induced transc	2	2	3.54	1E-05
1670	gi|42476007|r	hypothetical protein FLJ34922 [Homo	1	2	1.89	1E-05
1671	gi|11345460|r	hypothetical protein LOC60558 [Hom	1	3	1.79	3E-05
1672	gi|11496982|r	supervillin isoform 2 [Homo sapiens]	2	3	1.67	8E-06
1674	gi|44890068|r	zinc finger protein 262 [Homo sapiens	2	2	1.68	7E-06
1675	gi|41281518|r	hypothetical protein LOC9897 [Homo	1	4	1.73	2E-05
1676	gi|18644728|r	nucleolar RNA-associated protein alp	2	2	3.75	1E-05
1678	gi|4505917|re	exosome component 10 isoform 2 [H	1	2	1.74	1E-05
1680	gi|10835055|r	cell division cycle 2-like 1 (PITSLRE	1	2	1.64	1E-05
1694	gi|62243696|r	stromal antigen 1 [Homo sapiens]	2	2	2.15	9E-06
1695	gi|4507857|re	ubiquitin specific protease 7 (herpes	3	3	4.36	2E-05
1696	gi|24430149|r	nucleoporin 155kDa isoform 1 [Homo	2	3	2.88	1E-05
1698	gi|21264565|r	AT rich interactive domain 1A (SWI- l	2	2	1.53	5E-06
1700	gi|56549668|r	AT rich interactive domain 2 (ARID, R	2	4	2.02	1E-05
1701	gi|28559039|r	MEDIATOR_TRAP220 {peroxisome	3	4	3.98	1E-05
1702	gi|7662018|re	PHD finger protein 3 [Homo sapiens]	4	6	4.9	2E-05
1703	gi|32967601|r	ankyrin 3 isoform 1 [Homo sapiens]	2	2	0.87	3E-06
1704	gi|33504573|r	hypothetical protein LOC347918 [Hor	7	28	27.44	4E-04
1705	gi|17933772|r	S100 calcium binding protein A16 [Ho	4	16	53.4	9E-04
1706	gi|4827071|re	zinc finger protein 9 [Homo sapiens]	2	4	14.12	1E-04
1707	gi|42558250|r	membrane component chromosome	4	10	13.4	8E-05
1709	gi|42519916|r	forkhead box O3A [Homo sapiens]	2	2	6.54	2E-05
1711	gi|89052386|r	PREDICTED: widely-interspaced zinc	4	10	8.74	7E-05
1713	gi|33598968|r	LIM domain only 7 [Homo sapiens]	4	10	4.74	4E-05
1714	gi|4506699|re	ribosomal protein S21 [Homo sapiens	3	30	30.12	0.002
1715	gi|30410781|r	hypothetical protein LOC65095 isofor	9	18	27.58	2E-04
1717	gi|31083035|r	mitochondrial ribosomal protein L52 i	1	3	26.83	1E-04
1719	gi|4759276|re	RNA, U3 small nucleolar interacting p	8	41	31.58	5E-04
1720	gi|4506621|re	ribosomal protein L26 [Homo sapiens	3	5	22.07	2E-04
1721	gi|15147219|r	purine-rich element binding protein B	2	3	20.19	5E-05
1722	gi|9910244|re	mitochondrial ribosomal protein S22 [	4	9	19.72	1E-04
1723	gi|41148736|r	PREDICTED: similar to 40S ribosoma	4	17	19.66	3E-04
1730	gi|7705805|re	mitochondrial ribosomal protein S2 [H	2	3	18.92	6E-05
1731	gi|16950609|r	mitochondrial ribosomal protein S27 [	4	5	16.67	7E-05
1732	gi|7705738|re	mitochondrial ribosomal protein S7 [H	3	10	14.88	2E-04
1733	gi|16950603|r	mitochondrial ribosomal protein S35 [	2	4	14.24	7E-05
1734	gi|4506587|re	replication protein A3, 14kDa [Homo s	2	4	29.75	2E-04
1735	gi|7662645|re	mitochondrial ribosomal protein S18B	1	2	12.79	4E-05
1736	gi|4505941|re	PolII_Rpb2 {DNA directed RNA polym	9	24	11.84	1E-04
1737	gi|64368880|r	zinc finger protein 498 [Homo sapiens	2	2	9.74	2E-05
1738	gi|37588859|r	ring finger protein 41 isoform 2 [Hom	1	2	9.35	5E-05
1741	gi|14269586|r	mitochondrial ribosomal protein S26 [	1	2	8.78	6E-05
1742	gi|47271406|r	bin3, bicoid-interacting 3 [Homo sapie	4	12	13.5	1E-04
1743	gi|4503659|re	ubiquitin-like protein fubi and ribosom	2	5	8.27	2E-04
1744	gi|53759145|r	G-rich RNA sequence binding factor 1	2	3	5.19	4E-05
1745	gi|4557237|re	acetyl-Coenzyme A acetyltransferase	2	3	8.67	4E-05
1746	gi|42476127|r	polymerase (RNA) III (DNA directed)	2	3	4.15	2E-05
1747	gi|20336290|r	DEAH (Asp-Glu-Ala-His) box polypep	2	2	3.46	1E-05
1749	gi|4503265|re	dihydrolipoamide branched chain tran	1	3	3.53	4E-05
1750	gi|7705365|re	RNA binding motif protein 19 [Homo s	2	2	3.13	1E-05
1751	gi|18375637|r	HLA-B associated transcript 8 isoform	1	3	1.16	1E-05
1753	gi|89034039|r	PREDICTED: similar to heterogeneou	2	2	3.21	2E-05
1755	gi|22094079|r	thyroid hormone receptor interactor 3	4	11	34.19	4E-04
1756	gi|6912542|re	nuclear fragile X mental retardation p	9	42	18.38	5E-04
1757	gi|20149643|r	hypothetical protein LOC54680 [Hom	7	25	20	3E-04
1758	gi|46430495|r	basonuclin 2 [Homo sapiens]	2	2	3.43	1E-05
1759	gi|89037890|r	PREDICTED: similar to Ig gamma-1 c	2	5	4	5E-05
1760	gi|89062143|r	PREDICTED: similar to Ig gamma-4 c	2	5	8.84	7E-05
1761	gi|5729933|re	septin 9 [Homo sapiens]	4	5	13.73	5E-05
1762	gi|13375885|r	chromosome 14 open reading frame	2	2	5.62	2E-05
1763	gi|30795220|r	crooked neck-like 1 protein [Homo sa	1	2	1.65	1E-05
1764	gi|42716280|r	high density lipoprotein binding protei	2	3	2.29	1E-05
1766	gi|22202633|r	prefoldin 5 isoform alpha [Homo sapi	5	20	43.51	7E-04
1767	gi|4507873|re	von Hippel-Lindau binding protein 1 [	6	14	38.58	4E-04
1768	gi|24307981|r	exosome component 7 [Homo sapien	2	2	11.68	4E-05
1769	gi|4502801|re	regulator of chromosome condensati	2	2	9.74	3E-05
1770	gi|4757900|re	calreticulin precursor [Homo sapiens]	2	6	11.99	8E-05
1771	gi|33239451|r	proliferating cell nuclear antigen [Hor	1	2	8.05	4E-05
1773	gi|4507669|re	tumor protein, translationally-controlle	1	3	7.56	1E-04
1777	gi|21536449|r	prefoldin 1 [Homo sapiens]	1	3	7.38	1E-04
1778	gi|4758556|re	PRP3 pre-mRNA processing factor 3	3	4	11.86	3E-05
1779	gi|71143137|r	high-mobility group box 3 [Homo sapi	1	2	7	6E-05
1782	gi|50363217|r	serine (or cysteine) proteinase inhibit	2	3	6.94	4E-05
1785	gi|4826762|re	haptoglobin [Homo sapiens]	2	2	6.65	3E-05
1786	gi|4503609|re	electron-transfer-flavoprotein, beta po	1	2	6.67	4E-05
1788	gi|4502013|re	adenylate kinase 2 isoform a [Homo s	1	2	6.69	5E-05
1790	gi|31543653|r	signal recognition particle 14kDa (hor	1	2	6.62	8E-05
1791	gi|13376623|r	Ngg1 interacting factor 3 like 1 bindin	1	2	6.37	6E-05
1792	gi|31543419|r	polynucleotide kinase 3'-phosphatase	2	2	5.95	2E-05

1793	gi|4557321|re	apolipoprotein A-I preproprotein [Hom	1	2	5.99	4E-05	X	X	X	X	X	X	X	X	267	30778	5.8	N
1794	gi|45006986|r	small inducible cytokine subfamily E,	1	3	5.77	5E-05	X	X	X	X	X	X	X	X	312	34353	8.4	N
1795	gi|33469968|r	minichromosome maintenance protei	6	13	13.91	1E-04	X	X	X	X	X	X	X	X	719	81308	6.5	N
1796	gi|5454004|re	D4, zinc and double PHD fingers fam	2	3	8.7	4E-05	X	X	X	X	X	X	X	X	391	44156	6.3	N
1797	gi|4505257|re	moesin [Homo sapiens]	6	11	13	1E-04	X	X	X	X	X	X	X	X	577	67820	6.4	N
1798	gi|4507215|re	signal recognition particle 54kDa [Hor	2	4	5.16	5E-05	X	X	X	X	X	X	X	X	504	55705	8.8	N
1800	gi|17975755|r	male-specific lethal 3-like 1 isoform d	1	2	5.05	3E-05	X	X	X	X	X	X	X	X	416	47950	8.4	N
1806	gi|7706427|re	cleavage and polyadenylation specifi	2	4	6.14	3E-05	X	X	X	X	X	X	X	X	684	77486	5.6	N
1807	gi|4557871|re	transferrin [Homo sapiens]	2	3	4.3	2E-05	X	X	X	X	X	X	X	X	698	77050	7.1	N
1808	gi|6912400|re	general transcription factor IIIC, polyp	2	6	4.14	4E-05	X	X	X	X	X	X	X	X	822	92001	6.7	N
1809	gi|7661892|re	REST corepressor 1 [Homo sapiens]	1	3	4.15	4E-05	X	X	X	X	X	X	X	X	482	53028	7	N
1811	gi|48255889|r	protein kinase C substrate 80K-H isof	1	3	3.98	3E-05	X	X	X	X	X	X	X	X	528	59425	4.4	N
1813	gi|41281437|r	nucleoporin 93kDa [Homo sapiens]	1	2	3.91	1E-05	X	X	X	X	X	X	X	X	819	93557	5.8	N
1814	gi|18379349|r	vesicle amine transport protein 1 [Hor	1	2	3.82	3E-05	X	X	X	X	X	X	X	X	393	41920	6.3	N
1815	gi|4557343|re	antiquitin [Homo sapiens]	17	46	59.1	5E-04	X	X	X	X	X	X	X	X	511	55366	6.9	N
1816	gi|88988849|r	PREDICTED: similar to antiquitin [Ho	15	42	40.68	3E-04	X	X	X	X	X	X	X	X	703	75909	8.9	N
1817	gi|56788366|r	phosphatidylinositol-binding clathrin a	3	4	9.2	3E-05	X	X	X	X	X	X	X	X	652	70755	7.9	N
1819	gi|8923609|re	nuclear protein localization 4 [Homo s	1	3	2.96	3E-05	X	X	X	X	X	X	X	X	608	68183	6.3	N
1820	gi|4504035|re	guanine monophosphate synthetase	2	2	5.34	2E-05	X	X	X	X	X	X	X	X	693	76715	6.9	N
1821	gi|4503523|re	eukaryotic translation initiation factor	2	2	6.02	2E-05	X	X	X	X	X	X	X	X	548	63973	6	N
1822	gi|48762926|r	PWP2 periodic tryptophan protein ho	1	2	2.29	1E-05	X	X	X	X	X	X	X	X	919	102452	6.1	N
1823	gi|42542392|r	CCAAT/enhancer binding protein zeta	2	3	4.17	2E-05	X	X	X	X	X	X	X	X	1054	120974	5.9	N
1824	gi|4759172|re	splicing factor, arginine/serine-rich 2,	2	6	3.31	3E-05	X	X	X	X	X	X	X	X	1148	128875	8.3	N
1825	gi|5453998|re	importin 7 [Homo sapiens]	2	3	3.08	2E-05	X	X	X	X	X	X	X	X	1038	119516	4.8	N
1826	gi|4557385|re	complement component 3 precursor [	5	13	5.17	4E-05	X	X	X	X	X	X	X	X	1663	187163	6.4	N
1827	gi|31083367|r	SEC8 protein [Homo sapiens]	2	2	2.87	1E-05	X	X	X	X	X	X	X	X	974	110507	6.5	N
1828	gi|89056848|r	PREDICTED: hypothetical protein LO	1	3	1.23	1E-05	X	X	X	X	X	X	X	X	1303	140256	6.3	N
1830	gi|13259508|r	dynactin 1 isoform 2 [Homo sapiens]	2	2	2.71	1E-05	X	X	X	X	X	X	X	X	1144	127404	5.4	N
1833	gi|4557469|re	adaptor-related protein complex 2, be	2	2	3.31	1E-05	X	X	X	X	X	X	X	X	937	104553	5.4	N
1834	gi|4504349|re	beta globin [Homo sapiens]	10	24	70.75	9E-04	X	X	X	X	X	X	X	X	147	15998	7.3	N
1835	gi|21614544|r	S100 calcium-binding protein A8 [Hor	3	4	33.33	2E-04	X	X	X	X	X	X	X	X	93	10834	7	N
1836	gi|NTAP-BHD	N-terminal TAP-tagged BHD Mutant [	8	95	13.06	8E-04	X	X	X	X	X	X	X	X	651	72628	6.2	N
1838	gi|51988900|r	XPG-complementing protein [Homo s	24	77	32.8	4E-04	X	X	X	X	X	X	X	X	1186	133307	5.3	N
1839	gi|21359867|r	cytochrome c-1 [Homo sapiens]	5	28	23.08	5E-04	X	X	X	X	X	X	X	X	325	35390	9	N
1840	gi|4758086|re	cysteine and glycine-rich protein 1 [H	4	11	33.16	3E-04	X	X	X	X	X	X	X	X	193	20567	8.6	N
1841	gi|13236583|r	BRCA1/BRCA2-containing complex s	3	4	12.34	7E-05	X	X	X	X	X	X	X	X	316	36072	5.9	N
1848	gi|4506783|re	sin3 associated polypeptide p30 [Hon	1	2	5.45	5E-05	X	X	X	X	X	X	X	X	220	23306	9.2	N
1849	gi|8923405|re	RNA (guanine-9-) methyltransferase (	2	4	10.32	9E-05	X	X	X	X	X	X	X	X	252	29591	9.2	N
1850	gi|42476130|r	retinoid x receptor interacting protein	6	12	15.72	9E-05	X	X	X	X	X	X	X	X	719	79728	5.4	N
1851	gi|42544179|r	Cip1-interacting zinc finger protein [H	4	6	8.13	4E-05	X	X	X	X	X	X	X	X	898	100045	6.1	N
1852	gi|21361171|r	brain and reproductive organ-express	1	3	3.37	4E-05	X	X	X	X	X	X	X	X	415	46974	6.1	N
1857	gi|15147335|r	nuclear receptor coactivator 5 [Homo	2	4	7.25	4E-05	X	X	X	X	X	X	X	X	579	65536	9.6	N
1859	gi|5174745|re	ubiquinol-cytochrome c reductase hin	1	16	19.78	0.001	X	X	X	X	X	X	X	X	91	10755	4.4	N
1860	gi|4505119|re	methyl-CpG binding domain protein 3	2	3	18.9	6E-05	X	X	X	X	X	X	X	X	291	32844	5.3	N
1861	gi|4504517|re	heat shock 27kDa protein 1 [Homo sa	2	3	26.34	8E-05	X	X	X	X	X	X	X	X	205	22783	6.4	N
1862	gi|14141170|r	metastasis-associated protein 2 [Hom	7	11	18.86	9E-05	X	X	X	X	X	X	X	X	668	75023	9.7	N
1863	gi|7706499|re	DNA directed RNA polymerase III pol	1	2	12.96	1E-04	X	X	X	X	X	X	X	X	108	12320	7.8	N
1864	gi|19923502|r	GATA zinc finger domain containing 2	2	4	10	5E-05	X	X	X	X	X	X	X	X	490	52513	10.5	N
1865	gi|5453682|re	HMBA-inducible [Homo sapiens]	1	2	10.03	3E-05	X	X	X	X	X	X	X	X	359	40623	4.9	N
1866	gi|4505117|re	methyl-CpG binding domain protein 2	1	4	9.49	6E-05	X	X	X	X	X	X	X	X	411	43255	10	N
1867	gi|5454024|re	ribonuclease P (30kD) [Homo sapiens	3	3	21.64	6E-05	X	X	X	X	X	X	X	X	268	29321	8.9	N
1868	gi|11496885|r	enigma protein isoform 1 [Homo sapi	1	2	8.32	2E-05	X	X	X	X	X	X	X	X	457	49845	8.4	N
1870	gi|68160937|r	tripartite motif-containing 25 [Homo sa	4	7	9.68	6E-05	X	X	X	X	X	X	X	X	630	70974	8.1	N
1871	gi|6006001|re	plasma glutathione peroxidase 3 prec	1	2	7.52	5E-05	X	X	X	X	X	X	X	X	226	25402	8.1	N
1872	gi|75709192|r	hypothetical protein LOC29086 [Hom	1	2	6.99	3E-05	X	X	X	X	X	X	X	X	329	36560	4.6	N
1874	gi|19923106|r	paraoxonase 1 [Homo sapiens]	1	2	6.76	3E-05	X	X	X	X	X	X	X	X	355	39731	5.2	N
1875	gi|4504195|re	general transcription factor IIE, polype	1	2	6.53	4E-05	X	X	X	X	X	X	X	X	291	33044	9.7	N
1876	gi|31543212|r	macrophage stimulating 1 (hepatocyt	2	14	5.77	1E-04	X	X	X	X	X	X	X	X	711	80320	7.7	N
1877	gi|73623028|r	carnitine palmitoyltransferase 1A isof	1	3	5.16	2E-05	X	X	X	X	X	X	X	X	756	86239	8.4	N
1879	gi|4503635|re	coagulation factor II precursor [Homo	2	5	4.98	5E-05	X	X	X	X	X	X	X	X	622	70037	5.9	N
1880	gi|21361331|r	carbamoyl-phosphate synthetase 1, r	4	6	4.87	2E-05	X	X	X	X	X	X	X	X	1500	164939	6.7	N
1881	gi|8922532|re	family with sequence similarity 82, me	1	3	4.89	4E-05	X	X	X	X	X	X	X	X	470	52118	5.1	N
1882	gi|27363457|r	aarF domain containing kinase 4 [Hor	1	2	4.04	2E-05	X	X	X	X	X	X	X	X	544	60070	7.2	N
1883	gi|31542539|r	DnaJ (Hsp40) homolog, subfamily A,	2	2	8.33	2E-05	X	X	X	X	X	X	X	X	480	52538	9.3	N
1884	gi|18201911|r	vitronectin precursor [Homo sapiens]	1	2	3.35	2E-05	X	X	X	X	X	X	X	X	478	54336	5.8	N
1885	gi|6005872|re	SEC63-like protein [Homo sapiens]	1	2	2.76	1E-05	X	X	X	X	X	X	X	X	760	87997	5.3	N
1886	gi|12229217|r	activity-dependent neuroprotector [Ho	1	2	2.36	1E-05	X	X	X	X	X	X	X	X	1102	123563	7.3	N
1888	gi|26051278|r	nuclear pore membrane protein 121 [	1	2	2.44	1E-05	X	X	X	X	X	X	X	X	984	99037	9.8	N
1889	gi|38016947|r	complement component 5 [Homo sap	2	5	2.21	2E-05	X	X	X	X	X	X	X	X	1676	188304	6.5	N
1890	gi|21735569|r	claspin [Homo sapiens]	2	3	2.17	1E-05	X	X	X	X	X	X	X	X	1339	151093	4.8	N
1891	gi|41281612|r	hypothetical protein LOC283489 [Hor	1	2	1.97	1E-05	X	X	X	X	X	X	X	X	812	89099	8.4	N
1892	gi|67782358|r	complement factor B preproprotein [H	1	2	1.83	1E-05	X	X	X	X	X	X	X	X	764	85533	7.1	N
1893	gi|19923597|r	mSin3A-associated protein 130 [Hom	1	2	1.15	1E-05	X	X	X	X	X	X	X	X	1048	110324	9.8	N
1894	gi|22538461|r	nuclear receptor co-repressor 1 [Hom	3	5	2.34	1E-05	X	X	X	X	X	X	X	X	2440	270207	7.1	N
1895	gi|67190748|r	complement component 4A prepropr	1	2	0.69	7E-06	X	X	X	X	X	X	X	X	1744	192784	7.1	N
1896	gi|14211843|r	short coiled-coil protein [Homo sapien	3	16	44.26	7E-04	X	X	X	X	X	X	X	X	122	13895	4.8	N
1897	gi|4759154|re	synaptosomal-associated protein 29 [	5	10	27.13	2E-04	X	X	X	X	X	X	X	X	258	28970	5.8	N
1898	gi|89040213|r	PREDICTED: hypothetical protein XP	1	2	18.03	6E-05	X	X	X	X	X	X	X	X	183	20343	5.6	N
1899	gi|19923935|r	hypothetical protein LOC112869 [Hor	2	2	16.72	4E-05	X	X	X	X	X	X	X	X	293	33238	8.1	N
1900	gi|21361350|r	serologically defined colon cancer an	3	4	16.38	6E-05	X	X	X	X	X	X	X	X	354	39038	4.8	N
1901	gi|14249500|r	transforming growth factor beta regula	1	2	13.08	4E-05	X	X	X	X	X	X	X	X	260	29157	6.9	N
1902	gi|8923092|re	glutaminyl-peptide cyclotransferase-li	2	3	12.04	4E-05	X	X	X	X	X	X	X	X	382	42864	9.8	N
1903	gi|13435356|r	HCLS1 associated protein X-1 isofor	1	2	8.6	4E-05	X	X	X	X	X	X	X	X	279	31621	4.9	N
1905	gi|38049014|r	semenogelin I isoform b preproprotei	2	3	5.97	4E-05	X	X	X	X	X	X	X	X	402	45297	9.3	N
1907	gi|4505047|re	lumican precursor [Homo sapiens]	1	2	5.33	3E-05	X	X	X	X	X	X	X	X	338	38429	6.6	N
1908	gi|73747799|r	suppressor of actin mutations 2-like [	1	2	3.73	2E-05	X	X	X	X	X	X	X	X	723	82221	6	N
1909	gi|63252886|r	prolyl 4-hydroxylase, alpha I subunit i	3	6	8.43	6E-05	X	X	X	X	X	X	X	X	534	60967	6	N
1911	gi|4502005|re	alpha-2-HS-glycoprotein [Homo sapie	2	2	3.54	3E-05	X	X	X	X	X	X	X	X	367	39325	5.7	N
1912	gi|50582989|r	IQ motif and Sec7 domain 1 [Homo s	1	2	2.18	1E-05	X	X	X	X	X	X	X	X	963	108314	6.9	N
1913	gi|16753233|r	talin 1 [Homo sapiens]	2	2	1.81	4E-06	X	X	X	X	X	X	X	X	2541	269665	6	N
1914	gi|22748937|r	exportin 5 [Homo sapiens]	1	2	1.66	9E-06	X	X	X	X	X	X	X	X	1204	136311	5.8	N
1915	gi|4504951|re	laminin, beta 1 precursor [Homo sapi	1	2	1.23	6E-06	X	X	X	X	X	X	X	X	1786	198065	5	N
1916	gi|4506355|re	pregnancy-zone protein [Homo sapie	1	2	0.81	8E-06	X	X	X	X	X	X	X	X	1482	163835	6.4	N
1917	gi|13376798|r	hypothetical protein LOC80304 [Hom	13	38	29.4	3E-04	X	X	X	X	X	X	X	X	721	79136	6.7	N
1918	gi|7656936|re	zinc finger, HIT domain containing 2 [	24	368	65.76	0.005	X	X	X	X	24	358	65.76	0.091	403	42884	6	N
1920	gi|89041101|r	PREDICTED: hypothetical protein XP	1	3	2.67	5E-05	X	X	X	X	X	X	X	X	375	40778	8.7	N
1922	gi|4502787|re	glycoprotein hormones, alpha polype	1	2	10.34	1E-04	X	X	X	X	X	X	X	X	116	13075	8.2	N
1923	gi|44681484|r	cell division cycle associated 2 [Hom	2	3	5.67	2E-05	X	X	X	X	X	X	X	X	1023	112676	8.4	N
1924	gi|17402907|r	tripartite motif protein TRIM29 isoforn	2	3	4.74	3E-05	X	X	X	X	X	X	X	X	570	63844	7	N
1926	gi|7661790|re	hypothetical protein LOC29080 [Hom	1	2	4.56	5E-05	X	X	X	X	X	X	X	X	241	28660	9.9	N
1927	gi|16579828|r	zinc finger protein 91 isoform 1 [Hom	1	2	4.39	2E-05	X	X	X	X	X	X	X	X	570	63445	7.4	N
1929	gi|40255237|r	leucine zipper protein 5 [Homo sapier	4	6	5.62	3E-05	X	X	X	X	X	X	X	X	1156	132195	6.8	N
1930	gi|45356151|r	KIAA0056 protein [Homo sapiens]	3	5	4.07	2E-05	X	X	X	X	X	X	X	X	1498	168890	7.5	N
1931	gi|24430146|r	nucleoporin 153kDa [Homo sapiens]	3	6	3.93	2E-05	X	X	X	X	X	X	X	X	1475	153938	8.7	N
1932	gi|40254967|r	hypothetical protein LOC79832 [Hom	1	2	1.98	9E-06	X	X	X	X	X	X	X	X	1315	143709	6.6	N
1933	gi|67551265|r	transcription factor ELYS [Homo sapi	2	3	1.68	8E-06	X	X	X	X	X	X	X	X	2266	252496	6.6	N
1934	gi|39652628|r	hypothetical protein LOC23196 [Hom	1	2	1.52	1E-05	X	X	X	X	X	X	X	X	1118	121888	8.9	N
1935	gi|56550039|r	myeloid/lymphoid or mixed-lineage le	1	2	0.5	3E-06	X	X	X	X	X	X	X	X	3969	431768	9.1	N
1936	gi|17158023|r	hypothetical protein LOC85395 [Hom	1	2	10.43	5E-05	X	X	X	X	X	X	X	X	230	25456	11.1	N
1937	gi|5032161|re	elongin C [Homo sapiens]	2	2	26.79	1E-04	X	X	X	X	X	X	X	X	112	12473	4.8	N
1938	gi|7662502|re	malignant T cell amplified sequence 1	2	4	21.55	1E-04	X	X	X	X	X	X	X	X	181	20555	8.8	N
1939	gi|23110925|r	proteasome beta 6 subunit [Homo sa	1	2	16.32	5E-05	X	X	X	X	X	X	X	X	239	25358	4.9	N
1940	gi|4502389|re	barrier to autointegration factor 1 [Ho	1	2	15.73	1E-04	X	X	X	X	X	X	X	X	89	10059	6.1	N
1943	gi|4506193|re	proteasome beta 1 subunit [Homo sa	2	2	14.11	5E-05	X	X	X	X	X	X	X	X	241	26489	8.1	N
1944	gi|5174659|re	S100 calcium binding protein A13 [Ho	1	2	12.24	1E-04	X	X	X	X	X	X	X	X	98	11471	6.2	N
1949	gi|27765083|r	calpastatin isoform a [Homo sapiens]	3	3	12.15	2E-05	X	X	X	X	X	X	X	X	708	76573	5.1	N
1951	gi|38570081|r	CUG triplet repeat, RNA-binding prote	2	3	10.14	4E-05	X	X	X	X	X	X	X	X	483	51617	8.5	N
1954	gi|4502899|re	clathrin, light polypeptide A isoform a	1	2	9.63	5E-05	X	X	X	X	X	X	X	X	218	23662	4.5	N
1955	gi|22538467|r	proteasome beta 4 subunit [Homo sa	1	2	9.09	4E-05	X	X	X	X	X	X	X	X	264	29204	6	N
1956	gi|4506203|re	proteasome beta 7 subunit proprotein	1	2	7.22	4E-05	X	X	X	X	X	X	X	X	277	29965	7.7	N
1957	gi|4502101|re	annexin I [Homo sapiens]	1	2	6.94	3E-05	X	X	X	X	X	X	X	X	346	38714	7	N
1958	gi|31795538|r	replication factor C 3 isoform 2 [Hom	1	2	6.93	6E-05	X	X	X	X	X	X	X	X	202	22710	9	N
1960	gi|21361918|r	leucine proline-enriched proteoglycan	2	3	6.34	2E-05	X	X	X	X	X	X	X	X	804	90544	5.8	N
1961	gi|88998579|r	PREDICTED: similar to lactate dehyd	1	5	6.27	1E-04	X	X	X	X	X	X	X	X	271	29390	8.2	N
1964	gi|19923399|r	Ras-GTPase activating protein SH3 d	2	2	6.22	2E-05	X	X	X	X	X	X	X	X	482	54121	5.6	N
1967	gi|24430160|r	proteasome 26S ATPase subunit 6 [H	2	2	5.91	3E-05	X	X	X	X	X	X	X	X	389	44173	7.5	N
1968	gi|13540523|r	nucleosomal binding protein 1 [Homo	1	2	5.32	4E-05	X	X	X	X	X	X	X	X	282	31525	4.6	N
1969	gi|54124343|r	hypothetical protein LOC387680 [Hor	2	3	3.06	1E-05	X	X	X	X	X	X	X	X	1341	147183	4.8	N
1972	gi|21361437|r	HIV TAT specific factor 1 [Homo sapi	2	3	2.78	2E-05	X	X	X	X	X	X	X	X	755	85853	4.4	N
1973	gi|17505234|r	nucleolar and spindle associated prot	1	2	2.73	3E-05	X	X	X	X	X	X	X	X	440	49324	9.9	N
1975	gi|8922557|re	solute carrier family 4 (anion exchang	1	2	2.64	1E-05	X	X	X	X	X	X	X	X	796	88945	5.2	N
1976	gi|17505907|r	DEAD (Asp-Glu-Ala-Asp) box polype	1	2	2	1E-05	X	X	X	X	X	X	X	X	851	94087	10	N
1978	gi|4503351|re	DNA (cytosine-5-)-methyltransferase	2	3	1.92	1E-05	X	X	X	X	X	X	X	X	1616	183164	7.8	N
1979	gi|31652264|r	cutaneous T-cell lymphoma tumor an	1	2	1.43	1E-05	X	X	X	X	X	X	X	X	980	110666	9.1	N
1980	gi|51467601|r	PREDICTED: hypothetical protein LO	1	2	1.12	9E-06	X	X	X	X	X	X	X	X	1337	145904	5.5	N
1982	gi|71044479|r	death inducer-obliterator 1 isoform c [	1	2	0.67	5E-06	X	X	X	X	X	X	X	X	2240	243840	7.9	N
1983	gi|18034690|r	hypothetical protein LOC25980 [Hom	2	4	10.16	6E-05	X	X	X	X	2	4	10.16	0.001	384	43472	6	N
1984	gi|21071006|r	tumor suppressing subtransferable ca	2	4	9.42	7E-05	X	X	X	X	2	4	9.42	0.001	329	34326	5.2	N
1985	gi|42476022|r	hypothetical protein LOC55622 [Hom	3	9	6.52	6E-05	X	X	X	X	3	9	6.52	0.001	843	96632	5.6	N
1986	gi|6005784|re	suppressor of S. cerevisiae gcr2 [Hor	2	3	4.5	3E-05	X	X	X	X	2	3	4.5	5E-04	644	72758	4.9	N
		Total Spc		69291				1318				3424						
		FDR (%)		0.066				0.152				0.117						
		SHUFFLED_Spc		23				1				2						
140	SHUFFLED_g	FALSE POSITIVE	1	2	2.26	X	1	1	2.26	X	X	X	X	X	619	71527	5.9	N
1012	SHUFFLED_g	FALSE POSITIVE	1	5	1.63	X	X	X	X	X	X	X	X	X	492	53132	9.4	N
1326	SHUFFLED_g	FALSE POSITIVE	1	2	0.68	X	X	X	X	X	X	X	X	X	1036	113738	5.2	N
1843	SHUFFLED_g	FALSE POSITIVE	1	3	5.98	X	X	X	X	X	X	X	X	X	251	28638	7.8	N
1845	SHUFFLED_g	FALSE POSITIVE	1	3	5.96	X	X	X	X	X	X	X	X	X	151	16311	11.9	N
1858	SHUFFLED_g	FALSE POSITIVE	1	2	1.05	X	X	X	X	X	X	X	X	X	1147	124824	8.8	N
1919	SHUFFLED_g	FALSE POSITIVE	1	2	3.57	X	X	X	X	X	X	X	X	X	364	40315	9.5	N
1921	SHUFFLED_g	FALSE POSITIVE	1	2	0.46	X	X	X	X	X	X	X	X	X	3677	383851	7.3	N
1987	SHUFFLED_g	FALSE POSITIVE	1	2	4.37	X	X	X	X	X	1	2	4.37	X	641	68454	7.5	N

Supporting Table 1B. Detailed List of Proteins and Peptides Detected in the Combined Human TIP49a/b Dataset.

Proteins with peptides passing the selection criteria described in the table below are listed by decreasing sequence coverage (percent of the protein sequence covered by the detected peptides).

Criteria Set	Parameter	Value
	Minimum +1 XCorr	1.8
	Minimum +2 XCorr	2.5
	Minimum +3 XCorr	3.5
	Minimum DeltCN	0.08
	Minimum charge state	1
	Maximum charge state	3
	Minimum ion proportion	0
	Maximum Sp rank	10
	Minimum Sp score	-1
	Modified peptide inclusion	Include
	Tryptic status requirement	Full
	Multiple, ambiguous IDs allowed	FALSE
	Minimum sequence length	7
	Maximum sequence length	100
	Sequence completeness required	0
	Purge duplicate peptides by protein	XCorr
	nclude only loci with unique peptide	FALSE
	Remove subset proteins	TRUE
	Exclude protein names matching	Contaminant
	clude protein descriptions matching	KERATIN
	inimum modified peptides per locus	0
	m redundancy for low coverage loci	2
	Minimum peptides per locus	2

Locus	**Sequence Count**	**Spectrum Count**	**Sequence Coverage**	**Length**	**MW**	**pI**	**Description**				
Unique	**FileName**	**XCorr**	**DeltCN**	**M+H+**	**CalcM+H+**	**TotalIntensity**	**SpRank**	**SpScore**	**IonProportion**	**Redundancy**	**Sequence**
gi|Flag_peptid	2	26	100.00%	8	1013	4.3	[FLAG peptide]				
	HsFLAG-ARP6_Ti_2	2.7459	0.104	1013.29	1013.99	6803.8	7	644.8	71.4	25	-.DYKDDDDK.-
	HsFLAG-KIAA0515_	2.8841	0.119	1014.36	1013.99	4702.3	6	941.5	92.9	1	-.DYKDDDDK.-
gi|5730023|re	84	4389	89.80%	463	51157	5.6	RuvB-like 2 [Homo sapiens]				
*	HsMRGBP-FLAG_Ti	1.8186	0.142	890.79	891.021	3609.3	1	316.5	71.4	1	R.IGAHSHIR.G
*	HsFLAG-TIP49b_Ti_	3.0474	0.1734	890.87	891.021	6414.4	1	1053.3	92.9	25	R.IGAHSHIR.G
*	HsFlag-VPS71_Ti_1	2.7325	0.2286	1155.69	1156.281	3976.7	1	535.6	70	10	R.GLGLDDALEPR.Q
*	HsTIP60_Ti_103.464	4.254	0.3186	1156.26	1156.281	7541.3	1	1864.5	90	90	R.GLGLDDALEPR.Q
*	HsFLAG-TIP49b_Ti_	2.6105	0.2844	1316.72	1317.506	2348.3	4	89.8	50	3	R.QASQGMVGQLAAR.R
*	HsFLAG-FLJ20309_	4.0269	0.3081	1317.32	1317.506	7215.8	1	1286.2	79.2	60	R.QASQGMVGQLAAR.R
*	HsFLAG-TIP49b_Ti_	4.08	0.2048	1215.56	1215.5	6693.7	1	1602.5	95	151	R.RAAGVVLEMIR.E
*	HsFLAG-TIP49b_Ti_	3.3479	0.3071	1529.44	1529.841	3206.1	1	326.7	65.4	2	R.RAAGVVLEMIREGK.I
*	HsFlag-ZnF-HIT2_Ti	4.3047	0.2714	1530.61	1529.841	6725.7	1	1389.4	51.9	2	R.RAAGVVLEMIREGK.I
*	HsFLAG-TIP49b_Ti_	2.6442	0.2624	1058.5	1059.312	6456.9	1	482.5	66.7	15	R.AAGVVLEMIR.E
*	HsFlag-ZnF-HIT2_Ti	3.7815	0.2418	1059.45	1059.312	4722.6	1	1144	88.9	120	R.AAGVVLEMIR.E
*	HsFLAG-TIP49b_Ti_	4.202	0.3783	1372.83	1373.654	8192.6	1	1434.4	75	17	R.AAGVVLEMIREGK.I
*	HsMRGBP-FLAG_Ti	4.9341	0.374	1511.21	1509.792	5132	1	954.3	66.7	2	K.IAGRAVLIAGQPGTGK.T
*	HsFLAG-ARP8_Ti_2	2.9242	0.3714	1111.63	1112.315	6215.4	1	668.6	63.6	53	R.AVLIAGQPGTGK.T
*	HsFlag-FLJ90652_2	4.0959	0.32	1112.09	1112.315	5858.9	1	1313.8	81.8	74	R.AVLIAGQPGTGK.T
*	HsFlag-ZnF-HIT2_Ti	6.261	0.5104	3258.78	3258.787	7949.4	1	1126.2	29.8	50	K.TAIAMGMAQALGPDTPFTAIAGSEIFSLEMSK.T
*	HsFLAG-TIP49b_Ti_	2.3687	0.2152	1036.41	1037.161	4039.4	3	258.5	68.8	5	K.TEALTQAFR.R
*	HsFlag-ZnF-HIT2_Ti	3.2342	0.2096	1037.5	1037.161	5608.2	1	814.4	81.2	13	K.TEALTQAFR.R
*	HsFLAG-TIP49b_Ti_	5.5656	0.4212	2942.56	2943.278	7919.9	1	1194.7	46.2	192	R.IKEETEIIEGEVVEIQIDRPATGTGSK.V
*	HsFlag-DPCD_Ti_20	7.4369	0.4233	2943.62	2943.278	8877.3	1	1426	32.7	340	R.IKEETEIIEGEVVEIQIDRPATGTGSK.V
*	HsFlag-ZnF-HIT2_Ti	2.5973	0.1099	2701.1	2701.945	3307.7	3	236.5	33.3	1	K.EETEIIEGEVVEIQIDRPATGTGSK.V
*	HsFlag-ZnF-HIT2_Ti	2.9512	0.3793	1501.76	1502.677	5465.7	1	417.1	58.3	24	K.TTEMETIYDLGTK.M
*	HsFlag-VPS71_Ti_1	4.6242	0.443	1502.2	1502.677	7463.1	1	1651.9	79.2	117	K.TTEMETIYDLGTK.M
*	HsFlag-ZnF-HIT2_Ti	1.9467	0.1237	821.37	822.008	6775.1	5	519.5	83.3	1	K.MIESLTK.D
*	HsFLAG-ARP5_Ti_1	5.7887	0.3008	2561.62	2562.982	10507.3	1	1645.6	34.8	4	K.MIESLTKDKVQAGDVITIDKATGK.I
*	HsFLAG-ARP5_Ti_1	3.3125	0.1729	1403.24	1402.588	9198.8	1	1419.2	75	1	K.DKVQAGDVITIDK.A
*	HsFLAG-ARP5_Ti_1	5.4446	0.4171	1759.45	1759.998	10924.4	1	2173.8	68.8	3	K.DKVQAGDVITIDKATGK.I
*	HsFlag-VPS71_Ti_1	2.9973	0.204	1158.64	1159.325	12315.5	1	1070.8	65	37	K.VQAGDVITIDK.A
*	HsFlag-NUFIP_Ti_1	4.1257	0.2235	1159.62	1159.325	3236.9	1	805.5	90	41	K.VQAGDVITIDK.A
*	HsTIP60_Ti_106.18	1.9457	0.1353	1030.62	1031.244	4311.5	2	306.8	66.7	2	K.ATGKISKLGR.S
*	HsFlag-ZnF-HIT2_Ti	4.6068	0.3683	1343.39	1343.454	6063.3	1	1448.7	86.4	47	R.ARDYDAMGSQTK.F
*	HsFLAG-TIP49a_Ti_	3.0182	0.3123	1115.18	1116.188	4250.9	1	699.3	77.8	5	R.DYDAMGSQTK.F
*	HsH2AZ-FLAG_293_	3.3483	0.2553	1116.19	1116.188	6621.8	1	1592.5	83.3	6	R.DYDAMGSQTK.F
*	HsH2AZ-FLAG_293_	3.5647	0.237	1321.22	1321.439	5358.9	1	1099.5	85	42	K.FVQCPDGELQK.R

*	HsFlag-ZnF-HIT2_Ti_	2.8879	0.128	1321.55	1321.439	8620.1	1	870.3	70	14	K.FVQCPDGELQK.R
*	HsTIP60_Ti_104.144	3.5595	0.2741	1477.3	1477.626	5713.4	1	902.5	77.3	12	K.FVQCPDGELQKR.K
*	HsFLAG-ARP5_Ti_1	3.5053	0.2496	2076.03	2076.36	9179.2	1	1162.9	36.8	1	R.KEVVHTVSLHEIDVINSR.T
*	HsFLAG-ARP5_Ti_1	4.4954	0.4429	2077.82	2076.36	9845.7	1	1841.8	64.7	1	R.KEVVHTVSLHEIDVINSR.T
*	HsFlag-ZnF-HIT2_Ti_	5.4437	0.4377	1947.19	1948.186	8124.8	1	1649.5	68.8	418	K.EVVHTVSLHEIDVINSR.T
*	HsH2AZ-FLAG_293_	5.1341	0.3789	1948.3	1948.186	8683.9	1	2394.8	53.1	204	K.EVVHTVSLHEIDVINSR.T
*	HsFlag-VPS71_Ti_1	5.5333	0.428	1684.7	1684.886	6626.4	1	1964.1	80	439	R.TQGFLALFSGDTGEIK.S
*	HsH2AZ-FLAG_293_	5.348	0.3552	2156.09	2156.4	4111.9	1	1414.1	48.7	25	R.TQGFLALFSGDTGEIKSEVR.E
*	HsFlag-ZnF-HIT2_Ti_	4.9489	0.3948	2156.68	2156.4	7289.5	1	2054.5	65.8	50	R.TQGFLALFSGDTGEIKSEVR.E
*	HsFlag-ZnF-HIT2_Ti_	4.7876	0.2395	2840.28	2840.163	6275.5	1	707.4	30	4	R.TQGFLALFSGDTGEIKSEVREQINAK.V
*	HsFlag-ZnF-HIT2_Ti_	2.9386	0.1543	1174.11	1174.299	5382.5	1	873.2	83.3	1	K.SEVREQINAK.V
*	HsFlag-FLJ20643_Ti	3.1319	0.1954	1104.92	1104.208	7558	9	867.1	81.2	12	K.VAEWREEGK.A
*	HsFLAG-TIP49b_Ti_	6.0692	0.3438	3450.11	3449.943	6613.2	1	922.8	28.4	1	R.EEGKAEIIPGVLFIDEVHMLDIESFSFLNR.A
*	HsFlag-VPS71_Ti_1	4.7333	0.3626	3005.68	3006.486	7633.1	1	883.1	42	10	K.AEIIPGVLFIDEVHMLDIESFSFLNR.A
*	HsFLAG-TIP49a_Ti_	5.2894	0.4374	1732.51	1733.051	4493.7	1	1232.9	80	48	R.ALESDMAPVLIMATNR.G
*	HsFlag-ZnF-HIT2_Ti_	5.4504	0.2815	1733.54	1733.051	10207.2	1	3305.8	56.7	13	R.ALESDMAPVLIMATNR.G
*	HsFLAG-TIP49b_Ti_	5.1786	0.3925	2139.14	2139.419	5534.9	1	1976.3	54.2	20	R.IRGTSYQSPHGIPIDLLDR.L
*	HsFlag-ZnF-HIT2_Ti_	4.3602	0.3462	2140.09	2139.419	5156.2	1	593.3	52.8	10	R.IRGTSYQSPHGIPIDLLDR.L
*	HsFlag-ZnF-HIT2_Ti_	4.6718	0.4575	1869.92	1870.072	5318.1	1	1218.9	68.8	150	R.GTSYQSPHGIPIDLLDR.L
*	HsFLAG-ARP8_Ti_2	4.3364	0.2699	1870.26	1870.072	6297.4	1	930.2	43.8	3	R.GTSYQSPHGIPIDLLDR.L
*	HsFLAG-TIP49b_Ti_	6.3494	0.426	3201.09	3202.632	10578.6	1	2841	35.7	11	R.GTSYQSPHGIPIDLLDRLLIVSTTPYSEK.D
*	HsFLAG-TIP49b_Ti_	5.0446	0.3167	3547.34	3546.999	8774.2	1	1079.2	26.6	8	R.GTSYQSPHGIPIDLLDRLLIVSTTPYSEKDTK.Q
*	HsTIP60_Ti_103.31	3.8964	0.1671	1351.1	1351.583	6414.7	1	1290.2	77.3	109	R.LLIVSTTPYSEK.D
*	HsFlag-FLJ90652_2	2.3504	0.1836	1351.72	1351.583	5187.7	9	282.8	50	6	R.LLIVSTTPYSEK.D
*	HsFlag-DPCD_Ti_20	3.9005	0.3785	1695.41	1695.951	5589.8	1	906.2	67.9	24	R.LLIVSTTPYSEKDTK.Q
*	HsFLAG-TIP49b_Ti_	5.3901	0.4274	2446.77	2446.611	7495	1	1662.9	63.2	217	R.IRCEEEDVEMSEDAYTVLTR.I
*	HsFlag-ZnF-HIT2_Ti_	4.6837	0.2562	2447.77	2446.611	10400.5	1	1510	35.5	8	R.IRCEEEDVEMSEDAYTVLTR.I
*	HsFlag-ZnF-HIT2_Ti_	5.9352	0.475	2178.84	2177.264	8006	1	3109.9	82.4	13	R.CEEEDVEMSEDAYTVLTR.I
*	HsFLAG-TIP49a_Ti_	2.063	0.1974	888.78	889.04	3114	3	186.8	71.4	6	R.IGLETSLR.Y
*	HsFLAG-TIP49a_Ti_	3.3502	0.2685	1579.47	1579.846	2730.2	2	141.1	57.7	26	R.YAIQLITAASLVCR.K
*	HsFlag-ZnF-HIT2_Ti_	5.8071	0.4006	1579.77	1579.846	8967.4	1	2469.6	84.6	374	R.YAIQLITAASLVCR.K
*	HsFlag-ZnF-HIT2_Ti_	4.4493	0.2974	1579.97	1579.846	7599.9	1	1757.6	55.8	3	R.YAIQLITAASLVCR.K
*	HsFLAG-TIP49b_Ti_	3.5994	0.1977	1389.54	1388.564	5220.1	1	799.3	77.3	14	K.RKGTEVQVDDIK.R
*	HsFlag-ZnF-HIT2_Ti_	3.7116	0.213	1544.35	1544.751	6848.1	4	1069.6	75	2	K.RKGTEVQVDDIKR.V
*	HsFlag-ZnF-HIT2_Ti_	2.8789	0.2338	1231.65	1232.376	6274.3	5	699.7	65	2	R.KGTEVQVDDIK.R
*	HsYL1_Ti_103.1312.	4.2705	0.2646	1233.05	1232.376	3689.1	6	768.7	85	14	R.KGTEVQVDDIK.R
*	HsFLAG-TIP49b_Ti_	3.5582	0.2117	1388.63	1388.564	4933	1	867.2	77.3	6	R.KGTEVQVDDIKR.V
*	HsFlag-ZnF-HIT2_Ti_	4.9702	0.259	1389.26	1388.564	5769.6	1	2336.7	70.5	7	R.KGTEVQVDDIKR.V
*	HsFLAG-ARP5_Ti_1	4.1314	0.2275	1389.87	1388.564	7859.3	1	1890.9	81.8	22	R.KGTEVQVDDIKR.V
*	HsFLAG-TIP49b_Ti_	3.8749	0.2928	1104.57	1104.202	7166.7	2	1202.6	83.3	33	K.GTEVQVDDIK.R
*	HsFLAG-TIP49b_Ti_	3.2589	0.1651	1104.62	1104.202	9177.7	5	721.7	66.7	14	K.GTEVQVDDIK.R
*	HsFlag-ZnF-HIT2_Ti_	2.7725	0.2007	1259.68	1260.39	5023	7	442.7	65	3	K.GTEVQVDDIKR.V
*	HsFlag-ZnF-HIT2_Ti_	3.8759	0.3018	1260.27	1260.39	8227.1	2	1345.1	80	10	K.GTEVQVDDIKR.V

*	HsFLAG-TIP49b_Ti_	3.8473	0.249	1385.06	1385.563	5885.6	1	1340.4	85	126	K.RVYSLFLDESR.S
*	HsFlag-ZnF-HIT2_Ti_	3.1282	0.1979	1228.68	1229.375	4347	1	405.7	72.2	13	R.VYSLFLDESR.S
*	HsFlag-ZnF-HIT2_Ti_	4.1784	0.2824	1229.21	1229.375	6206.8	1	1349.5	88.9	43	R.VYSLFLDESR.S
*	HsFLAG-TIP49a_Ti_	3.1815	0.3807	2255.28	2256.535	7484.1	1	849.2	52.9	1	R.STQYMKEYQDAFLFNELK.G
*	HsFlag-FLJ90652_2	3.3551	0.2391	1516.6	1517.678	2788.8	4	221.8	59.1	20	K.EYQDAFLFNELK.G
*	HsFlag-FLJ90652_2	4.2331	0.3787	1516.9	1517.678	7559.5	1	1385.5	81.8	70	K.EYQDAFLFNELK.G
*	HsFlag-ZnF-HIT2_Ti_	5.4717	0.4709	2238.34	2239.415	8205.7	1	1559.2	61.1	192	K.EYQDAFLFNELKGETMDTS.-
gi|89067014|r	10	587	89.10%	55	6231	6	PREDICTED: similar to RuvB-like protein 1 [Homo sapiens]				
*	HsFLAG-TIP49b_Ti_	3.4053	0.153	1588.01	1588.888	6589.8	2	611.4	53.6	3	K.GYSVQLLTPANLLAK.I
*	HsFlag-ZnF-HIT2_Ti_	4.3395	0.3482	1588.85	1588.888	5736.5	1	1461.2	78.6	11	K.GYSVQLLTPANLLAK.I
	HsFlag-ZnF-HIT2_Ti_	2.9069	0.1316	1004.09	1004.128	7177.7	1	974.3	87.5	2	K.INGKDSIEK.E
	HsYL1_Ti_106.2439.	3.6273	0.2529	2695.79	2694.955	7013.3	1	455.5	36.4	2	K.INGKDSIEKEHVEEISELFYDAK.S
	HsYL1_Ti_106.2407.	4.4451	0.3107	2695.92	2694.955	8062.8	1	1309.4	33	5	K.INGKDSIEKEHVEEISELFYDAK.S
	HsFLAG-ARP5_Ti_1	4.5642	0.3039	2282.19	2282.466	8732.6	1	1462.3	41.7	4	K.DSIEKEHVEEISELFYDAK.S
	HsFLAG-ARP5_Ti_1	5.2945	0.411	2282.61	2282.466	9949	1	1655.3	58.3	7	K.DSIEKEHVEEISELFYDAK.S
	HsH2AZ-FLAG_293_	5.0684	0.2221	1709.32	1709.85	6194	1	1297.4	50	112	K.EHVEEISELFYDAK.S
	HsFLAG-TIP49b_Ti_	5.2652	0.3234	1710.45	1709.85	7449.9	1	1932	80.8	436	K.EHVEEISELFYDAK.S
	HsFLAG-ARP5_Ti_1	3.8999	0.273	1352.8	1353.576	8316	2	1259.4	80	5	K.ILADQQDKYMK.-
gi|8922764|re	23	224	87.70%	204	22417	5.8	MRG-binding protein [Homo sapiens]				
*	HsMRGBP-FLAG_Ti_	3.9004	0.3112	1306.54	1306.39	4625.3	1	2204.8	92.9	2	-.MGEAEVGGGGAAGDK.G
*	HsMRGBP-FLAG_Ti_	4.1661	0.2521	3438.57	3437.815	6819.1	1	1039.9	28.2	4	K.GPGEAATSPAEETVVWSPEVEVCLFHAMLGHK.P
*	HsTIP60_Ti_106.201	2.2951	0.191	1360.59	1361.544	3207.7	4	235.5	59.1	1	K.FSQNIGRQVPSK.V
*	HsMRGBP-FLAG_Ti_	3.5328	0.2122	1361.85	1361.544	3566.3	1	707.1	81.8	3	K.FSQNIGRQVPSK.V
*	HsMRGBP-FLAG_Ti_	5.8879	0.3969	3370.16	3370.822	8409.8	1	2602	38	7	K.VIWDHLSTMYDMQALHESEILPFPNPER.N
*	HsTIP60_Ti_106.288	3.4313	0.2211	1585.89	1586.828	2946.4	1	220.7	58.3	8	R.NFVLPEEIIQEVR.E
*	HsMRGBP-FLAG_Ti_	4.3223	0.258	1587.88	1586.828	4300.4	2	887.2	79.2	84	R.NFVLPEEIIQEVR.E
*	HsMRGBP-FLAG_Ti_	4.2543	0.2905	1902.58	1901.17	4216.9	1	1045.6	76.7	4	R.NFVLPEEIIQEVREGK.V
*	HsMRGBP-FLAG_Ti_	4.0814	0.298	1526.73	1526.818	8389	1	1551.7	81.8	4	K.VMIEEEMKEEMK.E
*	HsMRGBP-FLAG_Ti_	5.3502	0.3444	3641.21	3641.973	5808.2	1	790.4	28.1	20	K.VMIEEEMKEEMKEDVDPHNGADDVFSSSGSLGK.A
*	HsMRGBP-FLAG_Ti_	3.7213	0.3414	2651.93	2651.775	3513.1	1	235.2	37.5	1	K.EEMKEDVDPHNGADDVFSSSGSLGK.A
*	HsTIP60_Ti_105.171	4.4053	0.4357	2133.37	2134.177	4788.2	1	910.5	62.5	5	K.EDVDPHNGADDVFSSSGSLGK.A
*	HsMRGBP-FLAG_Ti_	4.0861	0.2638	2135.89	2134.177	6028.4	1	742	33.8	1	K.EDVDPHNGADDVFSSSGSLGK.A
*	HsTIP60_Ti_105.070	3.7571	0.3092	2183.36	2184.288	7379.6	1	461.2	44.7	1	K.SSKDKEKNSSDLGCKEGADK.R
*	HsTIP60_Ti_106.094	4.7789	0.2486	2624.61	2624.837	11242.9	1	1513.3	35.2	1	K.SSKDKEKNSSDLGCKEGADKRKR.S
*	HsMRGBP-FLAG_Ti_	2.2835	0.2325	880.61	880.896	2731.1	1	273.8	78.6	2	K.NSSDLGCK.E
*	HsTIP60_Ti_102.075	2.8437	0.1929	1536.69	1537.593	4944.6	1	580.8	65.4	1	K.NSSDLGCKEGADKR.K
*	HsMRGBP-FLAG_Ti_	5.3292	0.3909	1887.22	1888.085	7869.1	1	1111.7	55.6	9	R.VTDKVLTANSNPSSPSAAK.R
*	HsTIP60_Ti_106.198	5.1485	0.3419	2043.74	2044.272	8889.8	1	1142.3	52.6	2	R.VTDKVLTANSNPSSPSAAKR.R
*	HsTIP60_Ti_101.121	4.7002	0.4239	1444.03	1444.585	5675.4	1	1146.2	75	45	K.VLTANSNPSSPSAAK.R
*	HsTIP60_Ti_104.121	2.9609	0.4192	1444.42	1444.585	6623.5	1	781.2	64.3	11	K.VLTANSNPSSPSAAK.R
*	HsTIP60_Ti_106.180	3.0939	0.2775	1599.56	1600.772	4119	1	226.1	50	3	K.VLTANSNPSSPSAAKR.R
*	HsTIP60_Ti_106.169	3.4701	0.287	1599.64	1600.772	4983.6	1	396	53.3	5	K.VLTANSNPSSPSAAKR.R
gi|5803102|re	47	510	86.70%	323	37231	9.2	MORF-related gene 15 isoform 1 [Homo sapiens]				

	HsMRGBP-FLAG_Ti	3.6925	0.2645	2294.08	2294.581	7236.1	1	960.3	55.6	1	K.FQEGERVLCFHGPLLYEAK.C
	HsMRGBP-FLAG_Ti	3.6801	0.2363	2295.28	2294.581	5155.1	1	828.6	37.5	2	K.FQEGERVLCFHGPLLYEAK.C
	HsFLAG-TIP49b_Ti_	3.4994	0.2826	1547.54	1547.803	6903.6	1	997.7	66.7	3	R.VLCFHGPLLYEAK.C
	HsMRGBP-FLAG_Ti	4.4526	0.3423	1548.23	1547.803	6829.3	1	1393.6	79.2	16	R.VLCFHGPLLYEAK.C
	HsMRGBP-FLAG_Ti	3.5534	0.3471	1315.45	1315.473	6280.5	1	1401	88.9	3	K.YFIHYSGWNK.N
	HsMRGBP-FLAG_Ti	3.3498	0.2873	1317.5	1315.473	3505.5	1	339.2	72.2	5	K.YFIHYSGWNK.N
*	HsTIP60_Ti_104.222	2.2466	0.1791	1317.5	1318.388	3543.5	3	287.6	66.7	1	K.NWDEWVPESR.V
*	HsTIP60_Ti_104.221	3.582	0.2402	1318.13	1318.388	5314.2	4	1016.6	83.3	49	K.NWDEWVPESR.V
*	HsMRGBP-FLAG_Ti	3.5524	0.0803	1659.85	1658.854	8126.7	2	1068.1	66.7	4	K.NWDEWVPESRVLK.Y
	HsMRGBP-FLAG_Ti	2.6927	0.084	1320.71	1321.56	5629.3	2	702.8	70	2	R.VLKYVDTNLQK.Q
	HsMRGBP-FLAG_Ti	2.8309	0.1953	1321.85	1321.56	4294.8	1	1220.4	85	1	R.VLKYVDTNLQK.Q
	HsTIP60_Ti_106.195	4.1689	0.3537	1906.78	1907.111	6949.9	1	1011.6	58.8	1	K.ANQEQYAEGKMRGAAPGK.K
	HsMRGBP-FLAG_Ti	2.5271	0.2356	1371.58	1371.58	5716.6	1	548.9	61.5	1	R.GAAPGKKTSGLQQK.N
	HsTIP60_Ti_106.110	3.4596	0.2761	1444.35	1444.718	8672.1	1	966.3	72.7	4	K.NVEVKTKKNKQK.T
	HsTIP60_Ti_106.179	2.6818	0.0973	2268	2268.448	6305.6	2	270.7	35.7	1	K.QKTPGNGDGGSTSETPQPPRKK.R
	HsMRGBP-FLAG_Ti	4.4989	0.5168	1757.23	1755.795	8291.4	1	1693.3	64.7	25	K.TPGNGDGGSTSETPQPPR.K
	HsTIP60_Ti_104.105	3.7834	0.3354	1883.77	1883.969	8214.8	1	837.3	34.7	1	K.TPGNGDGGSTSETPQPPRK.K
	HsMRGBP-FLAG_Ti	4.0666	0.4613	1884.68	1883.969	7433	1	679.6	50	16	K.TPGNGDGGSTSETPQPPRK.K
	HsTIP60_Ti_106.101	4.2302	0.2704	2011.33	2012.144	8742	1	1485.7	40.8	4	K.TPGNGDGGSTSETPQPPRKK.R
	HsTIP60_Ti_106.102	3.0101	0.2389	2011.54	2012.144	7630.1	1	475.4	42.1	6	K.TPGNGDGGSTSETPQPPRKK.R
	HsTIP60_Ti_105.171	4.8547	0.2105	1907.75	1909.081	8648.5	2	1434.7	43.3	2	R.ARVDPTVENEETFMNR.V
	HsTIP60_Ti_105.170	4.8515	0.2822	1908.69	1909.081	3469.3	1	859.8	76.7	5	R.ARVDPTVENEETFMNR.V
	HsMRGBP-FLAG_Ti	5.0525	0.2906	2365.19	2364.635	5280.1	1	939.6	40.8	4	R.ARVDPTVENEETFMNRVEVK.V
	HsMRGBP-FLAG_Ti	4.4689	0.3201	1682.75	1681.814	5891.2	1	996.9	76.9	29	R.VDPTVENEETFMNR.V
	HsMRGBP-FLAG_Ti	3.978	0.2654	2138.04	2137.369	3667.1	3	263.6	50	9	R.VDPTVENEETFMNRVEVK.V
	HsMRGBP-FLAG_Ti	5.2994	0.3888	2237.87	2239.576	3968.2	1	797.7	64.7	29	K.IPEELKPWLVDDWDLITR.Q
	HsMRGBP-FLAG_Ti	5.972	0.2767	2240.47	2239.576	6504.6	1	1453.8	44.1	23	K.IPEELKPWLVDDWDLITR.Q
	HsMRGBP-FLAG_Ti	4.0056	0.378	2495.21	2495.881	4783.6	1	673.4	52.6	3	K.IPEELKPWLVDDWDLITRQK.Q
	HsMRGBP-FLAG_Ti	4.4484	0.237	1529.75	1529.736	6342.4	1	1662.1	86.4	6	K.PWLVDDWDLITR.Q
	HsTIP60_Ti_101.272	1.9098	0.1413	978.59	980.195	2631.6	6	209.1	71.4	1	K.QLFYLPAK.K
	HsTIP60_Ti_106.231	2.8007	0.1259	1107.48	1108.369	1961.8	1	162.9	75	2	K.QLFYLPAKK.N
	HsMRGBP-FLAG_Ti	3.7533	0.2863	1673.28	1672.832	5382.9	1	1323.9	76.9	1	K.KNVDSILEDYANYK.K
	HsMRGBP-FLAG_Ti	5.021	0.3066	1800.78	1801.006	8298.7	1	1615.3	71.4	4	K.KNVDSILEDYANYKK.S
	HsTIP60_Ti_104.403	4.7168	0.2931	1544.23	1544.658	6772	2	1172.3	75	58	K.NVDSILEDYANYK.K
	HsMRGBP-FLAG_Ti	3.2546	0.252	1544.64	1544.658	4804.1	1	550	62.5	8	K.NVDSILEDYANYK.K
	HsTIP60_Ti_106.256	4.1615	0.2784	1673.84	1672.832	6496	1	1332.8	76.9	14	K.NVDSILEDYANYKK.S
	HsTIP60_Ti_106.232	4.8411	0.3917	1921.7	1922.102	6504.8	1	1400.4	67.6	2	R.GNTDNKEYAVNEVVAGIK.E
	HsMRGBP-FLAG_Ti	3.4706	0.229	1291.59	1292.475	4128.7	2	414.9	68.2	11	K.EYAVNEVVAGIK.E
	HsTIP60_Ti_103.259	3.9686	0.3073	1292.31	1292.475	5695.1	1	1069.2	81.8	59	K.EYAVNEVVAGIK.E
	HsMRGBP-FLAG_Ti	4.7656	0.1574	1719.77	1720.036	6223.4	1	1626.6	84.6	21	K.EYFNVMLGTQLLYK.F
	HsMRGBP-FLAG_Ti	6.2804	0.383	3324.58	3323.753	7672	1	1125.3	29.5	2	K.FERPQYAEILADHPDAPMSQVYGAPHLLR.L
	HsMRGBP-FLAG_Ti	3.0795	0.2746	1421.62	1422.679	7413.3	1	670.5	58.3	9	R.IGAMLAYTPLDEK.S
	HsTIP60_Ti_105.222	4.9481	0.3579	1422.29	1422.679	6181.6	1	1429.5	83.3	30	R.IGAMLAYTPLDEK.S

	HsMRGBP-FLAG_Ti_	4.1157	0.3935	1661.9	1660.997	6753.1	1	1302.3	73.1	3	K.SLALLLNYLHDFLK.Y
	HsMRGBP-FLAG_Ti_	4.6934	0.3976	2254.87	2255.405	4821.5	1	614.4	50	16	K.NSATLFSASDYEVAPPEYHR.K
	HsMRGBP-FLAG_Ti_	4.2899	0.2286	2257.48	2255.405	5306	1	862.2	39.5	6	K.NSATLFSASDYEVAPPEYHR.K
	HsMRGBP-FLAG_Ti_	4.5169	0.4416	2382.92	2383.579	4869.7	1	544.7	45	7	K.NSATLFSASDYEVAPPEYHRK.A
gi|4506753|re	66	5441	85.10%	456	50228	6.4	TATA binding protein interacting protein 49 kDa [Homo sapiens]				
	HsFLAG-TIP49b_Ti_	3.7644	0.2317	1294.29	1294.549	6330	2	1212.8	85	1	-.MKIEEVKSTTK.T
	HsFLAG-FLJ20309_	3.0135	0.1418	879.39	879.007	5761.9	1	1030.6	92.9	26	R.IASHSHVK.G
	HsTIP60_Ti_102.180	2.7619	0.2823	1059.38	1060.192	9272.9	1	1073.1	75	21	K.GLGLDESGLAK.Q
	HsFlag-FLJ20643_Ti	3.4732	0.2135	1060.94	1060.192	5294	2	974.6	85	36	K.GLGLDESGLAK.Q
	HsFLAG-ARP8_Ti_2	2.3985	0.2171	1301.48	1301.402	1693.2	1	80.1	58.3	2	K.QAASGLVGQENAR.E
	HsFlag-FLJ90652_2	4.1807	0.3411	1302.45	1301.402	5603.1	1	1211.4	83.3	39	K.QAASGLVGQENAR.E
	HsFlag-VPS71_Ti_1	3.2303	0.227	2513.34	2513.82	8076.3	1	574.5	41.3	2	K.QAASGLVGQENAREACGVIVELIK.S
	HsFlag-ZnF-HIT2_Ti_	3.8758	0.4002	2513.51	2513.82	6533	1	851.1	33.7	1	K.QAASGLVGQENAREACGVIVELIK.S
	HsFlag-VPS71_Ti_1	3.1115	0.1457	1230.73	1231.441	5422.2	5	554.2	70	10	R.EACGVIVELIK.S
	HsFlag-NUFIP_Ti_1	3.3651	0.1491	1232.62	1231.441	5111	4	762.6	80	202	R.EACGVIVELIK.S
	HsFLAG-UTX1_Ti_2	2.9797	0.4321	1080.36	1081.301	6033.2	1	1063.8	77.3	95	R.AVLLAGPPGTGK.T
	HsFLAG-p53-DNA-D	3.6323	0.1834	1080.56	1081.301	5572.9	7	948.5	72.7	38	R.AVLLAGPPGTGK.T
	HsFLAG-ARP8_Ti_2	5.5641	0.3332	1386.17	1386.632	9061.9	1	2693.9	84.6	601	K.TALALAIAQELGSK.V
	HsFLAG-TIP49a_Ti_	3.9239	0.2681	1386.48	1386.632	6365.2	1	710.9	61.5	95	K.TALALAIAQELGSK.V
	HsFLAG-ARP6_Ti_2	4.7951	0.4599	1943.24	1944.216	4198.1	1	1202.3	78.1	152	K.VPFCPMVGSEVYSTEIK.K
	HsFlag-ZnF-HIT2_Ti_	4.756	0.4779	2071	2072.39	6054.6	1	1602.5	73.5	18	K.VPFCPMVGSEVYSTEIKK.T
	HsFlag-ZnF-HIT2_Ti_	5.0154	0.3952	2072.24	2072.39	6914	1	1586.8	47.1	10	K.VPFCPMVGSEVYSTEIKK.T
	HsFlag-ZnF-HIT2_Ti_	4.8331	0.4032	3192.11	3192.679	6214.5	1	956.1	33.7	1	K.VPFCPMVGSEVYSTEIKKTEVLMENFR.R
	HsFLAG-TIP49b_Ti_	4.1361	0.2625	1267.41	1267.486	6497.9	1	1311.6	88.9	74	K.KTEVLMENFR.R
	HsFLAG-TIP49b_Ti_	2.9972	0.1299	1269.5	1267.486	4703.7	1	328	66.7	40	K.KTEVLMENFR.R
	HsFlag-ZnF-HIT2_Ti_	3.3579	0.1554	1423.5	1423.673	7345.3	1	995.7	80	2	K.KTEVLMENFRR.A
	HsFLAG-TIP49b_Ti_	2.8243	0.2487	1138.42	1139.312	5653.5	1	428.1	68.8	9	K.TEVLMENFR.R
	HsTIP60_Ti_103.194	2.982	0.2394	1139	1139.312	6432.3	2	1164	87.5	2	K.TEVLMENFR.R
	HsFlag-ZnF-HIT2_Ti_	5.4639	0.3864	2690.49	2690.858	4649.6	1	627.3	47.8	174	K.EVYEGEVTELTPCETENPMGGYGK.T
	HsFLAG-ARP8_Ti_2	2.9975	0.3149	1082.58	1081.344	5439.2	1	856.2	83.3	84	K.TISHVIIGLK.T
	HsFlag-ZnF-HIT2_Ti_	2.97	0.1867	1082.64	1081.344	4841.9	1	700	77.8	73	K.TISHVIIGLK.T
	HsFlag-ZnF-HIT2_Ti_	4.445	0.2048	1646.08	1646.924	4451.1	1	927.7	51.9	16	K.QLKLDPSIFESLQK.E
	HsH2AZ-FLAG_293_	3.0978	0.23	1646.43	1646.924	3939.5	1	413.8	65.4	8	K.QLKLDPSIFESLQK.E
	HsFLAG-p53-DNA-D	2.618	0.2579	1276.7	1277.46	2958.2	1	317.5	65	7	K.LDPSIFESLQK.E
	HsFlag-ZnF-HIT2_Ti_	4.4699	0.2878	1277.13	1277.46	6174.4	1	1226.6	85	51	K.LDPSIFESLQK.E
	HsFlag-ZnF-HIT2_Ti_	7.0787	0.5505	2020.39	2021.235	7362.1	1	2930.8	80.6	685	K.ERVEAGDVIYIEANSGAVK.R
	HsFlag-DPCD_Ti_20	5.6078	0.3406	2020.89	2021.235	8149.8	1	1761.9	41.7	258	K.ERVEAGDVIYIEANSGAVK.R
	HsFLAG-ARP5_Ti_1	4.9899	0.2613	2176.96	2177.422	8457.9	1	1468.6	40.8	3	K.ERVEAGDVIYIEANSGAVKR.Q
	HsFlag-DPCD_Ti_20	5.262	0.4923	1736.64	1735.932	6005.2	1	1383.5	68.8	26	R.VEAGDVIYIEANSGAVK.R
	HsFlag-ZnF-HIT2_Ti_	4.1501	0.267	2391.51	2391.556	4705.4	1	971.4	43.4	2	R.CDTYATEFDLEAEEYVPLPK.G
	HsFlag-DPCD_Ti_20	6.884	0.4827	2392.04	2391.556	9046.3	1	2363.5	65.8	751	R.CDTYATEFDLEAEEYVPLPK.G
	HsH2AZ-FLAG_293_	4.9951	0.4147	1922.11	1923.133	7254.1	1	1433.3	68.8	13	K.EIIQDVTLHDLDVANAR.P
	HsFlag-ZnF-HIT2_Ti_	3.9724	0.2325	1923.47	1923.133	7884	1	1595	45.3	2	K.EIIQDVTLHDLDVANAR.P

	HsFLAG-TIP49a_Ti_	6.494	0.4369	3638.48	3639.195	7117.6	1	1475.9	32.8	85	K.EIIQDVTLHDLDVANARPQGGQDILSMMGQLMK.P
	HsFlag-VPS71_Ti_1	7.167	0.3672	3863.76	3864.485	8246.8	1	1384.8	28.7	112	K.EIIQDVTLHDLDVANARPQGGQDILSMMGQLMKPK.K
	HsFlag-ZnF-HIT2_Ti_	4.2516	0.3154	1734.32	1735.085	7584	1	1271.6	66.7	3	R.PQGGQDILSMMGQLMK.P
	HsFLAG-TIP49a_Ti_	5.416	0.3829	1959.7	1960.375	7011.4	1	1214.5	61.8	2	R.PQGGQDILSMMGQLMKPK.K
	HsFLAG-TIP49a_Ti_	5.7179	0.3974	1962.73	1960.375	4367	1	1299.3	51.5	8	R.PQGGQDILSMMGQLMKPK.K
	HsFLAG-TIP49b_Ti_	3.9521	0.1276	3794.93	3794.323	4685.7	1	369.5	23.4	2	K.YIDQGIAELVPGVLFVDEVHMLDIECFTYLHR.A
	HsFlag-NUFIP_Ti_1	6.0975	0.4225	1689.03	1688.965	10187.6	1	3157.2	56.7	102	R.ALESSIAPIVIFASNR.G
	HsFlag-NUFIP_Ti_1	4.9148	0.4132	1689.58	1688.965	4604.7	1	762.8	66.7	125	R.ALESSIAPIVIFASNR.G
	HsFlag-DPCD_Ti_20	4.5205	0.2042	1949.21	1950.156	5235.7	1	1784.1	51.5	45	R.GTEDITSPHGIPLDLLDR.V
	HsFLAG-FLJ20309_	4.7346	0.33	1950.04	1950.156	6887.2	1	1385.1	64.7	131	R.GTEDITSPHGIPLDLLDR.V
	HsFLAG-ARP5_Ti_1	4.152	0.283	2563.06	2562.987	6064.4	1	762.7	34.1	3	R.GTEDITSPHGIPLDLLDRVMIIR.T
	HsFlag-ZnF-HIT2_Ti_	3.2731	0.2494	1242.15	1242.491	5558.9	1	1038.7	83.3	12	R.TMLYTPQEMK.Q
	HsTIP60_Ti_103.171	1.9921	0.2233	1242.44	1242.491	4660.1	5	301.6	61.1	2	R.TMLYTPQEMK.Q
*	HsFlag-ZnF-HIT2_Ti_	5.7078	0.5012	2594.22	2594.885	10246.8	1	1151.5	45.7	16	K.IRAQTEGINISEEALNHLGEIGTK.T
*	HsFlag-ZnF-HIT2_Ti_	7.7226	0.446	2594.6	2594.885	8598.1	1	2773.9	44.6	48	K.IRAQTEGINISEEALNHLGEIGTK.T
*	HsFlag-ZnF-HIT2_Ti_	5.5352	0.4772	2324.79	2325.538	6562.1	1	869.2	50	215	R.AQTEGINISEEALNHLGEIGTK.T
*	HsFLAG-FLJ20309_	4.2899	0.2341	2326.96	2325.538	3826.3	1	421.2	31	17	R.AQTEGINISEEALNHLGEIGTK.T
*	HsFLAG-TIP49a_Ti_	4.6355	0.4058	2003.69	2003.393	5278.2	1	759.7	52.9	7	K.TTLRYSVQLLTPANLLAK.I
	HsFLAG-ARP6_Ti_1	4.4489	0.337	1532.19	1531.836	5640.9	1	993.6	73.1	244	R.YSVQLLTPANLLAK.I
	HsFLAG-TIP49b_Ti_	4.0508	0.3027	1532.79	1531.836	6673.1	1	538.8	53.8	59	R.YSVQLLTPANLLAK.I
	HsFlag-ZnF-HIT2_Ti_	2.9069	0.1316	1004.09	1004.128	7177.7	1	974.3	87.5	2	K.INGKDSIEK.E
	HsYL1_Ti_106.2439.	3.6273	0.2529	2695.79	2694.955	7013.3	1	455.5	36.4	2	K.INGKDSIEKEHVEEISELFYDAK.S
	HsYL1_Ti_106.2407.	4.4451	0.3107	2695.92	2694.955	8062.8	1	1309.4	33	5	K.INGKDSIEKEHVEEISELFYDAK.S
	HsFLAG-ARP5_Ti_1	4.5642	0.3039	2282.19	2282.466	8732.6	1	1462.3	41.7	4	K.DSIEKEHVEEISELFYDAK.S
	HsFLAG-ARP5_Ti_1	5.2945	0.411	2282.61	2282.466	9949	1	1655.3	58.3	7	K.DSIEKEHVEEISELFYDAK.S
	HsH2AZ-FLAG_293_	5.0684	0.2221	1709.32	1709.85	6194	1	1297.4	50	112	K.EHVEEISELFYDAK.S
	HsFLAG-TIP49b_Ti_	5.2652	0.3234	1710.45	1709.85	7449.9	1	1932	80.8	436	K.EHVEEISELFYDAK.S
	HsFLAG-ARP5_Ti_1	3.8999	0.273	1352.8	1353.576	8316	2	1259.4	80	5	K.ILADQQDKYMK.-
gi|45643135|r	45	457	84.30%	362	41474	9.3	MORF-related gene 15 isoform 2 [Homo sapiens]				
	HsMRGBP-FLAG_Ti_	3.6925	0.2645	2294.08	2294.581	7236.1	1	960.3	55.6	1	K.FQEGERVLCFHGPLLYEAK.C
	HsMRGBP-FLAG_Ti_	3.6801	0.2363	2295.28	2294.581	5155.1	1	828.6	37.5	2	K.FQEGERVLCFHGPLLYEAK.C
	HsFLAG-TIP49b_Ti_	3.4994	0.2826	1547.54	1547.803	6903.6	1	997.7	66.7	3	R.VLCFHGPLLYEAK.C
	HsMRGBP-FLAG_Ti_	4.4526	0.3423	1548.23	1547.803	6829.3	1	1393.6	79.2	16	R.VLCFHGPLLYEAK.C
	HsMRGBP-FLAG_Ti_	3.5534	0.3471	1315.45	1315.473	6280.5	1	1401	88.9	3	K.YFIHYSGWNK.K
	HsMRGBP-FLAG_Ti_	3.3498	0.2873	1317.5	1315.473	3505.5	1	339.2	72.2	5	K.YFIHYSGWNK.K
*	HsMRGBP-FLAG_Ti_	3.867	0.241	3936.37	3937.36	4959.8	1	563.3	25	1	K.THEDIVALFPVPEGAPSVHHPLLTSSWDEWVPESR.V
	HsMRGBP-FLAG_Ti_	2.6927	0.084	1320.71	1321.56	5629.3	2	702.8	70	2	R.VLKYVDTNLQK.Q
	HsMRGBP-FLAG_Ti_	2.8309	0.1953	1321.85	1321.56	4294.8	1	1220.4	85	1	R.VLKYVDTNLQK.Q
	HsTIP60_Ti_106.195	4.1689	0.3537	1906.78	1907.111	6949.9	1	1011.6	58.8	1	K.ANQEQYAEGKMRGAAPGK.K
	HsMRGBP-FLAG_Ti_	2.5271	0.2356	1371.58	1371.58	5716.6	1	548.9	61.5	1	R.GAAPGKKTSGLQQK.N
	HsTIP60_Ti_106.11	3.4596	0.2761	1444.35	1444.718	8672.1	1	966.3	72.7	4	K.NVEVKTKKNKQK.T
	HsTIP60_Ti_106.179	2.6818	0.0973	2268	2268.448	6305.6	2	270.7	35.7	1	K.QKTPGNGDGGSTSETPQPPRKK.R
	HsMRGBP-FLAG_Ti_	4.4989	0.5168	1757.23	1755.795	8291.4	1	1693.3	64.7	25	K.TPGNGDGGSTSETPQPPR.K

	HsTIP60_Ti_104.105	3.7834	0.3354	1883.77	1883.969	8214.8	1	837.3	34.7	1	K.TPGNGDGGSTSETPQPPRK.K
	HsMRGBP-FLAG_Ti_	4.0666	0.4613	1884.68	1883.969	7433	1	679.6	50	16	K.TPGNGDGGSTSETPQPPRK.K
	HsTIP60_Ti_106.101	4.2302	0.2704	2011.33	2012.144	8742	1	1485.7	40.8	4	K.TPGNGDGGSTSETPQPPRKK.R
	HsTIP60_Ti_106.102	3.0101	0.2389	2011.54	2012.144	7630.1	1	475.4	42.1	6	K.TPGNGDGGSTSETPQPPRKK.R
	HsTIP60_Ti_105.171	4.8547	0.2105	1907.75	1909.081	8648.5	2	1434.7	43.3	2	R.ARVDPTVENEETFMNR.V
	HsTIP60_Ti_105.170	4.8515	0.2822	1908.69	1909.081	3469.3	1	859.8	76.7	5	R.ARVDPTVENEETFMNR.V
	HsMRGBP-FLAG_Ti_	5.0525	0.2906	2365.19	2364.635	5280.1	1	939.6	40.8	4	R.ARVDPTVENEETFMNRVEVK.V
	HsMRGBP-FLAG_Ti_	4.4689	0.3201	1682.75	1681.814	5891.2	1	996.9	76.9	29	R.VDPTVENEETFMNR.V
	HsMRGBP-FLAG_Ti_	3.978	0.2654	2138.04	2137.369	3667.1	3	263.6	50	9	R.VDPTVENEETFMNRVEVK.V
	HsMRGBP-FLAG_Ti_	5.2994	0.3888	2237.87	2239.576	3968.2	1	797.7	64.7	29	K.IPEELKPWLVDDWDLITR.Q
	HsMRGBP-FLAG_Ti_	5.972	0.2767	2240.47	2239.576	6504.6	1	1453.8	44.1	23	K.IPEELKPWLVDDWDLITR.Q
	HsMRGBP-FLAG_Ti_	4.0056	0.378	2495.21	2495.881	4783.6	1	673.4	52.6	3	K.IPEELKPWLVDDWDLITRQK.Q
	HsMRGBP-FLAG_Ti_	4.4484	0.237	1529.75	1529.736	6342.4	1	1662.1	86.4	6	K.PWLVDDWDLITR.Q
	HsTIP60_Ti_101.272	1.9098	0.1413	978.59	980.195	2631.6	6	209.1	71.4	1	K.QLFYLPAK.K
	HsTIP60_Ti_106.231	2.8007	0.1259	1107.48	1108.369	1961.8	1	162.9	75	2	K.QLFYLPAKK.N
	HsMRGBP-FLAG_Ti_	3.7533	0.2863	1673.28	1672.832	5382.9	1	1323.9	76.9	1	K.KNVDSILEDYANYK.K
	HsMRGBP-FLAG_Ti_	5.021	0.3066	1800.78	1801.006	8298.7	1	1615.3	71.4	4	K.KNVDSILEDYANYKK.S
	HsTIP60_Ti_104.403	4.7168	0.2931	1544.23	1544.658	6772	2	1172.3	75	58	K.NVDSILEDYANYK.K
	HsMRGBP-FLAG_Ti_	3.2546	0.252	1544.64	1544.658	4804.1	1	550	62.5	8	K.NVDSILEDYANYK.K
	HsTIP60_Ti_106.256	4.1615	0.2784	1673.84	1672.832	6496	1	1332.8	76.9	14	K.NVDSILEDYANYKK.S
	HsTIP60_Ti_106.232	4.8411	0.3917	1921.7	1922.102	6504.8	1	1400.4	67.6	2	R.GNTDNKEYAVNEVVAGIK.E
	HsMRGBP-FLAG_Ti_	3.4706	0.229	1291.59	1292.475	4128.7	2	414.9	68.2	11	K.EYAVNEVVAGIK.E
	HsTIP60_Ti_103.259	3.9686	0.3073	1292.31	1292.475	5695.1	1	1069.2	81.8	59	K.EYAVNEVVAGIK.E
	HsMRGBP-FLAG_Ti_	4.7656	0.1574	1719.77	1720.036	6223.4	1	1626.6	84.6	21	K.EYFNVMLGTQLLYK.F
	HsMRGBP-FLAG_Ti_	6.2804	0.383	3324.58	3323.753	7672	1	1125.3	29.5	2	K.FERPQYAEILADHPDAPMSQVYGAPHLLR.L
	HsMRGBP-FLAG_Ti_	3.0795	0.2746	1421.62	1422.679	7413.3	1	670.5	58.3	9	R.IGAMLAYTPLDEK.S
	HsTIP60_Ti_105.222	4.9481	0.3579	1422.29	1422.679	6181.6	1	1429.5	83.3	30	R.IGAMLAYTPLDEK.S
	HsMRGBP-FLAG_Ti_	4.1157	0.3935	1661.9	1660.997	6753.1	1	1302.3	73.1	3	K.SLALLLNYLHDFLK.Y
	HsMRGBP-FLAG_Ti_	4.6934	0.3976	2254.87	2255.405	4821.5	1	614.4	50	16	K.NSATLFSASDYEVAPPEYHR.K
	HsMRGBP-FLAG_Ti_	4.2899	0.2286	2257.48	2255.405	5306	1	862.2	39.5	6	K.NSATLFSASDYEVAPPEYHR.K
	HsMRGBP-FLAG_Ti_	4.5169	0.4416	2382.92	2383.579	4869.7	1	544.7	45	7	K.NSATLFSASDYEVAPPEYHRK.A
gi|5174447|re	21	214	77.60%	317	35077	7.7	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_11	5.3864	0.2976	2628.04	2628.965	7020.3	1	2211.4	41.3	11	K.GHNGWVTQIATTPQFPDMILSASR.D
*	HsFlag-NUFIP_Ti_10	6.1819	0.4492	2628.77	2628.965	5280.1	1	1135.6	54.3	19	K.GHNGWVTQIATTPQFPDMILSASR.D
*	HsFlag-NUFIP_Ti_10	3.7934	0.1985	1563.79	1563.71	9204.2	1	1290.5	70.8	2	K.LTRDETNYGIPQR.A
*	HsFlag-NUFIP_Ti_10	3.335	0.2925	1193.15	1193.258	3842.5	1	642.1	83.3	1	R.DETNYGIPQR.A
*	HsFlag-NUFIP_Ti_11	5.2176	0.3939	2962.04	2963.192	8897.3	1	1691.4	34.3	11	R.GHSHFVSDVVISSDGQFALSGSWDGTLR.L
*	HsFlag-NUFIP_Ti_10	3.0533	0.2608	1265.45	1265.409	6637.7	1	893.3	75	3	R.LWDLTTGTTTR.R
*	HsFlag-NUFIP_Ti_10	4.3417	0.4235	1310.48	1310.406	8209.3	1	1557.2	81.8	34	K.DVLSVAFSSDNR.Q
*	HsFlag-NUFIP_Ti_10	3.9665	0.2909	1982.51	1983.067	7188.5	2	868	40	3	K.YTVQDESHSEWVSCVR.F
*	HsFlag-NUFIP_Ti_10	4.5155	0.3987	1983.32	1983.067	9732.8	1	1385.6	63.3	21	K.YTVQDESHSEWVSCVR.F
*	HsFlag-NUFIP_Ti_10	4.3128	0.3965	1908.59	1909.072	5854.4	1	1027.9	65.6	4	R.FSPNSSNPIIVSCGWDK.L
*	HsFlag-NUFIP_Ti_11	5.1331	0.4982	2743.7	2744.944	8155.5	1	1089.4	46.2	8	K.TNHIGHTGYLNTVTVSPDGSLCASGGK.D

*	HsFlag-NUFIP_Ti_11	6.2905	0.257	2745.01	2744.944	5912.2	1	1254.8	36.5	4	K.TNHIGHTGYLNTVTVSPDGSLCASGGK.D
	HsFlag-NUFIP_Ti_10	4.0515	0.3373	1477.12	1477.632	6419.9	1	1302.8	75	3	K.DGQAMLWDLNEGK.H
*	HsFlag-NUFIP_Ti_10	7.1411	0.4933	2276.07	2277.508	7228.2	1	2777	76.3	18	K.HLYTLDGGDIINALCFSPNR.Y
*	HsFlag-NUFIP_Ti_10	4.4399	0.3027	2277.38	2277.508	6651.3	2	781.5	34.2	2	K.HLYTLDGGDIINALCFSPNR.Y
*	HsFlag-NUFIP_Ti_11	5.2396	0.3982	3625.98	3626.038	4655.6	1	582.3	27.4	2	K.HLYTLDGGDIINALCFSPNRYWLCAATGPSIK.I
*	HsFlag-NUFIP_Ti_10	4.1489	0.3726	1367.51	1367.554	6270	1	1501.9	81.8	4	R.YWLCAATGPSIK.I
*	HsFlag-NUFIP_Ti_10	5.4239	0.4534	1789.6	1790.064	9965.2	1	2062.8	73.3	43	K.IIVDELKQEVISTSSK.A
*	HsFlag-NUFIP_Ti_11	3.8688	0.3396	3069.43	3070.308	10544.5	1	1096.1	26.9	1	K.AEPPQCTSLAWSADGQTLFAGYTDNLVR.V
*	HsFlag-NUFIP_Ti_10	4.6353	0.4509	3070.31	3070.308	4345.5	1	608.9	46.3	13	K.AEPPQCTSLAWSADGQTLFAGYTDNLVR.V
*	HsFlag-NUFIP_Ti_10	3.1903	0.2658	1060.4	1060.241	6730	1	1289.3	93.8	7	R.VWQVTIGTR.-
gi|24308444|r	32	659	75.90%	357	39740	8.1	hypothetical protein LOC116143 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_10	2.6217	0.1518	1047.66	1048.274	5291.2	3	542.2	68.8	13	K.PQIIAHIQK.G
*	HsFlag-NUFIP_Ti_10	3.2571	0.1339	1048.22	1048.274	6232	7	922	81.2	2	K.PQIIAHIQK.G
*	HsFLAG-p53-DNA-D	3.1431	0.3654	1250.41	1251.347	8814.2	1	784.8	66.7	4	K.GFNYTVFDCK.W
*	HsFlag-FLJ20643_Ti	3.778	0.3511	1251.46	1251.347	7469.4	1	1231.1	83.3	11	K.GFNYTVFDCK.W
*	HsFlag-FLJ20643_Ti	3.0161	0.3314	1043.51	1043.229	4188.4	1	877.8	87.5	6	K.FVTMGNFAR.G
*	HsFlag-DPCD_Ti_20	4.9626	0.393	1771.54	1772.011	9364.9	1	1659	66.7	94	R.GTGVIQLYEIQHGDLK.L
*	HsFlag-ZnF-HIT2_Ti_	3.6914	0.2482	1772.32	1772.011	5905.8	1	1095.5	45	1	R.GTGVIQLYEIQHGDLK.L
*	HsFlag-FLJ20643_Ti	2.4781	0.159	1325.65	1326.418	3085.6	4	144.7	63.6	2	K.CGTFGATSLQQR.Y
*	HsFLAG-RPB5MP_2	3.8848	0.4091	1326.17	1326.418	7017.7	1	1073.3	77.3	8	K.CGTFGATSLQQR.Y
*	HsFlag-NUFIP_Ti_10	5.1997	0.4292	3022.54	3023.433	7741.6	1	836.8	36.5	29	R.YLATGDFGGNLHIWNLEAPEMPVYSVK.G
*	HsFlag-ZnF-HIT2_Ti_	5.8278	0.4586	3023.37	3023.433	5025.5	1	1343.7	39.4	79	R.YLATGDFGGNLHIWNLEAPEMPVYSVK.G
*	HsFLAG-p53-DNA-D	5.2092	0.4397	2832.1	2832.186	6074	1	1727.4	37.5	3	K.GHKEIINAIDGIGGLGIGEGAPEIVTGSR.D
*	HsFlag-ZnF-HIT2_Ti_	6.5542	0.5651	2508.55	2509.819	8263.1	1	2610.2	62	127	K.EIINAIDGIGGLGIGEGAPEIVTGSR.D
*	HsFLAG-p53-DNA-D	5.3446	0.3715	2511.15	2509.819	8006.7	1	1826.8	39	1	K.EIINAIDGIGGLGIGEGAPEIVTGSR.D
*	HsFLAG-TIP49a_Ti_	3.0423	0.3307	1900.28	1900.07	5756.7	3	435	46.9	1	R.QKDDPVANMEPVQGENK.R
*	HsFlag-FLJ20643_Ti	3.6677	0.3719	2056.42	2056.258	7044.5	1	663.2	52.9	5	R.QKDDPVANMEPVQGENKR.D
*	HsFlag-FLJ20643_Ti	3.2414	0.2776	1800.75	1799.953	4984.2	1	483.3	56.7	1	K.DDPVANMEPVQGENKR.D
*	HsFLAG-RPB5MP_2	3.6306	0.3091	1961.69	1961.02	8594.4	1	1310.2	45	1	R.DCWTVAFGNAYNQEER.V
*	HsFlag-NUFIP_Ti_10	5.5578	0.4537	1962.51	1961.02	7556.5	1	1964.3	76.7	71	R.DCWTVAFGNAYNQEER.V
*	HsFLAG-p53-DNA-D	3.1817	0.2087	1310.37	1311.4	7092	1	854.3	68.2	6	R.VVCAGYDNGDIK.L
*	HsFLAG-RPB5MP_2	3.6406	0.3209	1311.13	1311.4	5902.3	1	1328	81.8	8	R.VVCAGYDNGDIK.L
*	HsFlag-FLJ20643_Ti	3.4258	0.2612	1326.68	1325.43	6951.4	1	816.1	70	18	K.NGVCSLEFDRK.D
*	HsFLAG-p53-DNA-D	2.1566	0.2168	917.54	918.078	8356.5	2	588	62.5	1	K.LVATSLEGK.F
*	HsFLAG-p53-DNA-D	2.794	0.1859	918.26	918.078	2421.2	1	570.1	93.8	1	K.LVATSLEGK.F
*	HsFlag-NUFIP_Ti_10	2.2538	0.2335	951.6	952.119	6779.8	4	685.6	83.3	10	K.FHVFDMR.T
*	HsFlag-ZnF-HIT2_Ti_	2.5009	0.236	952.35	952.119	3607.6	1	724.1	91.7	1	K.FHVFDMR.T
*	HsFLAG-BC014022_	3.8507	0.3697	1517.11	1517.682	4707.5	1	931	73.1	2	R.TQHPTKGFASVSEK.A
*	HsFlag-NUFIP_Ti_10	5.2692	0.3973	1671.71	1670.952	6937.8	1	1918.7	80	130	R.ELFLTAGGAGGLHLWK.Y
*	HsFLAG-BC014022_	5.5377	0.4476	2619.92	2621.013	5715	1	1754.7	43.2	1	R.ELFLTAGGAGGLHLWKYEYPIQR.S
*	HsFlag-NUFIP_Ti_11	5.0459	0.3556	3663.49	3663.045	6465.5	1	737.7	26.5	17	K.DSEGIEMGVAGSVSLLQNVTLSTQPISSLDWSPDK.R
*	HsFLAG-UTX1_Ti_20	3.952	0.3652	1685.98	1685.81	3786	1	758.4	76.9	4	K.RGLCVCSSFDQTVR.V
*	HsFlag-FLJ20643_Ti	2.5491	0.1999	1532.44	1529.622	8078.7	1	1076.8	66.7	1	R.GLCVCSSFDQTVR.V

gi|39812115|r	79	1098	75.50%	624	70484	7.8	actin-related protein 8 [Homo sapiens]				
*	HsFLAG-ARP8_Ti_2	4.3155	0.4299	1887.95	1889.208	5429.6	1	659.7	55.9	2	R.IGRATDTLPASIPHVIAR.R
*	HsFLAG-ARP8_Ti_2	2.7813	0.2683	1561.69	1562.809	4098.6	1	307.2	50	6	R.ATDTLPASIPHVIAR.R
*	HsFLAG-ARP8_Ti_2	4.3263	0.3803	1562.93	1562.809	3546	1	492.9	64.3	29	R.ATDTLPASIPHVIAR.R
*	HsFLAG-ARP8_Ti_2	3.546	0.238	1565.08	1562.809	3685.9	1	741.1	46.4	1	R.ATDTLPASIPHVIAR.R
*	HsFLAG-ARP5_Ti_1	2.2401	0.1862	1226.55	1227.409	6977	1	509.5	61.1	1	R.HKQQGQPLYK.D
*	HsFLAG-ARP5_Ti_1	2.799	0.0862	1227.34	1227.409	8084.3	4	832.4	72.2	1	R.HKQQGQPLYK.D
*	HsFLAG-ARP8_Ti_2	2.8681	0.3036	1732.4	1732.98	4510.4	2	331.9	53.8	1	K.QQGQPLYKDSWLLR.E
*	HsFLAG-ARP8_Ti_2	3.5546	0.1045	3115.32	3115.432	6674.5	1	445	24	1	K.QQGQPLYKDSWLLREGLNKPESNEQR.Q
*	HsFLAG-ARP8_Ti_2	4.5174	0.2651	2712.2	2712.982	8851.4	6	657.8	28.4	2	K.DSWLLREGLNKPESNEQRQNGLK.M
*	HsFLAG-ARP8_Ti_2	2.8889	0.2992	1401.35	1401.476	3482.6	1	273.4	63.6	1	R.EGLNKPESNEQR.Q
*	HsFLAG-ARP8_Ti_1	2.7718	0.2435	1401.67	1401.476	3237.8	4	336.6	63.6	6	R.EGLNKPESNEQR.Q
*	HsFLAG-ARP8_Ti_2	3.4759	0.1065	1078.34	1078.271	4205.5	2	932.8	87.5	5	K.MVDQAIWSK.K
*	HsFLAG-ARP8_Ti_2	2.5774	0.1462	1079.54	1078.271	10426.1	6	735.7	68.8	7	K.MVDQAIWSK.K
*	HsFLAG-TIP49b_Ti_	3.5298	0.2529	1153.47	1153.327	7382.9	1	1084.7	83.3	30	R.RIPVSPEQAR.S
*	HsFLAG-ARP8_Ti_2	3.8359	0.3849	1627.51	1627.825	6382.2	1	569.5	61.5	5	K.QMRPAILDHCSGNK.W
*	HsFLAG-ARP8_Ti_1	4.0173	0.2027	1630.37	1627.825	9114.2	1	1671.4	50	4	K.QMRPAILDHCSGNK.W
*	HsFLAG-ARP8_Ti_1	2.9937	0.3103	1211.14	1212.314	4402.7	1	482.8	70	3	R.PAILDHCSGNK.W
*	HsFLAG-ARP8_Ti_2	3.7251	0.2978	1213.13	1212.314	8263.4	1	1394.1	80	9	R.PAILDHCSGNK.W
*	HsFLAG-ARP8_Ti_2	7.0604	0.4135	3926.42	3926.305	10452.8	1	1903.3	31.5	40	K.WTNTSHHPEYLVGEEALYVNPLDCYNIHWPIR.R
*	HsFLAG-ARP8_Ti_2	3.7727	0.1921	4082.99	4082.492	4374	1	608.2	26.6	1	K.WTNTSHHPEYLVGEEALYVNPLDCYNIHWPIRR.G
*	HsFLAG-ARP8_Ti_2	2.6915	0.1594	1231.56	1232.506	6047.2	3	902.3	77.8	4	K.YLEIPLKDLK.Y
*	HsFLAG-ARP5_Ti_1	2.9162	0.164	1232.46	1232.506	5389.3	5	787.5	77.8	1	K.YLEIPLKDLK.Y
*	HsFLAG-ARP8_Ti_1	3.0031	0.3008	1844.2	1845.158	3733.5	1	392.3	57.7	1	K.YYRCILLIPDIYNK.Q
*	HsFLAG-ARP8_Ti_2	2.6867	0.1847	1361.42	1362.618	4676.7	2	420.7	60	3	R.CILLIPDIYNK.Q
*	HsFLAG-ARP8_Ti_1	2.3631	0.0842	1090.37	1091.413	6163.4	9	478.3	75	1	K.ELVNMILMK.M
*	HsFLAG-ARP8_Ti_2	2.8729	0.1386	1091.3	1091.413	6852.8	1	784	81.2	5	K.ELVNMILMK.M
*	HsFLAG-ARP8_Ti_2	6.8455	0.4104	3491.05	3490.796	10141.4	1	1883.8	30.5	66	K.MGFSGIVVHQESVCATYGSGLSSTCIVDVGDQK.T
*	HsFLAG-ARP8_Ti_1	1.9558	0.1085	1505.4	1506.545	5269.5	4	246	45.8	1	K.TSVCCVEDGVSHR.N
*	HsFLAG-ARP8_Ti_2	4.1342	0.4822	1507.19	1506.545	6566.2	1	1224.6	75	26	K.TSVCCVEDGVSHR.N
*	HsFLAG-ARP8_Ti_1	3.1116	0.3149	1297.68	1298.405	3516.5	1	331.8	72.7	9	R.LCLAYGGSDVSR.C
*	HsFLAG-ARP8_Ti_2	3.7487	0.2661	1299.32	1298.405	6959.8	1	1871.5	86.4	7	R.LCLAYGGSDVSR.C
*	HsFLAG-ARP8_Ti_2	2.9681	0.1829	2482.49	2483.779	9380	2	376.4	36.8	3	R.LCLAYGGSDVSRCFYWLMQR.A
*	HsFLAG-ARP8_Ti_1	2.2023	0.2834	1203.41	1204.398	3606.5	9	196.8	64.3	6	R.CFYWLMQR.A
*	HsFLAG-ARP8_Ti_2	3.4747	0.2497	1204.37	1204.398	7944.6	1	1323	92.9	24	R.CFYWLMQR.A
*	HsFLAG-ARP8_Ti_2	2.4782	0.098	1583.58	1584.738	3797.4	8	206.4	45.8	1	R.AGFPYRECQLTNK.M
*	HsFLAG-ARP8_Ti_2	4.0565	0.1901	1584.7	1584.738	7670.3	2	821.2	62.5	4	R.AGFPYRECQLTNK.M
*	HsFLAG-ARP8_Ti_2	4.3369	0.3972	2145.14	2145.454	9721	1	2620	51.6	2	R.ECQLTNKMDCLLLQHLK.E
*	HsFLAG-FLJ20309_	3.6119	0.2529	1271.12	1271.527	8200.6	2	1042.3	77.8	17	K.MDCLLLQHLK.E
*	HsFLAG-ARP8_Ti_2	3.1164	0.219	1271.22	1271.527	5583.6	1	541.4	66.7	3	K.MDCLLLQHLK.E
*	HsFLAG-ARP8_Ti_2	6.3072	0.3368	2589.31	2589.747	10794.9	1	1370.8	36.2	90	K.ETFCHLDQDISGLQDHEFQIR.H
*	HsFLAG-ARP8_Ti_2	5.931	0.3584	2589.74	2589.747	8562.9	1	1214.9	52.5	96	K.ETFCHLDQDISGLQDHEFQIR.H
*	HsFLAG-ARP8_Ti_2	5.3678	0.2854	4015.19	4015.356	7484.8	1	748.1	25	14	K.ETFCHLDQDISGLQDHEFQIRHPDSPALLYQFR.L

*	HsFLAG-ARP8_Ti_2	2.4409	0.3241	1443.84	1444.633	3299.8	1	297.7	59.1	5	R.HPDSPALLYQFR.L
*	HsFLAG-ARP8_Ti_2	3.4305	0.2987	1444.71	1444.633	5933.3	2	713.4	72.7	33	R.HPDSPALLYQFR.L
*	HsFLAG-ARP8_Ti_2	3.8861	0.1588	1444.9	1444.633	4902.8	3	1006.2	54.5	14	R.HPDSPALLYQFR.L
*	HsFLAG-ARP8_Ti_2	5.3521	0.3625	2594.14	2596.059	6271.5	1	1255.4	54.3	4	R.LGDEKLQAPMALFYPATFGIVGQK.M
*	HsFLAG-ARP8_Ti_2	4.6711	0.2336	2597.68	2596.059	5138.4	1	918.7	37	2	R.LGDEKLQAPMALFYPATFGIVGQK.M
*	HsFLAG-ARP8_Ti_2	6.2077	0.4365	2053.06	2053.47	6921.5	1	2114.1	50	6	K.LQAPMALFYPATFGIVGQK.M
*	HsFLAG-ARP8_Ti_2	5.2604	0.4039	2053.2	2053.47	8064.6	1	1976.1	72.2	18	K.LQAPMALFYPATFGIVGQK.M
*	HsFLAG-ARP8_Ti_2	2.6249	0.1023	884.93	887.045	6004	1	848.6	100	1	K.MTTLQHR.S
*	HsFLAG-ARP8_Ti_2	5.0733	0.4119	2269.68	2268.358	5099.2	1	954.2	63.2	29	R.SQGDPEDPHDEHYLLATQSK.Q
*	HsFLAG-ARP8_Ti_2	4.2687	0.2569	2270.83	2268.358	4207.6	2	684.1	39.5	6	R.SQGDPEDPHDEHYLLATQSK.Q
*	HsFLAG-ARP5_Ti_1	3.8845	0.3881	2939.07	2940.066	5643.1	1	1114.9	38	3	R.SQGDPEDPHDEHYLLATQSKQEQSAK.A
*	HsFLAG-ARP8_Ti_2	3.8173	0.2452	2940.14	2940.066	5176.8	1	489.9	40	1	R.SQGDPEDPHDEHYLLATQSKQEQSAK.A
*	HsFLAG-ARP5_Ti_1	3.442	0.3224	1505.93	1505.714	5263	1	1023.5	73.1	1	R.KSASKPIGFEGDLR.G
*	HsFLAG-TCF3_Ti_1(	3.495	0.2915	1377.74	1377.54	3552.5	2	534.8	70.8	11	K.SASKPIGFEGDLR.G
*	HsFLAG-ARP8_Ti_1	2.2742	0.1372	1003.58	1004.131	3584.7	7	340.3	75	1	K.PIGFEGDLR.G
*	HsFLAG-ARP8_Ti_2	3.409	0.2367	1003.96	1004.131	4220.1	1	1014.1	93.8	5	K.PIGFEGDLR.G
*	HsFLAG-ARP8_Ti_2	6.5971	0.4611	4275.21	4274.592	10453.8	1	1931.3	27.5	7	MSR.K
*	HsFLAG-ARP8_Ti_2	8.6309	0.5368	3303.86	3304.585	10003.3	1	5032.1	41.9	74	R.LHSQEVDLGSAQGDGLMAGNDSEEALTALMSR.K
*	HsFLAG-ARP8_Ti_2	3.3947	0.2344	1093.48	1094.296	5209.6	2	669.6	66.7	7	R.KTAISLFEGK.A
*	HsFLAG-ARP8_Ti_2	3.545	0.1686	1093.58	1094.296	4995.4	1	890.1	83.3	11	R.KTAISLFEGK.A
*	HsFLAG-ARP8_Ti_2	2.4017	0.1807	965.33	966.122	7055.9	8	483.6	62.5	8	K.TAISLFEGK.A
*	HsFLAG-ARP8_Ti_2	2.7094	0.0919	966.26	966.122	4129.3	1	769.3	87.5	3	K.TAISLFEGK.A
*	HsFlag-Ies6_293_Ti_	4.8274	0.3255	1722.02	1722.779	6485.6	1	1421.7	75	14	K.AILHSIDCCSSDDTK.K
*	HsFLAG-ARP8_Ti_1	3.8035	0.2305	1723.91	1722.779	5496.6	2	797.3	42.9	2	K.AILHSIDCCSSDDTK.K
*	HsFLAG-ARP8_Ti_1	4.0139	0.2433	1851.41	1850.953	6980.9	2	938	40	2	K.AILHSIDCCSSDDTKK.K
*	HsFLAG-ARP8_Ti_1	4.9264	0.3848	1851.51	1850.953	7567.7	1	1645.8	73.3	8	K.AILHSIDCCSSDDTKK.K
*	HsFLAG-ARP8_Ti_2	4.6611	0.3544	1979.54	1979.127	9487.7	1	2228.1	71.9	1	K.AILHSIDCCSSDDTKKK.M
*	HsFLAG-ARP8_Ti_2	5.6409	0.4464	1740.66	1740.132	6441.2	1	1666.9	76.7	17	K.MYSSILVVGGGLMFHK.A
*	HsFLAG-ARP8_Ti_2	3.9552	0.2912	1741.42	1740.132	3824.8	4	391.3	36.7	1	K.MYSSILVVGGGLMFHK.A
*	HsFLAG-FLJ20309_	2.0515	0.1865	1028.44	1029.144	6488.6	4	424.2	71.4	1	K.AQEFLQHR.I
*	HsFLAG-ARP8_Ti_2	2.8963	0.1873	1030.78	1029.144	6240.5	5	1024.2	92.9	9	K.AQEFLQHR.I
*	HsFLAG-ARP8_Ti_2	3.5256	0.2291	1497.94	1497.74	9766.6	1	1256.7	72.7	3	K.AQEFLQHRILNK.M
*	HsFLAG-ARP8_Ti_2	4.2295	0.2583	1553.8	1553.845	5770.5	1	1257.4	87.5	7	R.RIIENVDVITRPK.D
*	HsFLAG-ARP8_Ti_2	2.9765	0.1573	1553.91	1553.845	2910.1	1	211	66.7	9	R.RIIENVDVITRPK.D
*	HsFLAG-ARP8_Ti_2	4.2197	0.1436	1397.29	1397.658	7215.7	1	1681.6	86.4	29	R.IIENVDVITRPK.D
*	HsFLAG-ARP8_Ti_2	5.797	0.3732	2196.15	2195.446	7900.5	1	1980.9	45.8	50	K.GGAVLACLDTTQELWIYQR.E
*	HsFLAG-ARP8_Ti_2	6.0385	0.4596	2196.53	2195.446	8710.1	1	2370.1	66.7	156	K.GGAVLACLDTTQELWIYQR.E
gi|42822884|r	18	148	75.50%	192	20643	10	hypothetical protein LOC125476 [Homo sapiens]				
*	HsFLAG-ARP5_Ti_1	2.8521	0.1015	1904.26	1903.021	6150	1	393.2	42.1	2	K.KRPASPSHNGSSGGGYGASK.K
*	HsFlag-Ies6_293_Ti_	4.7623	0.5394	1774.28	1774.847	7315.2	1	1343	63.9	8	K.RPASPSHNGSSGGGYGASK.K
*	HsH2AZ-FLAG_293_	3.863	0.2922	1775.64	1774.847	8309.9	4	716.3	33.3	1	K.RPASPSHNGSSGGGYGASK.K
*	HsFlag-Ies6_293_Ti_	2.6681	0.2643	1903.59	1903.021	5265.7	2	384.7	44.7	1	K.RPASPSHNGSSGGGYGASKK.K
*	HsFLAG-ARP8_Ti_2	4.5531	0.3591	1946.08	1947.142	6181.4	1	1294.1	63.9	13	K.ASASSFAQGISMEAMSENK.M

*	HsFLAG-ARP5_Ti_1	2.9665	0.317	1407.97	1408.609	2869.7	7	293	66.7	1	K.MVPSEFSTGPVEK.A
*	HsFLAG-TIP49b_Ti_	2.0157	0.1162	871.64	872.098	3203.9	1	458.1	78.6	1	K.AAKPLPFK.D
*	HsFlag-Ies6_293_Ti_	3.4684	0.4127	1549.47	1550.674	2957.4	1	321.5	56.7	4	K.DPNFVHSGHGGAVAGK.K
*	HsFLAG-ARP8_Ti_2	4.5472	0.3358	1550.23	1550.674	3748.7	1	777.1	76.7	18	K.DPNFVHSGHGGAVAGK.K
*	HsFLAG-FLJ20309_	4.302	0.4046	2420.86	2421.714	6698.5	1	842.7	52.5	16	R.ALPWQLNDPNYFSIDAPPSFK.P
*	Hs293Flag-Ies2_Ti_1	3.2879	0.1237	2718.88	2718.084	6507.4	1	403.5	34.8	4	R.ALPWQLNDPNYFSIDAPPSFKPAK.K
*	HsFLAG-ARP5_Ti_1	5.6808	0.4579	1986.64	1987.174	6055.2	1	1662.3	73.5	15	K.KYSDVSGLLANYTDPQSK.L
*	HsH2AZ-FLAG_293_	5.0475	0.4461	1858.58	1859	6796.6	1	2040.4	75	13	K.YSDVSGLLANYTDPQSK.L
*	HsFLAG-FLJ20309_	4.2593	0.3548	1392.57	1392.551	5425.7	1	1326.5	90	17	R.FSTIEEFSYIR.R
*	HsFLAG-TCF3_Ti_1	4.6596	0.2825	1560.73	1560.837	6051.1	1	1432.8	51.9	2	R.RLPSDVVTGYLALR.K
*	HsFLAG-TCF3_Ti_1	4.7377	0.3624	1560.8	1560.837	5777	1	1344.1	80.8	28	R.RLPSDVVTGYLALR.K
*	HsFLAG-ARP5_Ti_1	4.8186	0.2947	1688.74	1689.011	6617.2	1	1678.8	51.8	2	R.RLPSDVVTGYLALRK.A
*	HsFLAG-TCF3_Ti_1	2.8612	0.201	1689.12	1689.011	5072.1	8	377.7	57.1	2	R.RLPSDVVTGYLALRK.A
gi|34577110|r	23	73	74.70%	364	39420	8.1	aldolase A [Homo sapiens]				
gi|4557305|re	23	73	74.70%	364	39420	8.1	aldolase A [Homo sapiens]				
gi|34577112|r	23	73	74.70%	364	39420	8.1	aldolase A [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.0629	0.1785	1069.22	1069.206	6103.3	1	981.6	87.5	1	K.KELSDIAHR.I
	HsFlag-VPS71_Ti_1	2.7354	0.3706	1332.59	1333.481	6706.1	1	662.3	61.5	2	K.GILAADESTGSIAK.R
	HsFlag-VPS71_Ti_1	4.436	0.3893	1334.59	1333.481	6440	1	1513.9	76.9	2	K.GILAADESTGSIAK.R
	HsFlag-VPS71_Ti_1	4.8945	0.343	1647.68	1647.742	6818.9	1	1563.9	84.6	1	K.RLQSIGTENTEENR.R
	HsFlag-VPS71_Ti_1	7.2182	0.5056	3115.17	3115.566	9009.8	1	1277.2	30.8	3	R.QLLLTADDRVNPCIGGVILFHETLYQK.A
	HsFlag-VPS71_Ti_1	3.5113	0.3738	2088.73	2089.408	7154.2	1	1072.6	58.8	1	R.VNPCIGGVILFHETLYQK.A
	HsFlag-DPCD_Ti_20	4.3599	0.1052	2273.73	2273.462	8043.6	1	608.1	43.2	1	K.GVVPLAGTNGETTTQGLDGLSER.C
	HsFlag-VPS71_Ti_1	4.8541	0.424	2107.1	2108.42	5082.2	1	1131.3	65.8	4	K.IGEHTPSALAIMENANVLAR.Y
	HsFlag-VPS71_Ti_1	4.7245	0.2305	2108.8	2108.42	6763.9	1	1308.9	40.8	6	K.IGEHTPSALAIMENANVLAR.Y
	HsFlag-VPS71_Ti_1	4.0335	0.3068	3022.16	3022.348	5181.6	2	408.1	36.5	3	R.YASICQQNGIVPIVEPEILPDGDHDLK.R
	HsFlag-VPS71_Ti_1	5.5709	0.2217	3022.85	3022.348	6479.9	2	791.7	30.8	6	R.YASICQQNGIVPIVEPEILPDGDHDLK.R
	HsH2AZ-FLAG_293_	1.9697	0.1264	763.69	763.955	6757.4	3	659.4	75	4	K.VLAAVYK.A
	HsFLAG-FLJ20729_	4.5159	0.2775	1711.48	1710.971	8217.6	1	1314.5	60.7	8	K.ALSDHHIYLEGTLLK.P
	HsFlag-VPS71_Ti_1	3.9602	0.2695	1441.76	1441.611	4335.9	1	973.2	83.3	2	K.PNMVTPGHACTQK.F
	HsFlag-VPS71_Ti_1	5.1914	0.4373	1676.71	1676.928	6375.4	1	1745.9	78.6	5	K.FSHEEIAMATVTALR.R
	HsFlag-VPS71_Ti_1	3.1517	0.2674	1832.64	1833.116	10853.7	5	760.8	50	1	K.FSHEEIAMATVTALRR.T
	HsFlag-VPS71_Ti_1	5.3631	0.3659	3216.07	3215.588	9152.7	1	2168.6	34.2	2	R.RTVPPAVTGITFLSGGQSEEEASINLNAINK.C
	HsFLAG-p53-DNA-D	3.1202	0.2367	1809.32	1810.115	3585.4	1	635.3	64.3	1	K.CPLLKPWALTFSYGR.A
	HsFlag-VPS71_Ti_1	3.5725	0.2934	1198.81	1198.367	5068.6	1	1115.9	88.9	2	K.PWALTFSYGR.A
	HsFLAG-p53-DNA-D	2.8641	0.1622	1094.36	1094.213	7427	2	935.6	81.2	1	K.AAQEEYVKR.A
	HsFlag-VPS71_Ti_1	4.136	0.2515	1290.1	1289.444	7380.7	1	1420.7	81.8	11	K.RALANSLACQGK.Y
	HsFlag-VPS71_Ti_1	2.54	0.1851	1133.56	1133.256	5973	1	440.8	60	1	R.ALANSLACQGK.Y
	HsFLAG-Lin9_Ti_20	4.3034	0.4796	2228.57	2229.367	5567.1	1	1277.6	61.9	5	K.YTPSGQAGAAASESLFVSNHAY.-
gi|17986283|r	29	507	74.30%	451	50136	5.1	tubulin, alpha 3 [Homo sapiens]				
	HsSrcap_Ti_205.362	5.2798	0.4255	4301.41	4299.657	10101.8	1	671.9	20.3	1	R.ECISIHVGQAGVQIGNACWELYCLEHGIQPDGQMPSDK.T
	HsFLAG-ARP6_Ti_1	5.5507	0.3763	2011.61	2009.093	9267.4	1	1408.9	57.9	84	K.TIGGGDDSFNTFFSETGAGK.H
	HsFLAG-ARP6_Ti_1	5.0349	0.3	1702.67	1702.945	4531.2	1	1118.7	78.6	44	R.AVFVDLEPTVIDEVR.T

	HsFLAG-ARP6_Ti_1	4.0678	0.2493	1703.54	1702.945	8950.2	1	1040.6	42.9	1	R.AVFVDLEPTVIDEVR.T
	HsFLAG-p53-DNA-D	3.8546	0.3066	2415.78	2416.655	9887	1	636.1	42.5	25	R.QLFHPEQLITGKEDAANNYAR.G
	HsSrcap_Ti_204.213	5.0964	0.4219	2416.38	2416.655	6002.3	1	934.1	37.5	18	R.QLFHPEQLITGKEDAANNYAR.G
	HsFLAG-ARP6_Ti_1	3.2026	0.111	1086.33	1086.274	5676.6	1	1026.6	93.8	15	K.EIIDLVLDR.I
	HsFLAG-ARP6_Ti_1	5.5288	0.4605	3519.46	3520.951	9178.7	1	1611.9	30.5	2	R.KLADQCTGLQGFLVFHSFGGGTGSGFTSLLMER.L
	HsFLAG-ARP6_Ti_1	6.8756	0.4682	3390.27	3392.777	8761.3	1	1604.7	31.5	13	K.LADQCTGLQGFLVFHSFGGGTGSGFTSLLMER.L
	HsScrap_Ti_106.239	2.55	0.1652	1877.45	1876.082	6295.5	1	349.4	53.6	1	R.RNLDIERPTYTNLNR.L
	HsFlag-ZnF-HIT2_Ti_	2.9442	0.2517	1719.52	1719.895	6354.4	3	522.7	57.7	12	R.NLDIERPTYTNLNR.L
	HsFLAG-ARP6_Ti_1	4.5345	0.4222	1458.63	1458.742	6748.6	1	1765.2	84.6	9	R.LIGQIVSSITASLR.F
	HsFLAG-ARP6_Ti_1	5.8116	0.4265	2410.46	2410.689	5990.7	1	1327.4	60	74	R.FDGALNVDLTEFQTNLVPYPR.I
	HsYL1_Ti_106.2380.	4.538	0.4145	1756.22	1758.07	4074.6	1	799.2	70	54	R.IHFPLATYAPVISAEK.A
	HsFLAG-ARP6_Ti_1	5.1723	0.3713	2751.88	2752.037	6388.1	1	727.7	32.6	7	K.AYHEQLSVAEITNACFEPANQMVK.C
	HsYL1_Ti_103.2152.	5.4112	0.353	2751.97	2752.037	8492.5	1	1660.1	52.2	3	K.AYHEQLSVAEITNACFEPANQMVK.C
	HsFLAG-ARP6_Ti_1	3.1777	0.2663	1250.3	1250.43	4496.7	1	907.7	93.8	7	K.YMACCLLYR.G
	HsH2AZ-FLAG_293_	2.3357	0.2535	1015.43	1016.183	6915.1	2	562	72.2	14	K.DVNAAIATIK.T
	HsSrcap_Ti_202.001	3.6793	0.2729	1017.71	1016.183	5879.8	1	1088.4	83.3	8	K.DVNAAIATIK.T
	HsSrcap_Ti_205.279	4.5969	0.4286	1755.42	1755.98	5429.1	1	785.6	65.4	26	K.RTIQFVDWCPTGFK.V
	HsSrcap_Ti_205.280	4.8872	0.2348	1757.48	1755.98	8327.5	1	2242.3	57.7	10	K.RTIQFVDWCPTGFK.V
	HsSrcap_Ti_202.300	2.6402	0.345	1598.54	1599.793	6635.7	1	411.8	50	2	R.TIQFVDWCPTGFK.V
	HsFLAG-TCF3_Ti_1(	4.0211	0.3559	1599.41	1599.793	6154.4	1	984.8	70.8	8	R.TIQFVDWCPTGFK.V
	HsFLAG-ARP6_Ti_2	4.0719	0.4153	1825.6	1826.103	3498.4	1	615.9	58.8	34	K.VGINYQPPTVVPGGDLAK.V
	HsFLAG-ARP6_Ti_1	6.0682	0.4321	1865.52	1866.108	10861.7	1	2782.2	75	18	R.AVCMLSNTTAIAEAWAR.L
	HsFLAG-ARP6_Ti_1	4.4765	0.3204	1867.57	1866.108	8904.4	1	1596.3	45.3	7	R.AVCMLSNTTAIAEAWAR.L
	HsFLAG-ARP6_Ti_1	3.7547	0.214	2330.07	2331.521	8623.8	3	888.4	34.2	2	R.AFVHWYVGEGMEEGEFSEAR.E
	HsFLAG-ARP6_Ti_1	4.334	0.4395	2330.87	2331.521	6787.1	1	1352.6	57.9	3	R.AFVHWYVGEGMEEGEFSEAR.E
	HsFlag-Ies6_293_Ti_	4.6127	0.3488	2350.09	2350.275	8478.9	1	1358.3	57.5	5	K.DYEEVGVDSVEGEGEEEGEEY.-
gi|4885431|re	58	1356	72.50%	641	70025	5.6	heat shock 70kDa protein 1B [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	5.785	0.3078	2265.88	2266.525	7092.9	1	1398.9	57.1	37	K.AAAIGIDLGTTYSCVGVFQHGK.V
	HsFLAG-ARP6_Ti_1	4.0748	0.3138	2267.01	2266.525	4372.5	1	773.6	35.7	14	K.AAAIGIDLGTTYSCVGVFQHGK.V
	HsFLAG-ARP6_Ti_1	5.0723	0.2775	3475.75	3476.837	7568.2	1	651.7	25	23	K.AAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNR.T
	HsFlag-FLJ90652_2!	3.6517	0.3726	1487.89	1488.594	3812.9	1	610.4	75	34	R.TTPSYVAFTDTER.L
	Hs293Flag-Ies2_Ti_1	3.2174	0.4318	1488.58	1488.594	3710.2	1	167.1	54.2	6	R.TTPSYVAFTDTER.L
	HsFLAG-ARP6_Ti_2	5.6419	0.2894	1659.34	1659.839	4755.5	1	1178	78.6	39	K.NQVALNPQNTVFDAK.R
	HsFLAG-TCF3_Ti_1(	3.9084	0.3083	1815.46	1816.027	4917	1	699.4	60	3	K.NQVALNPQNTVFDAKR.L
	HsFLAG-TCF3_Ti_1(	2.8868	0.2653	1222.47	1223.386	3364.3	1	525.2	75	7	K.FGDPVVQSDMK.H
	HsFlag-FLJ90652_2!	4.1764	0.3409	1222.48	1223.386	5313	1	1403.4	90	13	K.FGDPVVQSDMK.H
	HsFlag-FLJ90652_2!	2.6975	0.1757	1456.44	1456.601	4625.5	1	448	59.1	2	K.HWPFQVINDGDK.P
	HsFLAG-ARP6_Ti_1	3.7224	0.3578	1457.44	1456.601	3155.5	1	697.6	81.8	5	K.HWPFQVINDGDK.P
	HsFLAG-ARP6_Ti_1	5.4135	0.2578	1680.83	1681.891	5101	1	1587.9	59.6	43	K.HWPFQVINDGDKPK.V
	HsFlag-ZnF-HIT2_Ti_	4.2583	0.364	1681	1681.891	4034.1	1	1006.7	80.8	65	K.HWPFQVINDGDKPK.V
*	HsFLAG-ARP8_Ti_2	3.0492	0.1674	1139.2	1139.294	6594.2	2	723.8	72.2	8	K.VQVSYKGETK.A
*	HsFlag-FLJ20643_Ti	3.242	0.241	1140.07	1139.294	5287.2	2	856.4	83.3	9	K.VQVSYKGETK.A
	HsFLAG-FLJ20729_	4.0267	0.3494	1616.65	1615.882	4580.3	1	846.5	76.9	19	K.AFYPEEISSMVLTK.M

	HsFlag-NUFIP_Ti_1	4.3722	0.3972	3003.16	3003.338	5168.8	1	380.9	34.6	16	K.EIAEAYLGYPVTNAVITVPAYFNDSQR.Q
	HsFlag-NUFIP_Ti_1	4.3601	0.2186	3004.85	3003.338	4429.3	1	419.9	29.8	7	K.EIAEAYLGYPVTNAVITVPAYFNDSQR.Q
	HsFlag-FLJ20643_Ti	2.8122	0.287	1197.73	1198.408	3228.1	7	262.1	59.1	5	K.DAGVIAGLNVLR.I
	HsFLAG-ARP6_Ti_1	4.5976	0.2685	1198.23	1198.408	6316.9	1	2167	95.5	46	K.DAGVIAGLNVLR.I
	HsFlag-FLJ90652_2	5.0718	0.2176	1688.21	1688.921	6740.8	1	1838.4	51.7	10	R.IINEPTAAAIAYGLDR.T
	HsFLAG-ARP6_Ti_1	5.4263	0.43	1689.04	1688.921	5489.6	1	1548.3	80	52	R.IINEPTAAAIAYGLDR.T
	HsFlag-ZnF-HIT2_Ti	4.6766	0.4075	1675.9	1676.696	6824.2	1	1767	76.7	48	K.ATAGDTHLGGEDFDNR.L
	HsFLAG-TCF3_Ti_1	2.6951	0.2599	1261.45	1262.451	5998.8	1	521.8	66.7	20	R.LVNHFVEEFK.R
	HsFlag-NUFIP_Ti_2	3.8472	0.3159	1261.56	1262.451	6150.8	1	1081.9	83.3	88	R.LVNHFVEEFK.R
	HsFLAG-ARP5_Ti_1	3.5968	0.2665	1418.17	1418.638	8699.5	1	1270.3	80	23	R.LVNHFVEEFKR.K
	HsFLAG-TCF3_Ti_1	2.8914	0.2187	1418.62	1418.638	4140.4	1	446.4	70	1	R.LVNHFVEEFKR.K
	HsFlag-FLJ90652_2	3.2252	0.2635	3140.2	3139.443	4863.5	2	321.7	31.5	9	K.RTLSSSTQASLEIDSLFEGIDFYTSITR.A
	HsFlag-FLJ90652_2	5.3049	0.2495	3140.26	3139.443	10318.3	1	1612.5	30.6	2	K.RTLSSSTQASLEIDSLFEGIDFYTSITR.A
	HsFLAG-ARP6_Ti_1	4.809	0.3403	2983.09	2983.256	6992.5	1	683.9	36.5	22	R.TLSSSTQASLEIDSLFEGIDFYTSITR.A
	HsFLAG-ARP6_Ti_1	3.982	0.2027	1543.2	1543.686	7726	1	1819.5	56.8	8	R.ARFEELCSDLFR.S
	HsFLAG-TIP49b_Ti_	2.8901	0.2543	1543.7	1543.686	5209.7	8	240.3	54.5	1	R.ARFEELCSDLFR.S
	HsFlag-FLJ90652_2	4.4813	0.316	1544.45	1543.686	5279.2	1	1248.6	86.4	92	R.ARFEELCSDLFR.S
	HsFLAG-TCF3_Ti_1	3.5157	0.2378	1316.78	1316.419	6306.6	3	1058.7	83.3	9	R.FEELCSDLFR.S
	HsFLAG-ARP6_Ti_1	2.1699	0.1805	902.57	903.02	3454.5	4	265.1	64.3	2	R.STLEPVEK.A
	HsFLAG-ARP5_Ti_1	4.2482	0.3486	1822.54	1823.103	7778.4	1	1337.6	62.5	3	K.LDKAQIHDLVLVGGSTR.I
	HsFlag-FLJ90652_2	2.0672	0.1951	1109.54	1110.258	2531.8	4	138.1	62.5	2	K.LLQDFFNGR.D
	HsFlag-FLJ90652_2	3.2581	0.2081	1110.23	1110.258	5624	1	1107.9	93.8	24	K.LLQDFFNGR.D
	HsFLAG-ARP6_Ti_1	4.3587	0.1355	1580.35	1580.784	8035.3	3	1517.8	79.2	2	K.LLQDFFNGRDLNK.S
	HsFLAG-ARP6_Ti_1	6.6812	0.5227	2303.95	2305.608	7222.4	1	2114.5	63.6	124	K.SINPDEAVAYGAAVQAAILMGDK.S
	HsFLAG-ARP6_Ti_1	6.7971	0.4665	2304.11	2305.608	8353	1	2965.1	46.6	47	K.SINPDEAVAYGAAVQAAILMGDK.S
	HsFlag-ZnF-HIT2_Ti	4.7193	0.3858	3181.8	3182.741	4851.7	1	509.4	36.7	49	K.SENVQDLLLLDVAPLSLGLETAGGVMTALIK.R
	HsFlag-FLJ90652_2	6.8938	0.4375	3182.31	3182.741	9881.5	1	1770.7	30.8	34	K.SENVQDLLLLDVAPLSLGLETAGGVMTALIK.R
	HsFLAG-FLJ20309_	5.4572	0.4673	2788.6	2788.043	9884.1	1	1776.8	37	8	K.QTQIFTTYSDNQPGVLIQVYEGER.A
	HsFlag-ZnF-HIT2_Ti	4.6245	0.4536	2788.77	2788.043	6989.1	1	643	41.3	55	K.QTQIFTTYSDNQPGVLIQVYEGER.A
	HsFlag-NUFIP_Ti_11	4.3928	0.1486	2530.58	2531.822	9691	1	877.9	43.5	21	R.GVPQIEVTFDIDANGILNVTATDK.S
	HsFLAG-ARP5_Ti_1	3.9737	0.4094	1953.07	1954.162	7450.7	1	1448.8	70	1	R.MVQEAEKYKAEDEVQR.E
	HsFLAG-ARP5_Ti_1	4.0797	0.2004	2238.73	2239.465	6876.7	1	1014	42.6	1	R.MVQEAEKYKAEDEVQRER.V
	HsFLAG-TCF3_Ti_1	3.0245	0.244	1138.56	1138.222	3708.8	1	704.6	93.8	3	K.YKAEDEVQR.E
	HsFlag-FLJ90652_2	4.362	0.2456	1288.02	1288.461	6806.6	1	1526.8	90	24	K.NALESYAFNMK.S
	HsFLAG-ARP6_Ti_1	3.1355	0.2732	1289.43	1288.461	4692.1	1	433.4	70	18	K.NALESYAFNMK.S
	HsH2AZ-FLAG_293_	2.0691	0.1958	947.37	948.018	9365.8	3	803.1	68.8	4	K.SAVEDEGLK.G
	HsFlag-FLJ90652_2	5.4239	0.3384	1878.5	1878.055	6692.7	1	1641.9	76.7	7	K.CQEVISWLDANTLAEK.D
	HsFLAG-TCF3_Ti_1	5.0809	0.3353	2662.81	2663.866	9294.5	1	1178.4	50	16	K.CQEVISWLDANTLAEKDEFEHK.R
	HsFLAG-ARP6_Ti_1	4.827	0.2512	2663.16	2663.866	5386.4	1	1085.5	39.3	34	K.CQEVISWLDANTLAEKDEFEHK.R
	HsFLAG-ARP6_Ti_1	5.3629	0.4095	3184.98	3185.53	7847.8	1	1127.5	29.8	2	R.KELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
	HsFlag-NUFIP_Ti_1	6.1748	0.4351	3056.95	3057.356	7304.6	1	1142	43.3	49	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
	HsFlag-NUFIP_Ti_1	7.6261	0.4465	3056.96	3057.356	8868.5	1	2682.6	38.3	40	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G
gi|8923598|re	20	980	72.10%	290	32363	5.1	hypothetical protein LOC55011 [Homo sapiens]				

*	HsFlag-FLJ20643_Ti	3.2496	0.1945	1177.73	1178.371	8225.3	3	924.4	72.2	32 R.FEELLLQASK.E
*	HsFlag-NUFIP_Ti_1	4.1982	0.1758	1178.55	1178.371	6303.6	1	1516.9	88.9	118 R.FEELLLQASK.E
*	HsFlag-NUFIP_Ti_1	4.2842	0.378	2786.11	2787.068	6232.6	1	639.1	45.7	22 K.ELQQAQTTRPESTQIQPQPGFCIK.T
*	HsFlag-NUFIP_Ti_1	6.2347	0.3241	2787.14	2787.068	5926.7	1	1032.9	37	68 K.ELQQAQTTRPESTQIQPQPGFCIK.T
*	HsFlag-NUFIP_Ti_1	5.7677	0.4248	3882.79	3884.316	4664.7	1	518	25	44 K.VFINICHSPSIPPPADVTEEELLQMLEEDQAGFR.I
*	HsFlag-NUFIP_Ti_1	4.8352	0.3991	1608.24	1608.85	6233.6	1	1225.1	75	19 R.IPMSLGEPHAELDAK.G
*	HsFlag-FLJ20643_Ti	5.7838	0.5136	1924.1	1924	7235.5	1	1863.7	75	199 K.GQGCTAYDVAVNSDFYR.R
*	HsFlag-FLJ20643_Ti	3.1228	0.1285	1167.58	1167.328	4725.8	1	942	93.8	3 R.RMQNSDFLR.E
*	HsFlag-FLJ20643_Ti	3.6074	0.1166	1589.27	1586.826	7980.4	1	1010	69.2	1 R.ELVITIAREGLEDK.Y
*	HsFlag-FLJ20643_Ti	4.4473	0.454	2005.56	2005.194	8820.3	1	1460.2	66.7	6 R.EGLEDKYNLQLNPEWR.M
*	HsFlag-FLJ20643_Ti	2.332	0.1079	1332.68	1333.489	4363.8	1	311.3	72.2	2 K.YNLQLNPEWR.M
*	HsFlag-FLJ20643_Ti	3.7624	0.223	1333.66	1333.489	6776.2	2	1333.7	88.9	88 K.YNLQLNPEWR.M
*	HsFlag-NUFIP_Ti_11	4.9596	0.1362	1648.87	1648.88	6865.2	3	1433.1	53.8	4 K.NRPFMGSISQQNIR.S
*	HsFlag-NUFIP_Ti_1	4.6161	0.3975	1649.75	1648.88	5258.2	1	913.1	73.1	31 K.NRPFMGSISQQNIR.S
*	HsFlag-NUFIP_Ti_11	2.5487	0.2092	1377.45	1378.589	4488.2	1	325.9	63.6	1 R.PFMGSISQQNIR.S
*	HsFlag-FLJ20643_Ti	4.6205	0.4168	1530.59	1530.721	7673.6	1	1688.3	76.9	29 R.IQELGDLYTPAPGR.A
*	HsFlag-FLJ20643_Ti	4.5137	0.4176	2231.45	2229.451	6174.5	1	774.3	52.5	4 R.IQELGDLYTPAPGRAESGPEK.P
*	HsFlag-NUFIP_Ti_1	5.346	0.4343	1556.9	1557.744	7295.5	1	2145	82.1	288 K.LDGALGLSLEIGENR.L
*	HsFlag-NUFIP_Ti_11	4.6094	0.3335	2954.06	2953.386	6024.7	1	678.7	42	8 R.LVMGGPQQLYHLDAYIPLQINSHESK.A
*	HsFLAG-UTX1_Ti_2	5.1651	0.2345	2954.19	2953.386	3562.1	1	714.6	37	13 R.LVMGGPQQLYHLDAYIPLQINSHESK.A
gi|29788785|r	37	839	71.60%	444	49671	4.9	tubulin, beta polypeptide [Homo sapiens]			
*	HsFLAG-ARP6_Ti_1	6.5939	0.1945	3103.06	3104.273	6031.8	1	821.5	31.7	49 K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I
*	HsFlag-FLJ90652_2	3.6323	0.3152	3104.29	3104.273	4947.3	1	308.9	32.7	5 K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I
*	HsFLAG-TIP49b_Ti_	2.8634	0.2956	1301.53	1302.426	6152.8	1	570.9	63.6	10 R.ISVYYNEATGGK.Y
*	Hs293Flag-Ies2_Ti_1	3.5162	0.2889	1302.19	1302.426	5900	1	789.5	68.2	15 R.ISVYYNEATGGK.Y
*	HsFLAG-TCF3_Ti_1	3.8882	0.3998	1817.38	1818.039	8238.1	1	785	50	1 R.ISVYYNEATGGKYVPR.A
	HsFLAG-ARP6_Ti_1	4.2213	0.2479	1617.4	1616.87	4265.9	1	1041.3	78.6	14 R.AILVDLEPGTMDSVR.S
	HsFLAG-ARP6_Ti_1	5.3305	0.4496	2798.59	2800.065	6948.6	1	1444.6	52	59 R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-ARP6_Ti_1	7.0292	0.3487	2802.51	2800.065	7956.6	1	2098.3	39	59 R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-TCF3_Ti_1	7.1819	0.4728	1959.62	1960.151	9139.8	1	3610.1	82.4	73 K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-ARP6_Ti_1	4.9251	0.2887	1959.94	1960.151	7005.8	1	1288.7	41.2	34 K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-TIP49b_Ti_	5.684	0.3213	2087.63	2088.325	8116.7	1	2259	51.4	39 K.GHYTEGAELVDSVLDVVRK.E
	HsSrcap_Ti_206.286	6.4593	0.361	2087.84	2088.325	9352.8	1	2739.4	72.2	25 K.GHYTEGAELVDSVLDVVRK.E
	HsYL1_Ti_103.1035.	2.9392	0.1782	1078.13	1078.17	3062.5	4	568.7	85.7	4 K.IREEYPDR.I
	HsFLAG-TCF3_Ti_1	3.025	0.2204	2378.62	2379.736	6966.3	1	555.3	47.4	2 K.IREEYPDRIMNTFSVVPSPK.V
	HsFlag-VPS71_Ti_1	2.5434	0.1418	1319.6	1320.59	6897.3	9	431	59.1	1 R.IMNTFSVVPSPK.V
	HsFLAG-ARP6_Ti_1	4.5585	0.3954	1320.55	1320.59	7624	1	1689.8	86.4	26 R.IMNTFSVVPSPK.V
	HsFLAG-ARP6_Ti_1	6.4706	0.4855	4594.76	4595.903	4988.3	1	541.4	23.7	83 K.VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR.T
	HsFLAG-ARP6_Ti_1	4.7805	0.3574	2709.73	2710.041	10385.7	1	1165	31.2	30 K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsFLAG-ARP6_Ti_1	5.4731	0.383	2710.22	2710.041	8352.5	1	1412.5	47.9	39 K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsFLAG-ARP6_Ti_1	2.1817	0.2119	1130.19	1131.277	3484.6	1	331.1	72.2	1 R.FPGQLNADLR.K
	HsFLAG-ARP6_Ti_1	3.1035	0.1934	1133.31	1131.277	4537.1	1	968.3	94.4	20 R.FPGQLNADLR.K
	HsFLAG-ARP6_Ti_1	2.7216	0.2275	1259.45	1259.451	6377.3	1	1130.1	85	3 R.FPGQLNADLRK.L

	Hs293Flag-Ies2_Ti_1	4.1115	0.2404	1271.88	1272.594	7432.2	1	1437.4	85	9	R.KLAVNMVPFPR.L
	HsFLAG-Lin9_Ti_20	3.7432	0.2947	1144.31	1144.42	4934.2	1	1119.4	94.4	37	K.LAVNMVPFPR.L
	HsFLAG-ARP6_Ti_1	3.784	0.2563	1621.62	1621.94	4747.2	1	1118	76.9	9	R.LHFFMPGFAPLTSR.G
*	HsScrap_Ti_102.301	3.7284	0.3505	1661.17	1660.908	5522.5	2	655.5	41.1	2	R.ALTVPELTQQVFDAK.N
*	HsFLAG-TCF3_Ti_1	3.7064	0.1872	1662.5	1660.908	3477.1	1	666.1	75	18	R.ALTVPELTQQVFDAK.N
	HsFLAG-ARP6_Ti_1	3.1514	0.3044	1065.99	1066.201	5998.7	1	1325.1	87.5	4	K.NMMAACDPR.H
	HsFLAG-ARP6_Ti_1	3.3868	0.392	1040.35	1040.25	5162.1	1	1157.4	100	24	R.YLTVAAVFR.G
	Hs293Flag-Ies2_Ti_1	4.5214	0.2599	1447.29	1447.603	7900.2	2	1960.1	86.4	10	K.EVDEQMLNVQNK.N
	HsScrap_Ti_102.174	3.2133	0.1712	1447.35	1447.603	3682	1	435.8	72.7	4	K.EVDEQMLNVQNK.N
	HsFLAG-ARP6_Ti_1	4.0978	0.3327	1699.12	1697.888	5299.1	1	715	61.5	39	K.NSSYFVEWIPNNVK.T
	HsFLAG-TCF3_Ti_1	2.8997	0.2395	1029.45	1029.147	6481.9	1	1559.4	93.8	2	K.TAVCDIPPR.G
*	HsFLAG-ARP6_Ti_1	5.9778	0.4752	1871.55	1871.202	5636.8	1	1640.2	75	71	K.MAVTFIGNSTAIQELFK.R
*	HsFLAG-TCF3_Ti_1	3.2954	0.3863	2026.5	2027.389	8104.8	1	876.3	52.9	1	K.MAVTFIGNSTAIQELFKR.I
	HsFLAG-ARP6_Ti_1	4.1879	0.3996	1386.16	1386.612	7897.9	1	1417.6	85	10	K.RISEQFTAMFR.R
	HsFLAG-ARP6_Ti_1	3.7061	0.3498	1229.27	1230.424	8240.8	1	1542.7	88.9	7	R.ISEQFTAMFR.R
gi|5453603|re	38	245	70.80%	535	57488	6.4	chaperonin containing TCP1, subunit 2 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	5.6078	0.2716	1518.88	1518.837	6946	1	1902.4	78.6	22	R.LTSFIGAIAIGDLVK.S
*	HsFLAG-ARP6_Ti_1	2.5543	0.0907	1550.16	1549.78	5301.5	3	772	60.7	1	R.DASLMVTNDGATILK.N
*	HsFLAG-ARP6_Ti_1	6.3079	0.4938	2288.49	2289.502	8481.6	1	2069	64.3	30	R.VQDDEVGDGTTSVTVLAAELLR.E
*	HsFLAG-ARP6_Ti_1	5.8733	0.3925	2289.94	2289.502	9152.2	1	2045.3	41.7	8	R.VQDDEVGDGTTSVTVLAAELLR.E
*	HsFLAG-ARP6_Ti_1	3.4382	0.3048	1420.41	1420.701	3617.6	2	521.7	72.7	2	K.KIHPQTIIAGWR.E
*	HsFLAG-ARP6_Ti_1	5.1034	0.4073	1657.02	1657.775	8388.1	1	2235.4	76.7	2	R.EALLSSAVDHGSDEVK.F
*	HsFLAG-ARP5_Ti_1	4.7643	0.553	1960.48	1961.139	5997.3	1	1020.4	61.8	1	R.EALLSSAVDHGSDEVKFR.Q
*	HsFLAG-ARP6_Ti_1	5.4988	0.382	1781.5	1783.053	8572.2	1	2757.9	80	10	K.FRQDLMNIAGTTLSSK.L
*	HsFLAG-ARP6_Ti_1	3.7395	0.3096	1783.13	1783.053	6091.6	1	1122.5	46.7	1	K.FRQDLMNIAGTTLSSK.L
*	HsFLAG-ARP6_Ti_1	3.7852	0.2813	1479.22	1479.689	6208.4	1	794.7	65.4	1	R.QDLMNIAGTTLSSK.L
*	HsFLAG-ARP5_Ti_1	3.734	0.3276	1493.51	1493.79	7746	1	1155.3	69.2	2	R.LKGSGNLEAIHIIK.K
*	HsFLAG-ARP6_Ti_1	3.5127	0.2493	1252.45	1252.456	6236.8	2	918.3	72.7	6	K.GSGNLEAIHIIK.K
*	HsFLAG-ARP6_Ti_1	6.4408	0.5542	2042.33	2042.293	9304.7	1	3074.5	75	7	K.KLGGSLADSYLDEGFLLDK.K
*	HsFLAG-ARP6_Ti_1	5.0519	0.1669	2042.76	2042.293	7261.5	3	1329.2	41.7	2	K.KLGGSLADSYLDEGFLLDK.K
*	HsFLAG-TCF3_Ti_1	5.5032	0.5338	1913.72	1914.119	9135.3	1	1814.7	64.7	9	K.LGGSLADSYLDEGFLLDK.K
*	HsFLAG-ARP6_Ti_1	4.3389	0.3762	2041.83	2042.293	4998.8	1	1351.4	47.2	2	K.LGGSLADSYLDEGFLLDKK.I
*	HsFLAG-ARP6_Ti_1	4.6641	0.3401	2042.94	2042.293	7862.9	1	918.7	50	3	K.LGGSLADSYLDEGFLLDKK.I
*	HsFLAG-ARP6_Ti_1	4.3543	0.2203	1293.07	1292.49	6755	1	1611.7	86.4	2	K.ILIANTGMDTDK.I
*	HsFLAG-p53-DNA-D	3.376	0.1728	1284.36	1283.424	9860.1	1	1393.2	80	6	K.VAEIEHAEKEK.M
*	HsFLAG-ARP6_Ti_1	3.1884	0.3645	1131.15	1131.246	5542.9	1	1228.1	93.8	4	K.HGINCFINR.Q
*	HsFLAG-ARP5_Ti_1	4.8484	0.3736	3212.41	3211.619	5225.3	1	839.6	30.4	14	R.QLIYNYPEQLFGAAGVMAIEHADFAGVER.L
*	HsFLAG-ARP6_Ti_1	5.5575	0.4716	2097.44	2098.404	7321.2	1	1467.7	60.5	10	R.LALVTGGEIASTFDHPELVK.L
*	HsFLAG-ARP6_Ti_1	4.0822	0.284	2098.66	2098.404	3993.5	1	543.1	35.5	1	R.LALVTGGEIASTFDHPELVK.L
*	HsFLAG-ARP5_Ti_1	5.7674	0.3471	3215.32	3214.754	10919	1	1238.2	28.6	1	K.LIEEVMIGEDKLIHFSGVALGEACTIVLR.G
*	HsFLAG-ARP6_Ti_1	5.9259	0.5661	1956.22	1957.29	6516.3	1	2359.2	79.4	10	K.LIHFSGVALGEACTIVLR.G
*	HsFLAG-ARP6_Ti_1	4.3413	0.2248	1331.83	1331.425	8077.5	1	1577.7	81.8	1	R.GATQQILDEAER.S
*	HsFLAG-ARP6_Ti_1	4.9938	0.2994	1555.39	1555.781	6431.9	1	1695.1	80.8	20	R.SLHDALCVLAQTVK.D

*	HsFLAG-ARP6_Ti_1	4.5313	0.4281	2366.29	2367.666	8399	1	949	45.2	4	R.TVYGGGCSEMLMAHAVTQLANR.T
*	HsFLAG-ARP6_Ti_1	4.0331	0.3406	2366.69	2367.666	4058.4	1	633.6	34.5	1	R.TVYGGGCSEMLMAHAVTQLANR.T
*	HsFLAG-ARP6_Ti_1	2.4189	0.2359	1098.58	1099.244	4262.3	1	312.8	66.7	2	K.EAVAMESYAK.A
*	HsFLAG-ARP6_Ti_1	5.3053	0.3778	2348.32	2348.676	7932.2	1	1469.2	36.9	4	R.MLPTIIADNAGYDSADLVAQLR.A
*	HsFLAG-ARP6_Ti_1	6.283	0.511	2348.55	2348.676	7091.3	1	2264.6	69	14	R.MLPTIIADNAGYDSADLVAQLR.A
*	HsFLAG-ARP6_Ti_1	4.5175	0.451	1531.46	1531.64	8412.5	1	1714.2	75	5	R.AAHSEGNTTAGLDMR.E
*	HsFLAG-ARP6_Ti_1	5.2518	0.5299	2010.51	2010.31	8675.2	1	1553.6	63.9	15	R.EGTIGDMAILGITESFQVK.R
*	HsFLAG-ARP6_Ti_1	4.3424	0.2743	1739.07	1740.056	6375.6	1	1963.2	55	4	K.RQVLLSAAEAAEVILR.V
*	HsFLAG-ARP6_Ti_1	4.6365	0.2373	1740.75	1740.056	7763.4	1	1362.7	66.7	6	K.RQVLLSAAEAAEVILR.V
*	HsFLAG-ARP6_Ti_1	5.3266	0.3581	1583.39	1583.869	8951.6	1	2412.5	82.1	11	R.QVLLSAAEAAEVILR.V
*	HsFLAG-ARP5_Ti_1	2.8632	0.2353	1145.76	1146.26	4465	2	626.1	75	1	R.KRVPDHHPC.-
gi|57013276|r	29	591	70.70%	451	50152	5.1	tubulin, alpha, ubiquitous [Homo sapiens]				
	HsSrcap_Ti_205.362	5.2798	0.4255	4301.41	4299.657	10101.8	1	671.9	20.3	1	R.ECISIHVGQAGVQIGNACWELYCLEHGIQPDGQMPSDK.T
	HsFLAG-ARP6_Ti_1	5.5507	0.3763	2011.61	2009.093	9267.4	1	1408.9	57.9	84	K.TIGGGDDSFNTFFSETGAGK.H
	HsFLAG-ARP6_Ti_1	5.0349	0.3	1702.67	1702.945	4531.2	1	1118.7	78.6	44	R.AVFVDLEPTVIDEVR.T
	HsFLAG-ARP6_Ti_1	4.0678	0.2493	1703.54	1702.945	8950.2	1	1040.6	42.9	1	R.AVFVDLEPTVIDEVR.T
	HsFLAG-p53-DNA-D	3.8546	0.3066	2415.78	2416.655	9887	1	636.1	42.5	25	R.QLFHPEQLITGKEDAANNYAR.G
	HsSrcap_Ti_204.213	5.0964	0.4219	2416.38	2416.655	6002.3	1	934.1	37.5	18	R.QLFHPEQLITGKEDAANNYAR.G
	HsFLAG-ARP6_Ti_1	3.2026	0.111	1086.33	1086.274	5676.6	1	1026.6	93.8	15	K.EIIDLVLDR.I
	HsFLAG-ARP6_Ti_1	5.5288	0.4605	3519.46	3520.951	9178.7	1	1611.9	30.5	2	R.KLADQCTGLQGFLVFHSFGGGTGSGFTSLLMER.L
	HsFLAG-ARP6_Ti_1	6.8756	0.4682	3390.27	3392.777	8761.3	1	1604.7	31.5	13	K.LADQCTGLQGFLVFHSFGGGTGSGFTSLLMER.L
	HsScrap_Ti_106.239	2.55	0.1652	1877.45	1876.082	6295.5	1	349.4	53.6	1	R.RNLDIERPTYTNLNR.L
	HsFlag-ZnF-HIT2_Ti_	2.9442	0.2517	1719.52	1719.895	6354.4	3	522.7	57.7	12	R.NLDIERPTYTNLNR.L
	HsFLAG-ARP6_Ti_1	5.0973	0.4595	1487.62	1488.768	7314.4	1	1783.7	80.8	94	R.LISQIVSSITASLR.F
	HsFLAG-Lin9_Ti_20	3.9906	0.2202	1487.96	1488.768	5903.2	1	1035.4	48.1	1	R.LISQIVSSITASLR.F
	HsFLAG-ARP6_Ti_1	5.8116	0.4265	2410.46	2410.689	5990.7	1	1327.4	60	74	R.FDGALNVDLTEFQTNLVPYPR.I
	HsFLAG-ARP6_Ti_1	5.1723	0.3713	2751.88	2752.037	6388.1	1	727.7	32.6	7	K.AYHEQLSVAEITNACFEPANQMVK.C
	HsYL1_Ti_103.2152.	5.4112	0.353	2751.97	2752.037	8492.5	1	1660.1	52.2	3	K.AYHEQLSVAEITNACFEPANQMVK.C
	HsFLAG-ARP6_Ti_1	3.1777	0.2663	1250.3	1250.43	4496.7	1	907.7	93.8	7	K.YMACCLLYR.G
	HsH2AZ-FLAG_293_	2.3357	0.2535	1015.43	1016.183	6915.1	2	562	72.2	14	K.DVNAAIATIK.T
	HsSrcap_Ti_202.001	3.6793	0.2729	1017.71	1016.183	5879.8	1	1088.4	83.3	8	K.DVNAAIATIK.T
	HsSrcap_Ti_205.275	4.3851	0.1572	1742.07	1741.953	8212.2	1	1660.4	51.9	6	K.RSIQFVDWCPTGFK.V
	HsFLAG-ARP6_Ti_1	4.7996	0.4001	1743.87	1741.953	5585.1	1	1005.5	73.1	32	K.RSIQFVDWCPTGFK.V
	HsFLAG-TCF3_Ti_1	3.0532	0.402	1584.47	1585.766	5401	1	539.5	58.3	17	R.SIQFVDWCPTGFK.V
	HsSrcap_Ti_202.297	4.5222	0.2867	1585.72	1585.766	5721.7	1	1065.6	75	43	R.SIQFVDWCPTGFK.V
	HsFLAG-ARP6_Ti_2	4.0719	0.4153	1825.6	1826.103	3498.4	1	615.9	58.8	34	K.VGINYQPPTVVPGGDLAK.V
	HsFLAG-ARP6_Ti_1	6.0682	0.4321	1865.52	1866.108	10861.7	1	2782.2	75	18	R.AVCMLSNTTAIAEAWAR.L
	HsFLAG-ARP6_Ti_1	4.4765	0.3204	1867.57	1866.108	8904.4	1	1596.3	45.3	7	R.AVCMLSNTTAIAEAWAR.L
	HsFLAG-ARP6_Ti_1	3.7547	0.214	2330.07	2331.521	8623.8	3	888.4	34.2	2	R.AFVHWYVGEGMEEGEFSEAR.E
	HsFLAG-ARP6_Ti_1	4.334	0.4395	2330.87	2331.521	6787.1	1	1352.6	57.9	3	R.AFVHWYVGEGMEEGEFSEAR.E
	HsFlag-Ies6_293_Ti_	4.6127	0.3488	2350.09	2350.275	8478.9	1	1358.3	57.5	5	K.DYEEVGVDSVEGEGEEEGEEY.-
gi|4504349|re	10	24	70.70%	147	15998	7.3	beta globin [Homo sapiens]				
*	HsFLAG-RPB5MP_2	2.74	0.2036	933.43	933.095	5036.3	2	1074	93.8	2	K.SAVTALWGK.V

*	HsFLAG-RPB5MP_2	4.3112	0.3621	1315.16	1315.426	7819.3	1	1811.5	83.3	1	K.VNVDEVGGEALGR.L
	HsFLAG-RPB5MP_2	2.6604	0.1379	1275.17	1275.536	4903	1	1079.9	77.8	1	R.LLVVYPWTQR.F
	HsFLAG-RPB5MP_2	5.2862	0.3643	1798.54	1799.08	6971.4	1	1754.5	75	2	K.KVLGAFSDGLAHLDNLK.G
	HsFLAG-RPB5MP_2	3.1659	0.3061	1670.43	1670.906	9712.9	1	864.3	53.3	3	K.VLGAFSDGLAHLDNLK.G
*	HsFLAG-RPB5MP_2	3.764	0.3422	1479.55	1479.596	6253.8	6	628.6	58.3	3	K.GTFATLSELHCDK.L
*	HsFLAG-RPB5MP_2	4.1998	0.3122	1777.52	1778.117	7840.5	1	1264.3	66.7	2	R.LLGNVLVCVLAHHFGK.E
*	HsFLAG-RPB5MP_2	2.903	0.307	1379.03	1379.555	5650.6	1	634.2	68.2	1	K.EFTPPVQAAYQK.V
	HsFLAG-RPB5MP_2	3.7251	0.3125	1150.16	1150.366	6676.6	1	1376.6	86.4	5	K.VVAGVANALAHK.Y
	HsFLAG-RPB5MP_2	4.2178	0.3958	1451.37	1450.684	8857.4	1	1471.3	73.1	4	K.VVAGVANALAHKYH.-
gi|4506671|re	9	45	70.40%	115	11665	4.5	ribosomal protein P2 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	5.0226	0.3727	1870.54	1870.112	8039.2	1	1332	58.3	16	R.YVASYLLAALGGNSSPSAK.D
	HsFLAG-TCF3_Ti_1	4.5155	0.281	1870.97	1870.112	6879	2	1610	44.4	2	R.YVASYLLAALGGNSSPSAK.D
*	HsFLAG-ARP6_Ti_1	3.1562	0.3383	1546.09	1546.674	5007.3	1	479.8	73.1	1	K.KILDSVGIEADDDR.L
*	HsFLAG-TCF3_Ti_1	5.0163	0.349	1901.87	1902.112	8863.1	1	1489.7	62.5	4	K.KILDSVGIEADDDRLNK.V
*	HsFLAG-ARP6_Ti_1	4.101	0.3305	1902.38	1902.112	4880.3	1	1329	50	1	K.KILDSVGIEADDDRLNK.V
*	HsFlag-Ies6_293_Ti_	2.7559	0.3258	1419.14	1418.5	4935.1	1	1069.6	79.2	1	K.ILDSVGIEADDDR.L
*	HsFLAG-Lin9_Ti_20	3.289	0.301	1256.65	1257.429	4816.1	1	425.8	63.6	5	K.NIEDVIAQGIGK.L
*	HsFLAG-p53-DNA-D	4.8079	0.3147	1257.47	1257.429	7083.3	1	2078.4	86.4	12	K.NIEDVIAQGIGK.L
*	HsFLAG-ARP6_Ti_1	3.9503	0.3894	2777.06	2776.076	4529.6	1	401.6	34.4	3	K.LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK.K
gi|48762932|r	45	135	69.30%	548	59621	5.6	chaperonin containing TCP1, subunit 8 (theta) [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.1658	0.1703	963.27	963.183	4551.1	1	918.2	93.8	1	K.APGFAQMLK.E
*	HsFLAG-ARP6_Ti_1	2.3012	0.3361	1307.3	1308.436	5490.2	2	313.2	55	1	K.HFSGLEEAVYR.N
*	HsFLAG-ARP5_Ti_1	3.7186	0.3748	1308.46	1308.436	4703.5	1	1131.9	90	8	K.HFSGLEEAVYR.N
	HsFLAG-ARP6_Ti_1	4.3182	0.364	1334.27	1334.558	6639.1	1	1699.4	86.4	5	K.LFVTNDAATILR.E
	HsFLAG-ARP6_Ti_1	2.5138	0.2453	1121.44	1122.266	3301.7	3	280	66.7	2	R.ELEVQHPAAK.M
	HsFLAG-ARP6_Ti_1	2.8744	0.2847	1122.16	1122.266	5218.5	1	591.8	77.8	2	R.ELEVQHPAAK.M
	HsFLAG-ARP6_Ti_1	5.2339	0.4411	1895.48	1896.114	6267.7	1	1496.1	68.8	13	R.IGLSVSEVIEGYEIACR.K
*	HsFLAG-ARP5_Ti_1	4.4781	0.3367	1740.53	1740.973	4812.1	1	972.3	71.4	4	R.KAHEILPNLVCCSAK.N
*	HsFlag-NUFIP_Ti_2	3.2562	0.3529	1612.41	1612.799	4081	1	652.6	65.4	3	K.AHEILPNLVCCSAK.N
*	HsFLAG-ARP6_Ti_1	3.8507	0.1818	1613.03	1612.799	5566.5	3	1073.9	50	1	K.AHEILPNLVCCSAK.N
*	HsFLAG-ARP6_Ti_1	2.8333	0.1627	1146.27	1147.271	3867.1	3	525.4	77.8	1	R.DIDEVSSLLR.T
*	HsFLAG-ARP6_Ti_1	3.6741	0.1537	1146.48	1147.271	6595	4	1133.9	83.3	1	R.DIDEVSSLLR.T
*	HsFLAG-ARP6_Ti_1	4.1618	0.3458	2474.52	2474.745	6486.8	1	913.4	34.5	3	K.LIAQACVSIFPDSGHFNVDNIR.V
*	HsFLAG-ARP6_Ti_1	5.5315	0.5786	1820.57	1820.157	6330.6	1	1480.3	67.6	10	K.ILGSGISSSSVLHGMVFK.K
*	HsFLAG-ARP6_Ti_1	3.2091	0.3273	1833.43	1833.072	4482.8	1	504.7	53.3	2	K.IAVYSCPFDGMITETK.G
*	HsFLAG-ARP6_Ti_1	4.9075	0.4001	2384.42	2385.666	6484	1	1160.7	55	2	K.TAEELMNFSKGEENLMDAQVK.A
*	HsFLAG-ARP6_Ti_1	5.4024	0.4394	2385.32	2385.666	5764.9	1	1103.1	40	2	K.TAEELMNFSKGEENLMDAQVK.A
*	HsFLAG-ARP6_Ti_1	2.4727	0.2745	1372.64	1373.549	7057.5	1	448.8	46.4	2	K.AIADTGANVVVTGGK.V
*	HsFLAG-ARP6_Ti_1	4.8556	0.5084	1373.34	1373.549	8552.4	1	2276.1	78.6	3	K.AIADTGANVVVTGGK.V
*	HsFLAG-ARP6_Ti_1	2.9652	0.1945	1232.56	1233.428	5792.6	1	731.4	70	1	K.VADMALHYANK.Y
*	HsFLAG-ARP6_Ti_1	3.7196	0.2246	1234.11	1233.428	7902.4	1	1602.1	85	3	K.VADMALHYANK.Y
*	HsFLAG-ARP6_Ti_1	2.7088	0.2022	909.06	909.134	5219.6	2	1186.3	91.7	1	K.YNIMLVR.L
*	HsFLAG-ARP6_Ti_1	2.5074	0.1647	886.23	886.039	3503.9	6	689.4	81.2	1	K.TVGATALPR.L

*	HsFLAG-ARP6_Ti_1	4.8486	0.3453	3250.25	3250.654	9341.6	3	726.4	25	2	R.LTPPVLEEMGHCDSVYLSEVGDTQVVVFK.H
*	HsFLAG-ARP6_Ti_1	4.0743	0.2769	1569.39	1568.77	6811.9	1	1073.2	69.2	2	K.HEKEDGAISTIVLR.G
*	HsFLAG-ARP6_Ti_1	3.4544	0.2788	1367.33	1366.442	5578.9	2	854.5	77.3	2	R.GSTDNLMDDIER.A
*	HsFLAG-ARP6_Ti_1	2.336	0.3054	1065.44	1066.156	4665	2	341.9	55.6	2	R.AVDDGVNTFK.V
*	HsFLAG-TCF3_Ti_1	4.0566	0.2834	1511.67	1511.762	7211.1	1	980.6	60.7	7	K.RLVPGGGATEIELAK.Q
*	HsFLAG-ARP6_Ti_1	4.3901	0.3587	1511.76	1511.762	4370.4	1	999.8	51.8	1	K.RLVPGGGATEIELAK.Q
*	HsFLAG-ARP6_Ti_1	5.1959	0.4859	2057.94	2059.246	5222.2	1	1105.6	67.6	2	K.QITSYGETCPGLEQYAIK.K
*	HsFLAG-ARP6_Ti_1	4.5843	0.4256	2186.47	2187.421	5349.6	1	871.2	58.3	2	K.QITSYGETCPGLEQYAIKK.F
*	HsFLAG-ARP5_Ti_1	3.8814	0.2787	1279.45	1279.481	6591.5	1	1268.8	80	3	K.KFAEAFEAIPR.A
*	HsFLAG-ARP6_Ti_1	2.7507	0.1017	1150.6	1151.307	5004.9	8	501.3	72.2	1	K.FAEAFEAIPR.A
*	HsFLAG-ARP6_Ti_1	4.3663	0.2168	1151.49	1151.307	6252.5	1	1643.2	94.4	2	K.FAEAFEAIPR.A
*	HsFlag-VPS71_Ti_1	2.3948	0.106	1158.6	1159.287	5027.4	1	602.3	72.2	6	K.LYAVHQEGNK.N
*	HsFLAG-ARP6_Ti_1	3.0353	0.1784	1159.2	1159.287	5981.3	1	1165.9	83.3	8	K.LYAVHQEGNK.N
*	HsFLAG-ARP6_Ti_1	4.6048	0.368	1454.42	1454.663	8401.3	1	2688.5	88.5	2	K.NVGLDIEAEVPAVK.D
*	HsFLAG-ARP5_Ti_1	5.08	0.3993	2975.31	2975.424	10071.5	1	1376	30.6	2	K.NVGLDIEAEVPAVKDMLEAGILDTYLGK.Y
*	HsFLAG-ARP6_Ti_1	5.2161	0.3769	1539.82	1539.784	7409.2	1	2261.6	84.6	4	K.DMLEAGILDTYLGK.Y
*	HsFLAG-ARP6_Ti_1	4.0296	0.3394	1129.36	1129.345	7433.1	1	1549.8	90	2	K.LATNAAVTVLR.V
*	HsFLAG-ARP6_Ti_1	2.2848	0.146	917.66	918.139	7037.5	2	622.2	71.4	1	R.VDQIIMAK.P
*	HsFLAG-ARP5_Ti_1	3.6068	0.337	1891.56	1892.267	5757.5	1	773.1	52.8	4	R.VDQIIMAKPAGGPKPPSGK.K
*	HsFLAG-ARP5_Ti_1	4.0541	0.294	1892	1892.267	5963.2	9	820.8	38.9	4	R.VDQIIMAKPAGGPKPPSGK.K
*	HsFLAG-ARP6_Ti_1	2.2569	0.1078	992.47	993.151	4476.3	3	434.7	60	1	K.PAGGPKPPSGK.K
*	HsFLAG-ARP6_Ti_1	3.5588	0.2555	993.73	993.151	7386.5	4	1025	80	3	K.PAGGPKPPSGK.K
gi|5174735|re	33	691	67.60%	445	49831	4.9	tubulin, beta, 2 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	5.1932	0.4341	3117.35	3118.299	6212.7	1	1002.5	34.6	14	K.FWEVISDEHGIDPTGTYHGDSDLQLER.I
*	HsFLAG-TCF3_Ti_1	2.9907	0.2592	1328.45	1329.452	6425.8	1	548.6	63.6	5	R.INVYYNEATGGK.Y
*	HsFLAG-ARP6_Ti_1	3.5519	0.3531	1329.72	1329.452	4538.9	1	1127.3	86.4	5	R.INVYYNEATGGK.Y
*	HsFLAG-TCF3_Ti_1	3.9056	0.4507	1844.35	1845.065	8563.4	1	940.3	60	1	R.INVYYNEATGGKYVPR.A
	HsTIP60_Ti_104.237	4.1551	0.3271	1601.63	1602.843	4487.9	1	912.8	71.4	10	R.AVLVDLEPGTMDSVR.S
	HsFLAG-ARP6_Ti_1	5.3305	0.4496	2798.59	2800.065	6948.6	1	1444.6	52	59	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-ARP6_Ti_1	7.0292	0.3487	2802.51	2800.065	7956.6	1	2098.3	39	59	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-TCF3_Ti_1	7.1819	0.4728	1959.62	1960.151	9139.8	1	3610.1	82.4	73	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-ARP6_Ti_1	4.9251	0.2887	1959.94	1960.151	7005.8	1	1288.7	41.2	34	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-TIP49b_Ti_	5.684	0.3213	2087.63	2088.325	8116.7	1	2259	51.4	39	K.GHYTEGAELVDSVLDVVRK.E
	HsSrcap_Ti_206.286	6.4593	0.361	2087.84	2088.325	9352.8	1	2739.4	72.2	25	K.GHYTEGAELVDSVLDVVRK.E
	HsYL1_Ti_103.1035.	2.9392	0.1782	1078.13	1078.17	3062.5	4	568.7	85.7	4	K.IREEYPDR.I
	HsFLAG-TCF3_Ti_1	3.025	0.2204	2378.62	2379.736	6966.3	1	555.3	47.4	2	K.IREEYPDRIMNTFSVVPSPK.V
	HsFlag-VPS71_Ti_1	2.5434	0.1418	1319.6	1320.59	6897.3	9	431	59.1	1	R.IMNTFSVVPSPK.V
	HsFLAG-ARP6_Ti_1	4.5585	0.3954	1320.55	1320.59	7624	1	1689.8	86.4	26	R.IMNTFSVVPSPK.V
	HsFLAG-ARP6_Ti_1	6.4706	0.4855	4594.76	4595.903	4988.3	1	541.4	23.7	83	K.VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR.T
	HsFLAG-ARP6_Ti_1	4.7805	0.3574	2709.73	2710.041	10385.7	1	1165	31.2	30	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsFLAG-ARP6_Ti_1	5.4731	0.383	2710.22	2710.041	8352.5	1	1412.5	47.9	39	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsFLAG-ARP6_Ti_1	2.1817	0.2119	1130.19	1131.277	3484.6	1	331.1	72.2	1	R.FPGQLNADLR.K
	HsFLAG-ARP6_Ti_1	3.1035	0.1934	1133.31	1131.277	4537.1	1	968.3	94.4	20	R.FPGQLNADLR.K

	HsFLAG-ARP6_Ti_1	2.7216	0.2275	1259.45	1259.451	6377.3	1	1130.1	85	3	R.FPGQLNADLRK.L
	Hs293Flag-Ies2_Ti_1	4.1115	0.2404	1271.88	1272.594	7432.2	1	1437.4	85	9	R.KLAVNMVPFPR.L
	HsFLAG-Lin9_Ti_20	3.7432	0.2947	1144.31	1144.42	4934.2	1	1119.4	94.4	37	K.LAVNMVPFPR.L
	HsFLAG-ARP6_Ti_1	3.784	0.2563	1621.62	1621.94	4747.2	1	1118	76.9	9	R.LHFFMPGFAPLTSR.G
	HsTIP60_Ti_106.282	3.611	0.2365	1693.78	1692.968	3399.3	1	640.9	75	3	R.ALTVPELTQQMFDAK.N
	HsFLAG-ARP6_Ti_1	3.1514	0.3044	1065.99	1066.201	5998.7	1	1325.1	87.5	4	K.NMMAACDPR.H
	HsFLAG-ARP6_Ti_1	3.3868	0.392	1040.35	1040.25	5162.1	1	1157.4	100	24	R.YLTVAAVFR.G
	Hs293Flag-Ies2_Ti_1	4.5214	0.2599	1447.29	1447.603	7900.2	2	1960.1	86.4	10	K.EVDEQMLNVQNK.N
	HsScrap_Ti_102.174	3.2133	0.1712	1447.35	1447.603	3682	1	435.8	72.7	4	K.EVDEQMLNVQNK.N
	HsFLAG-ARP6_Ti_1	4.0978	0.3327	1699.12	1697.888	5299.1	1	715	61.5	39	K.NSSYFVEWIPNNVK.T
	HsFLAG-TCF3_Ti_1	2.8997	0.2395	1029.45	1029.147	6481.9	1	1559.4	93.8	2	K.TAVCDIPPR.G
	HsFLAG-ARP6_Ti_1	4.1879	0.3996	1386.16	1386.612	7897.9	1	1417.6	85	10	K.RISEQFTAMFR.R
	HsFLAG-ARP6_Ti_1	3.7061	0.3498	1229.27	1230.424	8240.8	1	1542.7	88.9	7	R.ISEQFTAMFR.R
gi|11968057|	29	340	67.20%	396	45810	5	ARP6 actin-related protein 6 homolog [Homo sapiens]				
*	HsH2AZ-FLAG_293_	4.644	0.3695	2023.56	2021.206	5296.9	1	1041.2	65.6	34	K.IGYSHENVSVIPNCQFR.S
*	HsVPS71-FLAG_Ti_	2.6601	0.193	1279.66	1280.42	7125.7	6	488.7	65	2	K.TFTANQIDEIK.D
*	HsFlag-VPS71_Ti_1	3.4598	0.1809	1281.48	1280.42	6464.2	1	985.1	80	10	K.TFTANQIDEIK.D
*	HsH2AZ-FLAG_293_	4.5229	0.2685	2786.13	2787.185	6095.6	1	1131.2	35.9	6	K.TFTANQIDEIKDPSGLFYILPFQK.G
*	HsYL1_Ti_103.3139.	4.2352	0.2267	2787.95	2787.185	4635.5	1	556.3	43.5	6	K.TFTANQIDEIKDPSGLFYILPFQK.G
*	HsFLAG-TIP49b_Ti_	3.6805	0.1067	1526.73	1525.787	3431.8	6	458.6	62.5	7	K.DPSGLFYILPFQK.G
*	HsFLAG-TIP49a_Ti_	4.6696	0.3284	1526.87	1525.787	4587.9	1	1153.1	79.2	65	K.DPSGLFYILPFQK.G
*	HsFlag-VPS71_Ti_1	3.9532	0.3283	1250.52	1250.399	5763.9	1	1194.2	88.9	6	K.GYLVNWDVQR.Q
*	HsFlag-VPS71_Ti_1	3.4547	0.2715	996.94	996.114	7016.2	9	1286	83.3	16	R.VNAGALSAHR.Y
*	HsFlag-VPS71_Ti_1	4.8727	0.4036	3471.7	3470.761	6903.6	1	1275.9	30.6	1	R.YFRDNPSELCCIIVDSGYSFTHIVPYCR.S
*	HsH2AZ-FLAG_293_	3.4104	0.1721	1790.56	1792.063	5959.5	1	633.2	57.1	7	R.QLHVMDETHVINQVK.E
*	HsH2AZ-FLAG_293_	4.8476	0.286	3353.03	3354.685	8199.3	1	1019.1	31.7	3	R.QLHVMDETHVINQVKEDVCYVSQDFYR.D
*	HsSrcap_Ti_202.008	4.1099	0.4546	1580.83	1581.645	5550.4	1	1122.5	81.8	30	K.EDVCYVSQDFYR.D
*	HsFlag-VPS71_Ti_1	2.3466	0.265	1581.68	1581.645	2987.2	3	223.9	59.1	1	K.EDVCYVSQDFYR.D
*	HsFLAG-TIP49b_Ti_	5.9355	0.4708	2411.93	2413.788	8949.3	1	2151	62.5	32	K.LKGEENTVMIDYVLPDFSTIK.K
*	HsFlag-VPS71_Ti_1	4.4822	0.4705	2172.79	2172.455	6428.1	1	691	47.2	4	K.GEENTVMIDYVLPDFSTIK.K
*	HsFlag-VPS71_Ti_1	2.621	0.0936	894.64	893.043	3909.8	2	664	100	2	K.KGFCKPR.E
*	HsFlag-VPS71_Ti_1	3.9922	0.2033	1638.6	1638.888	7206.1	1	1409.5	76.9	4	K.GFCKPREEMVLSGK.Y
*	HsFLAG-TIP49a_Ti_	3.4002	0.211	1147.43	1146.347	5929.7	2	1057.3	83.3	8	K.PREEMVLSGK.Y
*	HsFlag-VPS71_Ti_1	2.632	0.2339	893.65	893.043	3385	3	312.2	78.6	5	R.EEMVLSGK.Y
*	HsFlag-VPS71_Ti_1	3.9724	0.1281	4691.68	4691.413	6724.3	1	466.7	18.8	5	R.FAVPEILFNPSDIGIQEMGIPEAIVYSIQNLPEEMQPHFFK.N
*	HsYL1-FLAG_Ti_20	4.0162	0.327	1591.82	1592.838	2697.8	1	219.6	64.3	14	K.NIVLTGGNSLFPGFR.D
*	HsSrcap_Ti_202.315	4.9657	0.3716	1593.11	1592.838	6676.9	1	1358.5	75	43	K.NIVLTGGNSLFPGFR.D
*	HsFLAG-ARP6_Ti_1	3.8897	0.29	2925.48	2926.215	5947.6	1	427.9	36	20	R.CLTPTDYDVSVVLPENPITYAWEGGK.L
*	HsFlag-VPS71_Ti_1	3.5363	0.308	1783.51	1783.948	9129.9	1	1318	64.3	3	K.LISENDDFEDMVVTR.E
*	HsFlag-VPS71_Ti_1	3.9237	0.2161	3490.19	3490.61	7921	1	714	25	1	K.LISENDDFEDMVVTREDYEENGHSVCEEK.F
*	HsFlag-VPS71_Ti_1	4.0736	0.2295	3865.54	3866.035	9305.2	1	669.5	22.6	2	K.LISENDDFEDMVVTREDYEENGHSVCEEKFDI.-
*	HsFLAG-ARP6_Ti_2	3.2646	0.2304	1725.97	1725.686	9308.7	1	1008.7	61.5	1	R.EDYEENGHSVCEEK.F
*	HsH2AZ-FLAG_293_	2.9474	0.1952	2100.34	2101.11	7322.8	1	661.5	53.1	2	R.EDYEENGHSVCEEKFDI.-

gi|14389309|r	26	503	66.80%	449	49895	5.1	tubulin alpha 6 [Homo sapiens]				
	HsSrcap_Ti_205.362	5.2798	0.4255	4301.41	4299.657	10101.8	1	671.9	20.3	1	R.ECISIHVGQAGVQIGNACWELYCLEHGIQPDGQMPSDK.T
	HsFLAG-ARP6_Ti_1	5.5507	0.3763	2011.61	2009.093	9267.4	1	1408.9	57.9	84	K.TIGGGDDSFNTFFSETGAGK.H
	HsFLAG-ARP6_Ti_1	5.0349	0.3	1702.67	1702.945	4531.2	1	1118.7	78.6	44	R.AVFVDLEPTVIDEVR.T
	HsFLAG-ARP6_Ti_1	4.0678	0.2493	1703.54	1702.945	8950.2	1	1040.6	42.9	1	R.AVFVDLEPTVIDEVR.T
	HsFLAG-p53-DNA-D	3.8546	0.3066	2415.78	2416.655	9887	1	636.1	42.5	25	R.QLFHPEQLITGKEDAANNYAR.G
	HsSrcap_Ti_204.213	5.0964	0.4219	2416.38	2416.655	6002.3	1	934.1	37.5	18	R.QLFHPEQLITGKEDAANNYAR.G
	HsFLAG-ARP6_Ti_1	3.2026	0.111	1086.33	1086.274	5676.6	1	1026.6	93.8	15	K.EIIDLVLDR.I
	HsFLAG-ARP6_Ti_1	5.5288	0.4605	3519.46	3520.951	9178.7	1	1611.9	30.5	2	R.KLADQCTGLQGFLVFHSFGGGTGSGFTSLLMER.L
	HsFLAG-ARP6_Ti_1	6.8756	0.4682	3390.27	3392.777	8761.3	1	1604.7	31.5	13	K.LADQCTGLQGFLVFHSFGGGTGSGFTSLLMER.L
	HsScrap_Ti_106.239	2.55	0.1652	1877.45	1876.082	6295.5	1	349.4	53.6	1	R.RNLDIERPTYTNLNR.L
	HsFlag-ZnF-HIT2_Ti_	2.9442	0.2517	1719.52	1719.895	6354.4	3	522.7	57.7	12	R.NLDIERPTYTNLNR.L
	HsFLAG-ARP6_Ti_1	5.0973	0.4595	1487.62	1488.768	7314.4	1	1783.7	80.8	94	R.LISQIVSSITASLR.F
	HsFLAG-Lin9_Ti_20	3.9906	0.2202	1487.96	1488.768	5903.2	1	1035.4	48.1	1	R.LISQIVSSITASLR.F
	HsFLAG-ARP6_Ti_1	5.8116	0.4265	2410.46	2410.689	5990.7	1	1327.4	60	74	R.FDGALNVDLTEFQTNLVPYPR.I
*	HsFLAG-ARP6_Ti_1	3.5186	0.2052	2767.53	2766.064	5720.2	1	592.4	30.4	1	K.AYHEQLTVAEITNACFEPANQMVK.C
	HsFLAG-ARP6_Ti_1	3.1777	0.2663	1250.3	1250.43	4496.7	1	907.7	93.8	7	K.YMACCLLYR.G
	HsH2AZ-FLAG_293_	2.3357	0.2535	1015.43	1016.183	6915.1	2	562	72.2	14	K.DVNAAIATIK.T
	HsSrcap_Ti_202.001	3.6793	0.2729	1017.71	1016.183	5879.8	1	1088.4	83.3	8	K.DVNAAIATIK.T
	HsSrcap_Ti_205.279	4.5969	0.4286	1755.42	1755.98	5429.1	1	785.6	65.4	26	K.RTIQFVDWCPTGFK.V
	HsSrcap_Ti_205.280	4.8872	0.2348	1757.48	1755.98	8327.5	1	2242.3	57.7	10	K.RTIQFVDWCPTGFK.V
	HsSrcap_Ti_202.300	2.6402	0.345	1598.54	1599.793	6635.7	1	411.8	50	2	R.TIQFVDWCPTGFK.V
	HsFLAG-TCF3_Ti_1	4.0211	0.3559	1599.41	1599.793	6154.4	1	984.8	70.8	8	R.TIQFVDWCPTGFK.V
	HsFLAG-ARP6_Ti_2	4.0719	0.4153	1825.6	1826.103	3498.4	1	615.9	58.8	34	K.VGINYQPPTVVPGGDLAK.V
	HsFLAG-ARP6_Ti_1	3.7547	0.214	2330.07	2331.521	8623.8	3	888.4	34.2	2	R.AFVHWYVGEGMEEGEFSEAR.E
	HsFLAG-ARP6_Ti_1	4.334	0.4395	2330.87	2331.521	6787.1	1	1352.6	57.9	3	R.AFVHWYVGEGMEEGEFSEAR.E
*	HsTIP60_Ti_101.185	5.112	0.4792	2080.32	2079.947	11152	1	1820.3	61.1	3	K.DYEEVGADSADGEDEGEEY.-
gi|31542680|r	48	643	66.70%	607	68241	5.2	ARP5 actin-related protein 5 homolog [Homo sapiens]				
*	HsFLAG-ARP5_Ti_1	2.9357	0.1722	1054.18	1053.267	4864.4	1	911.6	93.8	2	-.MAANVFPFR.D
*	HsFLAG-TCF3_Ti_1	3.6556	0.3941	3133.06	3134.605	4722.8	1	481.1	38.3	21	R.AAPDPVLEAGPVAHGPLPVPLVLDNGSFQVR.A
*	HsFLAG-TCF3_Ti_1	5.8306	0.4279	3134.31	3134.605	6648.3	1	1359.2	34.2	60	R.AAPDPVLEAGPVAHGPLPVPLVLDNGSFQVR.A
*	HsFLAG-TCF3_Ti_1	3.8247	0.3023	1595.32	1595.678	4497.9	1	863.8	71.4	7	R.AGWACPGQDPGPEPR.L
*	HsFLAG-TCF3_Ti_1	4.6302	0.3905	1723.6	1723.927	6008.5	1	1023.2	61.8	21	R.GASGPQVGNALGSLEPLR.W
*	HsFLAG-ARP5_Ti_1	4.5705	0.3305	1848.2	1847.161	6585.2	1	1164.1	67.9	9	R.QMMSELLFECYGIPK.V
*	HsFLAG-ARP5_Ti_1	4.1009	0.3474	1985.59	1987.265	8175.8	1	1061	56.2	25	K.VAYGIDSLFSFYHNKPK.N
*	HsFLAG-ARP8_Ti_2	4.5637	0.3757	2792.9	2794.127	7153.4	1	892.4	43.8	6	K.NSMCSGLIISSGYQCTHVLPILEGR.L
*	HsFLAG-ARP8_Ti_2	4.3186	0.3706	2795.14	2794.127	6844.2	1	764.1	30.2	3	K.NSMCSGLIISSGYQCTHVLPILEGR.L
*	HsFLAG-ARP5_Ti_1	4.8683	0.3492	1604.21	1604.809	6808.6	1	1130.7	71.4	7	K.RINLGGSQAAGYLQR.L
*	HsFlag-FLJ90652_2	5.3206	0.4376	1448.19	1448.622	8396.6	1	2255.4	84.6	19	R.INLGGSQAAGYLQR.L
*	HsFLAG-TCF3_Ti_1	3.1152	0.3514	1448.61	1448.622	3598.4	5	161.3	50	3	R.INLGGSQAAGYLQR.L
*	HsFLAG-ARP5_Ti_1	3.2037	0.2493	1298.62	1299.516	5163.5	1	636.5	68.2	7	K.YPGHLAAITLSR.M
*	HsFLAG-ARP8_Ti_2	4.4572	0.3908	1298.94	1299.516	6753	1	1926.9	90.9	28	K.YPGHLAAITLSR.M
*	HsFLAG-ARP5_Ti_1	3.7188	0.0886	1299.64	1299.516	6935.2	1	1741.9	59.1	1	K.YPGHLAAITLSR.M

*	HsFLAG-ARP5_Ti_1	6.7824	0.4162	2615.25	2615.874	8274.7	1	2425.6	45	26	R.MEEILHEHSYIAEDYVEELHK.W
*	HsFLAG-ARP5_Ti_1	6.0855	0.4807	2958.25	2958.274	9159	1	1202.8	35.2	3	R.MEEILHEHSYIAEDYVEELHKWR.C
*	HsFLAG-ARP5_Ti_1	3.5377	0.2024	1438.38	1439.49	8801.9	1	1328.1	80	5	R.CPDYYENNVHK.M
*	HsFLAG-ARP5_Ti_1	2.8725	0.3129	1179.42	1178.325	4549.1	1	675	80	2	K.LLGSTLTSEEK.Q
*	HsFLAG-ARP5_Ti_1	3.9203	0.3154	1591.59	1591.759	6454.1	1	889.5	65.4	11	K.LLGSTLTSEEKQER.L
*	HsFLAG-ARP5_Ti_1	4.0542	0.1471	2206.47	2207.506	3691	1	723.3	42.6	6	R.LLYVQELLEDGQMDQFHK.A
*	HsFLAG-ARP5_Ti_1	5.2725	0.3184	2206.5	2207.506	7513.7	1	1134.3	61.8	19	R.LLYVQELLEDGQMDQFHK.A
*	HsFLAG-TCF3_Ti_1	5.9178	0.4549	2221.44	2222.515	7116.6	1	2118	72.2	15	K.ALIELNMDSPEELQSYIQK.L
*	HsFLAG-ARP5_Ti_1	5.3129	0.2534	2221.55	2222.515	10159.5	2	1838.7	41.7	2	K.ALIELNMDSPEELQSYIQK.L
*	HsFLAG-FLJ20309_	2.3125	0.1947	958.56	959.131	7258.2	2	599.3	68.8	5	K.LSIAVEQAK.Q
*	HsFLAG-ARP5_Ti_1	3.1008	0.1783	959.11	959.131	5362.4	1	1112	93.8	4	K.LSIAVEQAK.Q
*	HsFLAG-ARP8_Ti_2	4.4742	0.3492	2589.34	2588.969	6138.3	1	1019.9	37.5	2	K.PVTTVQPVFNLAAYHQLFVGTER.I
*	HsFLAG-ARP5_Ti_1	6.8296	0.477	3386.74	3385.885	9613.6	1	1725.3	31	4	R.IRAPEIIFQPSLIGEEQAGIAETLQYILDR.Y
*	HsFlag-FLJ90652_2	7.0808	0.4529	3774.58	3774.352	8275.3	1	1868	31.2	8	R.IRAPEIIFQPSLIGEEQAGIAETLQYILDRYPK.D
*	HsFLAG-ARP5_Ti_1	2.9859	0.2443	3115.43	3116.538	6040.9	2	313.1	29.6	1	R.APEIIFQPSLIGEEQAGIAETLQYILDR.Y
*	HsFLAG-FLJ20309_	4.5769	0.4812	3116.57	3116.538	11597.1	1	1718.4	31.5	4	R.APEIIFQPSLIGEEQAGIAETLQYILDR.Y
*	HsFLAG-FLJ20309_	6.2168	0.418	3504.65	3505.005	4789.2	1	797	31.7	37	R.APEIIFQPSLIGEEQAGIAETLQYILDRYPK.D
*	HsFLAG-ARP5_Ti_1	4.9714	0.3899	2573.49	2574	7902.3	1	2159.7	59.1	2	K.DVQEMLVQNVFLTGGNTMYPGMK.A
*	HsFLAG-ARP5_Ti_1	3.0988	0.1167	1579.44	1579.916	9251.3	1	966.9	72.7	1	R.MEKELLEMRPFR.S
*	HsFLAG-ARP5_Ti_1	5.6024	0.4082	2209.42	2210.454	10986.6	1	2376.1	43.4	17	R.SSFQVQLASNPVLDAWYGAR.D
*	HsFLAG-ARP5_Ti_1	6.0082	0.445	2210.69	2210.454	6755.5	1	1513.1	63.2	98	R.SSFQVQLASNPVLDAWYGAR.D
*	HsFLAG-ARP5_Ti_1	5.6651	0.4526	1997.52	1998.162	8515	1	2171.6	76.7	81	R.DWALNHLDDNEVWITR.K
*	HsFLAG-ARP5_Ti_1	4.3808	0.2974	1997.77	1998.162	5228.9	1	1252.2	50	10	R.DWALNHLDDNEVWITR.K
*	HsFLAG-ARP5_Ti_1	4.8409	0.4197	2124.52	2126.336	10892.3	1	1577.5	59.4	1	R.DWALNHLDDNEVWITRK.E
*	HsFLAG-ARP5_Ti_1	4.8337	0.3509	2125.86	2126.336	7140.8	1	1312	45.3	12	R.DWALNHLDDNEVWITRK.E
*	HsFLAG-ARP5_Ti_1	4.2965	0.348	2785.73	2786.036	11377.3	1	1037.1	31.8	1	K.EYEEKGGEYLKEHCASNIYVPIR.L
*	HsFLAG-ARP5_Ti_1	4.3656	0.2411	3123.51	3124.486	10657.4	1	878.8	26	2	K.EYEEKGGEYLKEHCASNIYVPIRLPK.Q
*	HsFLAG-ARP5_Ti_1	5.2292	0.4025	2106.17	2107.34	6894	1	1779.3	67.6	3	K.GGEYLKEHCASNIYVPIR.L
*	HsFLAG-ARP5_Ti_1	4.609	0.2436	2106.69	2107.34	7466.5	1	938.1	36.8	6	K.GGEYLKEHCASNIYVPIR.L
*	HsFLAG-ARP5_Ti_1	4.2802	0.4221	2444.89	2445.79	6957.9	1	993.4	52.5	4	K.GGEYLKEHCASNIYVPIRLPK.Q
*	HsFLAG-ARP5_Ti_1	4.2462	0.3274	2445.67	2445.79	7180.1	1	783.7	33.8	10	K.GGEYLKEHCASNIYVPIRLPK.Q
*	HsFLAG-FLJ20309_	3.5453	0.3432	1459.53	1459.611	10532.9	1	1258.3	68.2	2	K.EHCASNIYVPIR.L
*	Hs293Flag-Ies2_Ti_	4.7875	0.2817	1797.03	1798.061	7344	1	1176.2	67.9	20	K.EHCASNIYVPIRLPK.Q
gi|52632383|	26	146	66.20%	589	64133	8.2	heterogeneous nuclear ribonucleoprotein L isoform a [Homo sapiens]				
*	HsFLAG-p53-DNA-D	2.701	0.1531	1299.73	1299.385	6378.6	1	1007.1	75	3	R.YYGGGSEGGRAPK.R
*	HsFLAG-FLJ20729_	7.1048	0.4474	2981.82	2982.883	9868.9	1	1263.8	26.5	1	K.TDNAGDQHGGGGGGGGGAGAAGGGGGGENYDDPHK.T
*	HsFLAG-FLJ20729_	3.5673	0.244	1077.35	1077.272	5334.6	1	921.5	88.9	15	K.TPASPVVHIR.G
*	HsFLAG-p53-DNA-D	5.3204	0.4201	3089.15	3089.614	7603.4	1	999.4	39.3	2	R.GLIDGVVEADLVEALQEFGPISYVVVMPK.K
*	HsFlag-VPS71_Ti_1	6.5737	0.4153	3090.19	3089.614	7736.7	1	1929.6	36.6	12	R.GLIDGVVEADLVEALQEFGPISYVVVMPK.K
	HsFLAG-p53-DNA-D	5.2966	0.4182	4389.27	4390.775	5953.7	1	1022.5	26.3	8	.I
	HsFlag-DPCD_Ti_20	2.5658	0.1898	1204.4	1205.227	3967	7	513.2	70	1	K.ISRPGDSDDSR.S
	HsFLAG-Lin9_Ti_20	4.9404	0.3755	3870.55	3870.41	8887.5	1	961.7	23.5	6	R.SVNSVLLFTILNPIYSITTDVLYTICNPCGPVQR.I
	HsFLAG-ARP6_Ti_1	4.3773	0.3767	1867.33	1867.044	6592.4	1	1745.3	75	2	K.NGVQAMVEFDSVQSAQR.A

	HsFLAG-Lin9_Ti_20	4.395	0.3827	1729.72	1730.845	6013.8	1	1261	70	6	K.ASLNGADIYSGCCTLK.I
	HsFLAG-ARP6_Ti_1	6.5887	0.4485	3336.87	3337.5	8369.5	1	1983.4	35.3	2	R.LNVFKNDQDTWDYTNPNLSGQGDPGSNPNK.R
	HsFLAG-p53-DNA-D	4.8912	0.3664	3492.72	3493.687	6498.2	1	972.8	30.8	1	R.LNVFKNDQDTWDYTNPNLSGQGDPGSNPNKR.Q
	HsFLAG-Lin9_Ti_20	4.6102	0.2579	2735.19	2735.753	8434.7	1	809.1	30.2	1	K.NDQDTWDYTNPNLSGQGDPGSNPNK.R
	HsFLAG-Lin9_Ti_20	4.5005	0.4405	2736.24	2735.753	6742.2	1	1132.8	50	5	K.NDQDTWDYTNPNLSGQGDPGSNPNK.R
	HsFLAG-p53-DNA-D	2.6483	0.3336	908.33	908.066	2797.9	4	390	81.2	3	R.MGPPVGGHR.R
	HsFLAG-Lin9_Ti_20	5.3022	0.3694	1589.53	1589.797	5876.7	1	1552.2	83.3	28	R.VFNVFCLYGNVEK.V
	HsFLAG-ARP6_Ti_1	4.3527	0.5048	1868.15	1869.118	6281.1	1	1323.9	67.6	3	K.SKPGAAMVEMADGYAVDR.A
	HsFlag-NUFIP_Ti_11	4.7574	0.4725	1635.58	1635.881	7045.2	1	1436.6	73.1	11	R.AITHLNNNFMFGQK.L
	HsFLAG-FLJ20729_	4.4276	0.4642	2188.34	2189.367	4886.7	1	672.9	55.3	5	K.QPAIMPGQSYGLEDGSCSYK.D
	HsFLAG-p53-DNA-D	6.9269	0.4661	3774.22	3775.175	11528.8	1	2872.2	33.9	10	R.IQHPSNVLHFFNAPLEVTEENFFEICDELGVK.R
	HsFLAG-p53-DNA-D	2.5485	0.1331	1222.48	1223.325	8580.1	4	542	55	2	R.SSSGLLEWESK.S
	HsFLAG-ARP6_Ti_1	3.2195	0.2979	1223.28	1223.325	6505.7	1	997.9	80	2	R.SSSGLLEWESK.S
	HsFlag-VPS71_Ti_1	5.2543	0.4626	1868.14	1868.114	5837.1	1	824.8	63.3	12	K.SDALETLGFLNHYQMK.N
	HsFLAG-p53-DNA-D	3.6562	0.3116	1868.25	1868.114	4030.8	3	585.5	41.7	1	K.SDALETLGFLNHYQMK.N
	HsFLAG-Lin9_Ti_20	2.9035	0.1903	1264.11	1264.423	6557.7	5	439.1	60	2	K.NPNGPYPYTLK.L
	HsFLAG-p53-DNA-D	2.4439	0.3385	1121.44	1122.189	4573.2	4	315.6	61.1	2	K.LCFSTAQHAS.-
gi|7656936|re	32	368	65.80%	403	42884	6	zinc finger, HIT domain containing 2 [Homo sapiens]				
*	HsFlag-ZnF-HIT2_Ti_	3.0239	0.3296	1141.11	1141.201	4100.9	1	633.2	87.5	1	R.CNAPYCSLR.C
*	HsFlag-ZnF-HIT2_Ti_	3.679	0.2365	2747.76	2746.931	6883.3	1	584.9	31	1	R.CYRTHGTCAENFYRDQVLGELR.G
*	HsFlag-ZnF-HIT2_Ti_	3.9363	0.4412	1355.52	1356.403	4153.9	1	825.4	85	6	R.THGTCAENFYR.D
*	HsFlag-ZnF-HIT2_Ti_	2.6744	0.2493	1355.72	1356.403	4606.6	1	304.8	65	4	R.THGTCAENFYR.D
*	HsFlag-ZnF-HIT2_Ti_	3.8261	0.1563	2266.78	2267.429	6169.5	7	363.4	41.7	8	R.THGTCAENFYRDQVLGELR.G
*	HsFlag-ZnF-HIT2_Ti_	3.0511	0.2163	1443.53	1443.612	7438.9	1	611.4	61.5	1	R.GCSAPPSRLASALR.R
*	HsFlag-ZnF-HIT2_Ti_	4.8171	0.2361	3280.93	3281.523	8007.8	1	1067.5	29.2	6	R.LRQQRETEDEPGEAGLSSGPAPGGLSGLWER.L
*	HsFlag-ZnF-HIT2_Ti_	7.2242	0.4703	3011.8	3012.176	7651.5	1	2439.5	41.1	5	R.QQRETEDEPGEAGLSSGPAPGGLSGLWER.L
*	HsFlag-ZnF-HIT2_Ti_	3.5291	0.2389	3012.22	3012.176	6161.6	1	492.9	37.5	4	R.QQRETEDEPGEAGLSSGPAPGGLSGLWER.L
*	HsFlag-ZnF-HIT2_Ti_	5.6709	0.3404	3608.79	3607.872	11353.8	1	1008.2	25	5	R.QQRETEDEPGEAGLSSGPAPGGLSGLWERLAPGEK.A
*	HsFlag-ZnF-HIT2_Ti_	5.4607	0.3739	3195.8	3195.423	5646.2	1	974.3	30.6	2	R.ETEDEPGEAGLSSGPAPGGLSGLWERLAPGEK.A
*	HsFlag-ZnF-HIT2_Ti_	2.8441	0.182	1708.43	1708.024	6838.8	1	477.5	59.1	2	R.LLPPWRPWWWNR.G
*	HsFlag-ZnF-HIT2_Ti_	6.1915	0.4233	2706.26	2705.938	5018.6	1	991.2	50	35	R.GAGPQLLEELDNAPGSDAAELELAPAR.T
*	HsFlag-ZnF-HIT2_Ti_	6.6636	0.4491	3428.87	3430.75	6173.7	1	842.1	28	20	R.GAGPQLLEELDNAPGSDAAELELAPARTPPDSVK.D
*	HsFlag-ZnF-HIT2_Ti_	1.8676	0.1455	743.44	743.835	4027.3	2	287.7	75	1	R.TPPDSVK.D
*	HsFlag-ZnF-HIT2_Ti_	3.9806	0.3366	1639.57	1638.871	3776.5	1	576.9	63.3	1	R.VLGDVPGACTPVVPTR.I
*	HsFlag-ZnF-HIT2_Ti_	2.4963	0.1605	955.64	956.173	3516.8	2	283.8	68.8	2	R.IPAIVSLSR.G
*	HsFlag-ZnF-HIT2_Ti_	2.6368	0.0943	956.38	956.173	4624.8	1	982.7	93.8	2	R.IPAIVSLSR.G
*	HsFlag-ZnF-HIT2_Ti_	2.5022	0.1256	826.43	824.999	4155.1	9	688.6	85.7	1	R.GPVSPLVR.F
*	HsFlag-ZnF-HIT2_Ti_	1.8985	0.1205	870.56	871.002	4361.4	1	455.9	71.4	1	R.GAMHEVAR.I
*	HsFlag-ZnF-HIT2_Ti_	2.6821	0.1808	871.03	871.002	5362.3	3	728.9	85.7	1	R.GAMHEVAR.I
*	HsFlag-ZnF-HIT2_Ti_	2.2598	0.2297	1169.51	1170.351	5720.1	1	412.3	60	1	R.ILLGEGPTNQK.G
*	HsFlag-ZnF-HIT2_Ti_	3.1876	0.1937	1170.41	1170.351	5750.7	7	781.3	75	2	R.ILLGEGPTNQK.G
*	HsFlag-ZnF-HIT2_Ti_	4.1615	0.3954	2772	2772.174	7975.8	1	850	38.5	1	R.ILLGEGPTNQKGYTLAALGDLAQTLGR.A
*	HsFlag-ZnF-HIT2_Ti_	5.3886	0.402	1620.67	1620.846	9148.4	1	2211	73.3	26	K.GYTLAALGDLAQTLGR.A

*	HsFlag-ZnF-HIT2_Ti_	2.5518	0.1678	1643.52	1643.803	5951.4	6	374.6	54.2	1	K.QAVAREERDHLYR.A
*	HsFlag-ZnF-HIT2_Ti_	5.4527	0.4168	2777.85	2779.054	7284	1	1921.4	58.7	62	K.CQFLLAWTNENEAALTPLALDCAR.A
*	HsFlag-ZnF-HIT2_Ti_	4.7417	0.2973	2779.36	2779.054	7472.8	1	1299.4	34.8	4	K.CQFLLAWTNENEAALTPLALDCAR.A
*	HsFlag-ZnF-HIT2_Ti_	4.7329	0.3126	2201.4	2202.432	4853.6	1	1506.8	46.2	35	R.AHQAHAVVAEEVAALTGELER.L
*	HsFlag-ZnF-HIT2_Ti_	7.5752	0.4801	2202.28	2202.432	9009.2	1	5097.7	85	96	R.AHQAHAVVAEEVAALTGELER.L
*	HsFlag-ZnF-HIT2_Ti_	2.6022	0.2503	1146.81	1147.365	7164.9	1	483.6	60	7	R.LWGGPVPPAPR.T
*	HsFlag-ZnF-HIT2_Ti_	3.802	0.2164	1147.7	1147.365	4707	1	1414.8	95	24	R.LWGGPVPPAPR.T
gi|7669492|re	26	152	65.70%	335	36053	8.5	glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.8083	0.2957	3311.79	3310.763	4266.1	1	601.5	30.6	4	K.VDIVAINDPFIDLNYMVYMFQYDSTHGK.F
*	HsFLAG-p53-DNA-D	4.5533	0.4635	1614.62	1614.885	6017.3	1	1396.5	84.6	4	K.LVINGNPITIFQER.D
*	HsFLAG-p53-DNA-D	4.2321	0.4568	2041.67	2042.343	7594.5	1	781.9	50	18	K.LVINGNPITIFQERDPSK.I
*	HsFLAG-ARP6_Ti_1	3.5495	0.2152	2042.39	2042.343	3991.1	1	554.4	33.8	1	K.LVINGNPITIFQERDPSK.I
*	HsFlag-VPS71_Ti_1	4.2703	0.3533	2278.54	2278.495	8622.7	1	762.6	31.2	2	K.WGDAGAEYVVESTGVFTTMEK.A
*	HsFlag-VPS71_Ti_1	5.4889	0.4446	2278.87	2278.495	5896.5	1	986.8	52.5	15	K.WGDAGAEYVVESTGVFTTMEK.A
*	HsFLAG-p53-DNA-D	2.8939	0.2135	909.47	910.021	3953.3	1	559	72.2	5	K.AGAHLQGGAK.R
*	HsFLAG-ARP6_Ti_1	5.2043	0.2791	2369.71	2370.79	6120.7	1	1195.9	41.7	6	K.RVIISAPSADAPMFVMGVNHEK.Y
*	HsFlag-VPS71_Ti_1	5.0204	0.3935	2369.99	2370.79	5856.5	1	984.6	57.1	3	K.RVIISAPSADAPMFVMGVNHEK.Y
*	HsFLAG-p53-DNA-D	5.698	0.4177	3090.89	3091.57	10058.4	1	1368	30.6	2	K.RVIISAPSADAPMFVMGVNHEKYDNSLK.I
*	HsFlag-VPS71_Ti_1	3.7709	0.3387	2215.37	2214.603	5099.4	1	609.9	52.5	4	R.VIISAPSADAPMFVMGVNHEK.Y
*	HsFLAG-TCF3_Ti_1	4.4938	0.3128	1835.5	1835.04	8673.7	1	2387.6	71.9	10	K.IISNASCTTNCLAPLAK.V
*	HsFlag-VPS71_Ti_1	6.977	0.5041	2597.06	2597.004	5962.1	1	1328.1	41.3	8	K.VIHDNFGIVEGLMTTVHAITATQK.T
*	HsFlag-VPS71_Ti_1	5.7979	0.4764	2597.94	2597.004	8350.3	1	1794.4	56.5	6	K.VIHDNFGIVEGLMTTVHAITATQK.T
*	HsFLAG-p53-DNA-D	3.3	0.1945	1411.61	1412.629	5478	1	534.8	57.1	2	R.GALQNIIPASTGAAK.A
*	HsFLAG-ARP6_Ti_1	3.4656	0.1531	1411.97	1412.629	4458.2	1	820.5	75	7	R.GALQNIIPASTGAAK.A
*	HsFlag-VPS71_Ti_1	4.3698	0.2851	2307.32	2308.667	4232.3	2	388.3	45	1	K.LTGMAFRVPTANVSVVDLTCR.L
*	HsFlag-VPS71_Ti_1	5.681	0.3511	2679.46	2679.116	8374	1	1413.5	37	2	K.LTGMAFRVPTANVSVVDLTCRLEK.P
*	HsFlag-VPS71_Ti_1	2.8845	0.2813	1530.69	1531.715	4474.4	7	216.9	50	2	R.VPTANVSVVDLTCR.L
*	HsFlag-VPS71_Ti_1	4.2187	0.3472	1531.82	1531.715	6179.1	1	1276	76.9	10	R.VPTANVSVVDLTCR.L
*	HsFlag-VPS71_Ti_1	4.5399	0.3334	1904.79	1902.164	7410.5	1	1225.1	62.5	6	R.VPTANVSVVDLTCRLEK.P
*	HsFLAG-p53-DNA-D	2.8826	0.0892	1320.42	1320.528	4949.5	6	786.6	75	1	R.LEKPAKYDDIK.K
*	HsFLAG-p53-DNA-D	3.4536	0.2241	1448.17	1448.703	5841.8	1	1045.8	81.8	1	R.LEKPAKYDDIKK.V
*	HsFLAG-p53-DNA-D	4.6813	0.4329	1765.63	1764.891	9002.4	1	1256.2	65.4	20	K.LISWYDNEFGYSNR.V
*	HsFlag-VPS71_Ti_1	2.9913	0.351	1330.51	1331.588	5778.1	1	846.8	68.2	3	R.VVDLMAHMASKE.-
*	HsFLAG-p53-DNA-D	4.3568	0.4109	1331.6	1331.588	9818.1	1	2228.2	86.4	9	R.VVDLMAHMASKE.-
gi|6912448|re	37	399	65.60%	288	32308	9.7	MORF-related gene X [Homo sapiens]				
*	HsTIP60_Ti_106.065	3.5654	0.2743	2048.72	2049.164	8476.3	1	529.8	47.1	1	R.KQGSQPRGQQSAEEENFK.K
*	HsTIP60_Ti_101.119	2.429	0.1688	1266.4	1267.294	8250.9	1	526.9	55	1	R.GQQSAEEENFK.K
*	HsTIP60_Ti_102.086	3.4734	0.3282	1267.14	1267.294	7827	1	1221.3	80	4	R.GQQSAEEENFK.K
*	HsTIP60_Ti_106.197	2.838	0.2517	1685.13	1685.84	3787.1	1	508.8	63.3	1	R.WGGRSAENPPSGSVRK.T
*	HsTIP60_Ti_103.113	4.4286	0.4647	1725.45	1725.769	8744.7	1	1479	61.8	21	K.TPGNGDGGSTSEAPQPPR.K
*	HsTIP60_Ti_104.118	4.4354	0.3609	1853.38	1853.943	7195.7	1	1249.2	41.7	4	K.TPGNGDGGSTSEAPQPPRK.K
*	HsMRGBP-FLAG_Ti_	4.4395	0.442	1855	1853.943	8237	1	999.4	55.6	21	K.TPGNGDGGSTSEAPQPPRK.K
*	HsTIP60_Ti_106.101	3.7623	0.4113	1981.74	1982.117	7523.7	1	497.4	42.1	7	K.TPGNGDGGSTSEAPQPPRKK.R

*	HsTIP60_Ti_106.138	3.9261	0.3545	1981.96	1982.117	6502.4	1	938.7	38.2	5	K.TPGNGDGGSTSEAPQPPRKK.R
*	HsMRGBP-FLAG_Ti_	2.7635	0.2315	1549.71	1550.665	3765.1	1	326.6	53.8	3	R.ARADPTVESEEAFK.N
*	HsTIP60_Ti_103.164	4.6019	0.3656	1550.28	1550.665	4190.7	1	1470.7	88.5	13	R.ARADPTVESEEAFK.N
*	HsMRGBP-FLAG_Ti_	2.5259	0.2816	1322.56	1323.399	2700.9	3	242.9	54.5	1	R.ADPTVESEEAFK.N
*	HsTIP60_Ti_102.158	3.1361	0.2389	1326.22	1323.399	4691.2	1	666.6	72.7	5	R.ADPTVESEEAFK.N
*	HsTIP60_Ti_103.149	3.0342	0.3207	1593.47	1593.69	3654.1	1	384.4	65.4	2	R.ADPTVESEEAFKNR.M
*	HsMRGBP-FLAG_Ti_	3.1612	0.199	2467.33	2466.883	3672.4	1	558.7	52.6	1	K.VKIPEELKPWLVEDWDLVTR.Q
*	HsMRGBP-FLAG_Ti_	6.2555	0.2843	2240.57	2239.576	8943.8	1	2424.7	48.5	9	K.IPEELKPWLVEDWDLVTR.Q
*	HsMRGBP-FLAG_Ti_	5.0807	0.2766	2240.96	2239.576	3322.7	1	758.2	67.6	6	K.IPEELKPWLVEDWDLVTR.Q
*	HsMRGBP-FLAG_Ti_	4.1463	0.3255	2495.29	2495.881	4961.6	1	790.6	55.3	2	K.IPEELKPWLVEDWDLVTRQK.Q
*	HsMRGBP-FLAG_Ti_	5.494	0.2835	2496.37	2495.881	7512.3	1	1312.1	40.8	5	K.IPEELKPWLVEDWDLVTRQK.Q
*	HsMRGBP-FLAG_Ti_	2.6901	0.305	1528.64	1529.736	4783.1	1	488.5	63.6	5	K.PWLVEDWDLVTR.Q
*	HsMRGBP-FLAG_Ti_	4.543	0.3925	1530.37	1529.736	5969.5	1	1742	90.9	10	K.PWLVEDWDLVTR.Q
*	HsMRGBP-FLAG_Ti_	3.1298	0.3509	1667.87	1667.822	9150.6	3	974.4	61.5	1	K.KNVDAILEEYANCK.K
*	HsMRGBP-FLAG_Ti_	3.6276	0.3215	1796.14	1795.997	8211	1	1208	64.3	1	K.KNVDAILEEYANCKK.S
*	HsTIP60_Ti_105.238	3.5378	0.4499	1538.49	1539.648	4882.5	1	677.7	70.8	20	K.NVDAILEEYANCK.K
*	HsTIP60_Ti_105.023	5.1521	0.4343	1539.14	1539.648	7850.4	1	1948.5	83.3	62	K.NVDAILEEYANCK.K
*	HsMRGBP-FLAG_Ti_	4.6234	0.2302	1667.61	1667.822	6888.6	1	1373.7	76.9	9	K.NVDAILEEYANCKK.S
*	HsTIP60_Ti_106.234	5.4488	0.3045	2134.17	2135.338	8410.7	1	1759	42.1	1	K.SQGNVDNKEYAVNEVVAGIK.E
*	HsTIP60_Ti_106.233	4.9209	0.4012	2134.5	2135.338	9675	1	1966.9	60.5	2	K.SQGNVDNKEYAVNEVVAGIK.E
	HsMRGBP-FLAG_Ti_	3.4706	0.229	1291.59	1292.475	4128.7	2	414.9	68.2	11	K.EYAVNEVVAGIK.E
	HsTIP60_Ti_103.259	3.9686	0.3073	1292.31	1292.475	5695.1	1	1069.2	81.8	59	K.EYAVNEVVAGIK.E
	HsMRGBP-FLAG_Ti_	4.7656	0.1574	1719.77	1720.036	6223.4	1	1626.6	84.6	21	K.EYFNVMLGTQLLYK.F
	HsMRGBP-FLAG_Ti_	3.0795	0.2746	1421.62	1422.679	7413.3	1	670.5	58.3	9	R.IGAMLAYTPLDEK.S
	HsTIP60_Ti_105.222	4.9481	0.3579	1422.29	1422.679	6181.6	1	1429.5	83.3	30	R.IGAMLAYTPLDEK.S
*	HsMRGBP-FLAG_Ti_	3.8896	0.3722	1603.74	1603.945	4329.4	1	1020.6	80.8	2	K.SLALLLGYLHDFLK.Y
*	HsMRGBP-FLAG_Ti_	3.1291	0.3342	1303.53	1304.399	4202.4	1	301.7	59.1	22	K.NSASLFTASDYK.V
*	HsTIP60_Ti_102.196	4.3094	0.3314	1304.18	1304.399	6923.2	1	1650.3	86.4	19	K.NSASLFTASDYK.V
*	HsTIP60_Ti_106.067	2.6368	0.2511	1060.64	1061.186	7502.9	1	873.5	81.2	3	K.VASAEYHRK.A
gi|5032051|re	8	46	65.60%	151	16273	10.1	ribosomal protein S14 [Homo sapiens]				
gi|68160922|r	8	46	65.60%	151	16273	10.1	ribosomal protein S14 [Homo sapiens]				
gi|68160915|r	8	46	65.60%	151	16273	10.1	ribosomal protein S14 [Homo sapiens]				
	HsFlag-NUFIP_Ti_11	5.0601	0.4308	4506.19	4507.967	7720.4	1	1030.7	23.8	3	K.E
	HsFlag-NUFIP_Ti_10	4.1233	0.1648	2265.68	2266.447	7950.7	1	2004	43.8	3	K.ADRDESSPYAAMLAAQDVAQR.C
	HsFlag-NUFIP_Ti_10	4.9474	0.359	2266.13	2266.447	6108.5	1	1703.3	70	6	K.ADRDESSPYAAMLAAQDVAQR.C
	HsFLAG-ARP6_Ti_1	2.9255	0.1516	1096.69	1095.327	4952.2	1	651	77.8	8	K.ELGITALHIK.L
	HsFLAG-TIP49b_Ti_	1.91	0.1633	1054.64	1055.179	3230.1	1	207.2	65	1	K.TPGPGAQSALR.A
	HsFLAG-ARP6_Ti_1	3.6757	0.37	1055.38	1055.179	7957.1	1	1146.6	80	15	K.TPGPGAQSALR.A
	HsFLAG-ARP6_Ti_1	4.1363	0.4185	1756.45	1756.954	5107.2	1	1179.6	73.3	6	K.IGRIEDVTPIPSDSTR.R
	HsFlag-NUFIP_Ti_10	4.2111	0.2605	1430.48	1430.555	4864.7	2	717.5	70.8	4	R.IEDVTPIPSDSTR.R
gi|50593002|r	11	121	65.10%	255	28416	8.6	small nuclear ribonucleoprotein polypeptide A' [Homo sapiens]				
*	HsFlag-NUFIP_Ti_10	5.6285	0.5078	1891.65	1892.119	8528.5	1	2017.4	68.8	23	K.LTAELIEQAAQYTNAVR.D
*	HsFlag-NUFIP_Ti_10	6.101	0.4502	2808.17	2807.086	11083.7	1	1666.7	47.9	31	K.IPVIENLGATLDQFDAIDFSDNEIR.K

*	HsFlag-NUFIP_Ti_10	3.4163	0.2226	1059.58	1059.297	4656	2	868.9	87.5	9	R.KLDGFPLLR.R
*	HsFlag-NUFIP_Ti_11	7.1876	0.3997	3735.47	3737.246	10977	1	2588.3	30.9	31	R.IGEGLDQALPCLTELILTNNSLVELGDLDPLASLK.S
	HsFLAG-ARP6_Ti_1	3.3081	0.3152	1065.89	1066.286	4598.7	1	986.4	93.8	3	K.SLTYLSILR.N
	HsFLAG-ARP6_Ti_1	2.2435	0.1879	1217.52	1218.352	5587.4	1	735.9	63.6	3	K.TFNPGAGLPTDK.K
	HsFLAG-ARP6_Ti_1	3.0774	0.1574	1218.25	1218.352	4254.1	1	1395	86.4	4	K.TFNPGAGLPTDK.K
	HsFlag-NUFIP_Ti_10	3.9536	0.2775	1255.59	1255.414	7459.6	2	1257.9	75	4	K.KGGPSPGDVEAIK.N
	HsFlag-NUFIP_Ti_10	4.8532	0.4808	1459.62	1459.599	8564.8	1	1906.6	80.8	8	K.NAIANASTLAEVER.L
	HsFLAG-ARP6_Ti_1	4.1075	0.3496	1126.52	1126.301	5124.1	1	1204.5	90	4	K.GLLQSGQIPGR.E
*	HsFlag-NUFIP_Ti_10	2.7281	0.2561	2257.2	2256.227	9502.8	6	418.6	35	1	R.RSGPTDDGEEEMEEDTVTNGS.-
gi|57863257|r	34	159	64.70%	556	60344	6.1	T-complex protein 1 isoform a [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	5.9928	0.4353	1517.44	1517.784	8788.7	1	2762.7	85.7	5	R.SQNVMAAASIANIVK.S
*	HsFLAG-ARP6_Ti_1	5.9654	0.4738	2105.32	2105.408	6147.3	1	1619.3	68.4	17	K.MLVDDIGDVTITNDGATILK.L
*	HsFLAG-ARP6_Ti_1	3.1348	0.2694	1107.01	1107.295	5367.6	3	1012.8	83.3	3	K.LLEVEHPAAK.V
*	HsFLAG-ARP6_Ti_1	3.4989	0.337	1303.51	1304.449	8508.1	1	1367.1	75	2	K.VLCELADLQDK.E
*	HsFLAG-ARP6_Ti_1	4.3224	0.2782	1305.55	1304.449	6702.9	1	1993.8	90	3	K.VLCELADLQDK.E
*	HsFLAG-ARP5_Ti_1	4.4763	0.2378	3101.44	3101.528	9737.7	1	1487.3	33	4	K.VLCELADLQDKEVGDGTTSVVIIAAELLK.N
*	HsFLAG-ARP6_Ti_1	4.0401	0.267	1816.64	1816.102	8006.9	1	1520.2	45.6	1	K.EVGDGTTSVVIIAAELLK.N
*	HsFLAG-ARP6_Ti_1	5.058	0.3974	1816.68	1816.102	7191.2	1	1262.7	64.7	22	K.EVGDGTTSVVIIAAELLK.N
*	HsFLAG-ARP6_Ti_1	2.345	0.1975	1229.39	1230.409	5030.4	1	379.8	70	2	K.IHPTSVISGYR.L
*	HsFLAG-ARP6_Ti_1	5.3485	0.3516	1763.5	1763.945	6735.4	1	1689.3	82.1	2	R.YINENLIVNTDELGR.D
*	HsFLAG-ARP6_Ti_1	3.9221	0.2116	2648.93	2649.927	8335.6	1	548.2	36.4	1	R.YINENLIVNTDELGRDCLINAAK.T
	HsFLAG-ARP6_Ti_1	3.6117	0.3492	2220.56	2221.663	8230.4	1	950.8	47.5	1	K.IIGINGDFFANMVVDAVLAIK.Y
	HsFLAG-ARP6_Ti_1	2.5651	0.191	1146.56	1147.36	5513.3	6	406.9	61.1	1	R.YPVNSVNILK.A
	HsFLAG-ARP6_Ti_1	3.0741	0.1526	1147.54	1147.36	5055.3	3	1147.6	88.9	2	R.YPVNSVNILK.A
	HsFLAG-ARP6_Ti_1	5.0505	0.4554	2589.02	2588.978	6292.6	1	1156.3	50	2	R.SQMESMLISGYALNCVVGSQGMPK.R
	HsFLAG-ARP6_Ti_1	3.1886	0.2571	1195.48	1195.367	6215.5	2	1179.7	83.3	2	K.IACLDFSLQK.T
	HsFLAG-ARP6_Ti_1	5.0254	0.3731	1925.18	1924.248	5118.2	1	930.5	65.6	10	K.LGVQVVITDPEKLDQIR.Q
	HsFLAG-ARP6_Ti_1	4.4544	0.2171	1925.36	1924.248	6646.5	2	1212.2	43.8	2	K.LGVQVVITDPEKLDQIR.Q
	HsFLAG-ARP6_Ti_1	6.1939	0.51	2178.73	2177.527	7333	1	1000.4	52.5	12	K.ILATGANVILTTGGIDDMCLK.Y
	HsFLAG-ARP6_Ti_1	3.8537	0.3359	3566.05	3566.916	9807	4	546.2	21.2	1	K.ASGATILSTLANLEGEETFEAAMLGQAEEVVQER.I
	HsFLAG-ARP6_Ti_1	3.6488	0.1485	1232.98	1232.426	4299.4	7	844.5	88.9	2	R.ICDDELILIK.N
	HsFLAG-ARP6_Ti_1	2.9702	0.2955	1141.51	1142.307	5062.9	1	712.2	72.2	4	R.SLHDALCVVK.R
	HsFLAG-ARP6_Ti_1	2.8588	0.2575	1142.64	1142.307	3951.7	1	644.4	83.3	2	R.SLHDALCVVK.R
	HsFLAG-ARP6_Ti_1	3.3022	0.2432	1148.47	1148.304	5294.7	1	988.1	94.4	4	R.EQLAIAEFAR.S
	HsFLAG-ARP6_Ti_1	5.2436	0.3569	2353.08	2354.706	5685.8	1	1123.6	56.8	20	R.SLLVIPNTLAVNAAQDSTDLVAK.L
	HsFLAG-ARP6_Ti_1	5.1419	0.4138	2354.48	2354.706	7405.8	1	1770.1	40.9	2	R.SLLVIPNTLAVNAAQDSTDLVAK.L
	HsFLAG-ARP6_Ti_1	3.889	0.2515	1412.46	1412.505	6741.9	1	1320.1	77.3	4	R.AFHNEAQVNPER.K
	HsFLAG-ARP6_Ti_1	3.9094	0.2305	1539.71	1540.679	9772.4	2	1442	70.8	6	R.AFHNEAQVNPERK.N
	HsFLAG-ARP6_Ti_1	3.7491	0.2012	1541.27	1540.679	6164.8	8	996.7	52.1	2	R.AFHNEAQVNPERK.N
	HsFLAG-ARP5_Ti_1	3.7468	0.2536	1356.45	1356.567	7650.2	1	1594.1	86.4	9	K.WIGLDLSNGKPR.D
	HsFLAG-ARP6_Ti_1	2.5309	0.0814	1189.5	1189.397	4242.3	1	635.8	80	1	K.QAGVFEPTIVK.V
	HsFLAG-ARP6_Ti_1	3.9507	0.4135	1206.32	1206.428	6763.7	1	1637.1	90	4	K.FATEAAITILR.I
	HsFLAG-ARP6_Ti_1	2.5451	0.359	1571.15	1572.588	6631.4	1	595.8	57.1	1	K.HGSYEDAVHSGALND.-

	HsFLAG-ARP6_Ti_1	4.4542	0.4599	1572.3	1572.588	8526.1	1	1990.6	75	3	K.HGSYEDAVHSGALND.-
gi|4505813|re	5	20	64.00%	89	10366	7.4	cytoplasmic dynein light polypeptide [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	5.338	0.4111	2514.97	2515.646	8560	1	1680.9	57.1	5	K.NADMSEEMQQDSVECATQALEK.Y
*	HsFLAG-ARP5_Ti_1	2.8894	0.0968	1415.48	1415.632	11640.8	1	1814.8	77.3	2	K.YNIEKDIAAHIK.K
	HsFlag-NUFIP_Ti_1	3.3398	0.2026	1531.61	1531.723	5250.6	1	948.4	81.8	2	K.KYNPTWHCIVGR.N
	HsFlag-VPS71_Ti_1	2.5216	0.2135	1282.54	1283.383	3899.1	3	254	55	2	R.NFGSYVTHETK.H
	HsFLAG-p53-DNA-D	3.5733	0.2828	1283.22	1283.383	6733.3	1	1034.2	80	9	R.NFGSYVTHETK.H
gi|13375809|r	61	958	63.80%	665	75703	7.1	hypothetical protein LOC79657 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	3.5556	0.0926	1042.35	1042.264	5934.1	3	1244.3	93.8	50	K.AIELQLQVK.Q
*	HsFlag-FLJ20643_Ti	3.4499	0.2124	1381.67	1381.503	5334.1	1	868.3	85	7	K.QNAEELQDFMR.D
*	HsFLAG-BC014022_	4.4025	0.3041	1619.29	1619.821	7831.8	1	1438.7	76.9	25	R.RQNGVPEENLPPIR.N
*	HsFlag-NUFIP_Ti_1	4.2704	0.1105	1621.14	1619.821	5424.8	1	1397.4	57.7	5	R.RQNGVPEENLPPIR.N
*	HsFlag-FLJ20643_Ti	3.2884	0.3331	1464.82	1463.633	4381	1	580	70.8	4	R.QNGVPEENLPPIR.N
*	HsFLAG-p53-DNA-D	2.512	0.1472	1132.45	1133.202	8687.9	6	564.8	62.5	3	K.SYDYEAWAK.L
*	HsFlag-FLJ20643_Ti	3.5687	0.3256	1133.78	1133.202	3720	2	683.9	87.5	8	K.SYDYEAWAK.L
*	HsFLAG-UTX1_Ti_2	4.3223	0.3872	3614.93	3616.695	7958.9	1	752.1	25	1	R.ILDELDKDDSTHESLSQESESEEDGIHVDSQK.A
*	HsFlag-NUFIP_Ti_1	4.0948	0.3041	2790	2789.75	13042	1	1319.7	30.2	1	K.DDSTHESLSQESESEEDGIHVDSQK.A
*	HsFlag-FLJ20643_Ti	3.2325	0.243	1592.34	1591.681	5030.1	5	358.8	58.3	3	K.QGKYDEAIDCYTK.G
*	HsFlag-ZnF-HIT2_Ti_	2.9579	0.3015	1277.51	1278.324	5711.6	1	741.1	77.8	5	K.YDEAIDCYTK.G
*	HsFlag-FLJ20643_Ti	3.7424	0.27	1280.04	1278.324	6496.1	1	1336.9	88.9	8	K.YDEAIDCYTK.G
*	HsFlag-NUFIP_Ti_1	3.8407	0.3524	1660.26	1660.842	4854.1	1	1301.4	75	2	K.GMDADPYNPVLPTNR.A
*	HsFLAG-p53-DNA-D	6.5629	0.4544	1878.09	1879.089	8908.8	1	3855.7	87.5	13	K.KFAVAESDCNLAVALNR.S
*	HsFlag-FLJ20643_Ti	5.5771	0.4228	1750.57	1750.915	8040.7	1	1935.4	73.3	113	K.FAVAESDCNLAVALNR.S
*	HsFLAG-UTX1_Ti_2	3.3145	0.087	1178.37	1177.386	6314.7	6	1055	77.8	9	R.FALQKLEEAK.K
*	HsFlag-FLJ20643_Ti	5.3117	0.3834	1888.95	1889.072	3419.7	1	790.5	76.7	42	R.VLELEPNNFEATNELR.K
*	HsFLAG-RPB5MP_2	4.2731	0.2992	2016.5	2017.246	4713.4	1	543.8	59.4	23	R.VLELEPNNFEATNELRK.I
*	HsFlag-FLJ20643_Ti	2.8175	0.0999	947.23	946.135	3805.7	1	541.1	81.2	2	R.KISQALASK.E
*	HsFlag-FLJ20643_Ti	2.9017	0.1159	818.46	817.961	4493.2	4	787	85.7	1	K.ISQALASK.E
*	HsFlag-FLJ20643_Ti	3.4515	0.1894	1537.35	1536.725	7283.6	3	584.4	53.8	1	K.ISQALASKENSYPK.E
*	HsFLAG-UTX1_Ti_2	4.2246	0.2634	1424.41	1424.6	4325.7	1	1047.8	78.6	16	R.GIAADGANALLPANR.A
*	HsFlag-NUFIP_Ti_1	2.0903	0.2319	1424.92	1424.6	3109.2	2	184.7	46.4	1	R.GIAADGANALLPANR.A
*	HsFLAG-p53-DNA-D	2.6595	0.0885	1137.94	1138.263	5013.9	3	622.2	81.2	1	K.IQKYEEAEK.D
*	HsFLAG-p53-DNA-D	4.652	0.3822	2689.34	2690.93	9065.5	1	1172.5	47.7	2	K.IQKYEEAEKDCTQAILLDGSYSK.A
*	HsFlag-FLJ20643_Ti	3.8041	0.3267	2320.84	2321.466	9400.8	1	1303	52.6	1	K.YEEAEKDCTQAILLDGSYSK.A
*	HsFlag-FLJ20643_Ti	3.9786	0.3434	1571.58	1571.691	5697.5	1	844.1	69.2	13	K.DCTQAILLDGSYSK.A
*	HsFLAG-p53-DNA-D	5.5704	0.2047	1571.66	1571.691	7609	1	2156.2	84.6	81	K.DCTQAILLDGSYSK.A
*	HsFLAG-UTX1_Ti_2	4.963	0.3513	2158.84	2159.444	6423.7	1	1060.9	55.6	7	K.LNEAKQDFETVLLLEPGNK.Q
*	HsFlag-FLJ20643_Ti	4.5597	0.3292	1604.31	1603.813	9433.7	1	1547.6	76.9	63	K.QDFETVLLLEPGNK.Q
*	HsFLAG-p53-DNA-D	3.7069	0.4036	1575.57	1576.665	7070.5	1	1086.8	66.7	4	K.GHWDDVFLDSTQR.Q
*	HsFlag-NUFIP_Ti_1	4.5596	0.4257	1575.94	1576.665	7822.8	1	1700.5	79.2	114	K.GHWDDVFLDSTQR.Q
*	HsFlag-NUFIP_Ti_1	3.8081	0.1395	1576.22	1576.665	8083.3	5	1246.1	47.9	1	K.GHWDDVFLDSTQR.Q
*	HsFLAG-UTX1_Ti_2	3.8748	0.3545	1829.52	1829.066	5555	1	552.7	53.1	6	R.QNVVKPIDNPPHPGSTK.P
*	HsFlag-NUFIP_Ti_1	4.1971	0.2479	1829.59	1829.066	8879.9	2	1216.6	42.2	4	R.QNVVKPIDNPPHPGSTK.P

*	HsFLAG-p53-DNA-D	3.9613	0.1012	2168.4	2167.516	8682.7	1	1250.9	38.2	1	R.QNVVKPIDNPPHPGSTKPLK.K
*	HsFlag-FLJ20643_Ti	2.4691	0.1523	1259.94	1260.392	6627	2	510.2	59.1	1	K.PIDNPPHPGSTK.P
*	HsFlag-FLJ20643_Ti	3.4362	0.2362	1260.68	1260.392	6359.1	3	1025.9	72.7	5	K.PIDNPPHPGSTK.P
*	HsFlag-NUFIP_Ti_11	3.305	0.2051	1598.68	1598.842	7339.6	4	673	57.1	1	K.PIDNPPHPGSTKPLK.K
*	HsFlag-NUFIP_Ti_10	5.5365	0.4219	4509.2	4508.037	6869	1	709.8	21.5	17	K.K
*	HsFlag-NUFIP_Ti_10	4.4519	0.3072	4507.21	4508.037	7038.8	1	749.8	20.9	2	K.N
*	HsFLAG-UTX1_Ti_2	5.6196	0.3638	2172.88	2173.469	4321.3	1	988.4	42.1	4	K.VLKIEEVSDTSSLQPQASLK.Q
*	HsFLAG-p53-DNA-D	6.3	0.4578	2173.8	2173.469	7753.2	1	2149.2	68.4	20	K.VLKIEEVSDTSSLQPQASLK.Q
*	HsFlag-FLJ20643_Ti	5.3533	0.3832	1833.14	1833.003	6388.4	1	1570.2	75	31	K.IEEVSDTSSLQPQASLK.Q
*	HsFlag-FLJ20643_Ti	4.4672	0.3179	3058.54	3058.246	8288.5	1	1387.3	34.6	1	K.IEEVSDTSSLQPQASLKQDVCQSYSEK.M
*	HsFlag-NUFIP_Ti_10	2.8207	0.2839	1245.26	1244.267	3691.8	4	418.6	72.2	3	K.QDVCQSYSEK.M
*	HsFlag-FLJ20643_Ti	2.557	0.0876	987.53	988.187	5562	2	611.1	78.6	1	K.MPIEIEQK.P
*	HsFlag-ZnF-HIT2_Ti_	5.1543	0.3966	3615.05	3617.154	5486.8	2	380	22.6	36	K.MPIEIEQKPAQFATTVLPPIPANSFQLESDFR.Q
*	HsFlag-NUFIP_Ti_10	4.7083	0.3391	2648.78	2647.99	4293.4	1	548.2	50	17	K.PAQFATTVLPPIPANSFQLESDFR.Q
*	HsFLAG-p53-DNA-D	2.5763	0.1975	1344.49	1345.553	7331.9	9	451.7	55	1	K.SSPDMLYQYLK.Q
*	HsFLAG-p53-DNA-D	3.3362	0.2577	1345.33	1345.553	3353.5	6	442.1	75	11	K.SSPDMLYQYLK.Q
*	HsFlag-FLJ20643_Ti	2.495	0.1791	1402.67	1402.59	3513.6	2	413.1	63.6	2	K.NLDPDVFNQIVK.I
*	HsFLAG-UTX1_Ti_2	3.6891	0.3014	1402.89	1402.59	3443.3	1	663	77.3	18	K.NLDPDVFNQIVK.I
*	HsFlag-FLJ20643_Ti	2.6608	0.1812	1177.67	1178.373	5375.7	1	652.7	75	10	K.ILHDFYIEK.E
*	HsFlag-NUFIP_Ti_10	3.0812	0.1556	1178.68	1178.373	5075.5	1	793.6	87.5	13	K.ILHDFYIEK.E
*	HsFLAG-p53-DNA-D	6.3037	0.3511	2658.78	2659.187	7238.6	1	2529.5	48.8	4	K.ILHDFYIEKEKPLLIFEILQR.L
*	HsFLAG-p53-DNA-D	2.5717	0.2006	1498.88	1499.837	2956	4	195.6	59.1	1	K.EKPLLIFEILQR.L
*	HsFlag-NUFIP_Ti_11	3.9368	0.2468	1499.5	1499.837	6451.5	1	1316.8	86.4	55	K.EKPLLIFEILQR.L
*	HsFlag-NUFIP_Ti_11	4.3279	0.3043	1242.36	1242.547	6656.4	1	1656.9	94.4	21	K.PLLIFEILQR.L
*	HsFlag-NUFIP_Ti_10	5.0511	0.47	1722.83	1723.03	8694.6	1	2249.3	80.8	17	K.RFDMAVMFMSETEK.K
*	HsFlag-NUFIP_Ti_10	3.087	0.1817	958.23	958.105	3971	1	754.6	92.9	25	R.ALFNHIDK.S
gi|30795231|r	8	20	63.40%	227	22693	4.6	brain abundant, membrane attached signal protein 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.3309	0.316	1428.21	1428.496	6815.3	1	1640.7	80.8	2	K.ESEPQAAAEPAEAK.E
*	HsFLAG-ARP6_Ti_1	4.0613	0.1502	2298.56	2299.502	5149.1	2	650	32.6	1	K.AEPPKAPEQEQAAPGPAAGGEAPK.A
*	HsFLAG-ARP6_Ti_1	4.7961	0.3958	1776.05	1776.9	3665	1	747.3	63.9	1	K.APEQEQAAPGPAAGGEAPK.A
*	HsFLAG-ARP6_Ti_1	3.8195	0.3308	2636.52	2637.773	4830.2	1	427.3	37	3	K.AAEAAAAPAESAAPAAGEEPSKEEGEPK.K
*	HsFLAG-p53-DNA-D	4.8424	0.3281	1412.73	1413.571	5229	1	1207.5	80.8	4	K.KTEAPAAPAAQETK.S
*	HsFLAG-p53-DNA-D	3.819	0.2585	1933.07	1933.981	6215.9	1	656.1	47.5	2	K.SDGAPASDSKPGSSEAAPSSK.E
*	HsFLAG-ARP6_Ti_1	3.2337	0.3191	1387.41	1387.486	5460.8	3	666.8	65.4	5	K.ETPAATEAPSSTPK.A
*	HsFLAG-ARP6_Ti_1	5.6163	0.3948	2894.54	2894.122	6862.3	1	1720.8	35.7	2	K.AQGPAASAEEPKPVEAPAANSDQTVTVKE.-
gi|4501885|re	29	925	62.90%	375	41737	5.5	beta actin [Homo sapiens]				
gi|4501887|re	29	925	62.90%	375	41793	5.5	actin, gamma 1 propeptide [Homo sapiens]				
	HsFLAG-ARP6_Ti_2	3.3564	0.3342	977.23	977.021	5082.6	1	1225.5	88.9	17	K.AGFAGDDAPR.A
	HsFlag-VPS71_Ti_10	2.159	0.1032	977.47	977.021	5226.9	1	385.5	61.1	2	K.AGFAGDDAPR.A
	HsFLAG-ARP5_Ti_1	3.43	0.2899	1199.05	1199.442	6548.6	1	831.6	80	27	R.AVFPSIVGRPR.H
	HsFLAG-TIP49a_Ti_	3.2318	0.3146	1171.37	1172.406	4944.3	1	760.2	75	54	R.HQGVMVGMGQK.D
	HsFLAG-p53-DNA-D	3.5553	0.3623	1172.01	1172.406	5155.7	1	1022.8	85	49	R.HQGVMVGMGQK.D
	HsFLAG-ARP8_Ti_2	3.7228	0.4	1198.34	1199.216	4824	1	494.9	65	7	K.DSYVGDEAQSK.R

	HsFlag-VPS71_Ti_1	3.4611	0.3002	1199.21	1199.216	3911.9	1	959.2	85	11	K.DSYVGDEAQSK.R
	HsFLAG-p53-DNA-D	2.8615	0.2497	1355.19	1355.404	5881	1	646.6	63.6	2	K.DSYVGDEAQSKR.G
	HsFLAG-TIP49b_Ti_	3.4873	0.339	1515.54	1516.702	6235.6	1	470.4	65	12	K.IWHHTFYNELR.V
	HsFLAG-p53-DNA-D	3.5256	0.379	1516.47	1516.702	6570.8	1	921.4	75	44	K.IWHHTFYNELR.V
	HsFLAG-ARP6_Ti_1	3.5437	0.1582	1517.38	1516.702	6065.3	1	1106.2	57.5	2	K.IWHHTFYNELR.V
	HsFLAG-ARP6_Ti_1	4.9174	0.311	1954.66	1955.261	5544.9	1	1253.1	70.6	126	R.VAPEEHPVLLTEAPLNPK.A
	HsFLAG-RPB5MP_2	4.2199	0.2289	1955.32	1955.261	7535.1	2	889.4	38.2	9	R.VAPEEHPVLLTEAPLNPK.A
	HsFlag-DPCD_Ti_20	6.8014	0.4506	3184.41	3185.622	9447.8	1	2159.6	34.5	71	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L
	HsFlag-VPS71_Ti_1	4.4039	0.381	3185.72	3185.622	4009.7	1	384.2	34.5	20	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L
	HsFLAG-p53-DNA-D	2.7022	0.1896	998.54	999.167	6873.8	9	806.7	78.6	9	R.DLTDYLMK.I
	HsFlag-DPCD_Ti_20	3.2886	0.3833	1133.04	1133.203	8829.6	1	1635.8	88.9	22	R.GYSFTTTAER.E
	HsFLAG-ARP6_Ti_1	7.0209	0.5236	2551.96	2551.791	10583.7	1	3086.5	61.4	147	K.LCYVALDFEQEMATAASSSSLEK.S
	HsFLAG-ARP6_Ti_1	4.8294	0.2968	2553.82	2551.791	8405.8	1	1387.9	37.5	6	K.LCYVALDFEQEMATAASSSSLEK.S
	HsFLAG-Lin9_Ti_20	3.6505	0.1696	1791.77	1791.955	7019.8	1	1188.6	45	2	K.SYELPDGQVITIGNER.F
	HsSrcap_Ti_202.259	5.2016	0.2868	1791.82	1791.955	5255.9	1	1548	80	115	K.SYELPDGQVITIGNER.F
	HsFLAG-ARP6_Ti_1	7.2763	0.4542	3537.02	3536.974	8917.3	1	2225.4	36.2	12	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C
	HsFLAG-ARP8_Ti_2	5.7731	0.4192	3235.09	3233.61	5258	1	782.6	30.6	39	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C
	HsFLAG-p53-DNA-D	6.4056	0.5053	2343.3	2344.645	7130.2	1	1400.7	59.5	9	R.KDLYANTVLSGGTTMYPGIADR.M
	HsFLAG-p53-DNA-D	5.4325	0.3458	2346.45	2344.645	7814.2	1	1648.5	41.7	6	R.KDLYANTVLSGGTTMYPGIADR.M
	HsFLAG-ARP6_Ti_1	5.2133	0.4255	2215.38	2216.471	9210.3	1	1666.4	60	62	K.DLYANTVLSGGTTMYPGIADR.M
	HsFLAG-ARP6_Ti_1	2.8881	0.328	1161.46	1162.387	4673.7	1	620.1	75	20	K.EITALAPSTMK.I
	HsFLAG-ARP6_Ti_1	2.895	0.2843	1161.87	1162.387	4881.7	1	872.9	80	8	K.EITALAPSTMK.I
	HsFLAG-TIP49b_Ti_	3.7056	0.1119	1518.27	1517.595	7339.9	1	1239.5	75	15	K.QEYDESGPSIVHR.K
gi|38455427|r	25	152	62.30%	539	57924	7.8	chaperonin containing TCP1, subunit 4 (delta) [Homo sapiens]				
	HsFLAG-TCF3_Ti_1	1.9042	0.0915	837.42	837.951	6621.4	3	475.4	64.3	2	R.FSNISAAK.A
*	HsFLAG-ARP6_Ti_1	5.0658	0.3183	2091.34	2091.384	7840.6	1	1891.7	68.4	3	K.MIQDGKGDVTITNDGATILK.Q
*	HsFLAG-ARP6_Ti_1	3.0607	0.1396	1150.4	1151.372	5743.4	1	1156.4	88.9	2	K.QMQVLHPAAR.M
*	HsFLAG-ARP6_Ti_1	5.8144	0.5241	2620.73	2622.852	7185	1	1834.9	58	10	K.AQDIEAGDGTTSVVIIAGSLLDSCTK.L
*	HsFLAG-ARP6_Ti_1	3.4969	0.3917	1456.72	1457.67	6188.7	1	786.3	62.5	2	K.GIHPTIISESFQK.A
*	HsFLAG-ARP6_Ti_1	3.6931	0.4173	1457.4	1457.67	3811.9	1	715.9	79.2	16	K.GIHPTIISESFQK.A
*	HsFLAG-ARP6_Ti_1	3.9312	0.2221	1459.95	1457.67	5628	8	906.9	50	4	K.GIHPTIISESFQK.A
*	HsFLAG-ARP6_Ti_1	5.0702	0.4369	3389.96	3392.804	9914.5	4	473.6	20.8	6	K.GIEILTDMSRPVELSDRETLLNSATTSLNSK.V
*	HsFLAG-ARP6_Ti_1	5.5812	0.3126	2040.69	2041.429	4804.6	1	1467.3	69.4	4	K.VVSQYSSLLSPMSVNAVMK.V
*	HsFLAG-ARP6_Ti_1	4.6887	0.3941	1358.28	1358.535	6950.4	1	1620.5	83.3	3	K.VIDPATATSVDLR.D
*	HsFLAG-ARP6_Ti_1	6.6163	0.5017	2188.81	2189.477	8436.9	1	2289.5	68.4	12	K.KLGGTIDDCELVEGLVLTQK.V
*	HsFLAG-ARP6_Ti_1	4.1616	0.268	2189.18	2189.477	7832.9	1	1076.5	36.8	4	K.KLGGTIDDCELVEGLVLTQK.V
*	HsFLAG-ARP6_Ti_1	4.9137	0.4705	2061.12	2061.303	8539.6	1	1615.4	61.1	11	K.LGGTIDDCELVEGLVLTQK.V
*	HsFLAG-ARP6_Ti_1	3.1748	0.2373	1190.56	1190.342	8688	2	1138.5	75	2	K.VSNSGITRVEK.A
*	HsFLAG-ARP6_Ti_1	4.227	0.2476	1347.16	1347.607	5482.2	2	788.1	72.7	10	K.IGLIQFCLSAPK.T
*	HsFLAG-ARP6_Ti_1	3.7365	0.2181	1146.28	1146.339	7002.8	1	1282.3	83.3	1	K.TGCNVLLIQK.S
*	HsFLAG-ARP6_Ti_1	5.0861	0.3174	1458.21	1457.67	8242.3	1	1945.1	79.2	25	R.DALSDLALHFLNK.M
*	HsFLAG-ARP6_Ti_1	3.5476	0.2454	1567.25	1567.702	6261.4	2	740.3	63.6	10	K.DIEREDIEFICK.T
*	HsFLAG-ARP6_Ti_1	4.5576	0.2997	3515.03	3515.917	9715.5	3	617.3	20.5	2	K.TIGTKPVAHIDQFTADMLGSAELAEEVNLNGSGK.L

*	HsFLAG-ARP6_Ti_1	5.1591	0.4296	1708.58	1708.014	7998	1	1951.4	75	10	K.RALIAGGGAPEIELALR.L
*	HsFLAG-ARP6_Ti_1	3.8759	0.1353	1708.97	1708.014	5111.4	1	1543.1	51.6	4	K.RALIAGGGAPEIELALR.L
*	HsFLAG-ARP6_Ti_1	4.8549	0.343	1553.77	1551.826	4938.2	1	1248.2	80	4	R.ALIAGGGAPEIELALR.L
*	HsFLAG-ARP6_Ti_1	3.9655	0.3746	3031.42	3032.436	9781.8	1	821.1	35.7	2	R.AFADAMEVIPSTLAENAGLNPISTVTELR.N
*	HsFLAG-Lin9_Ti_20	4.7841	0.4258	3125.27	3123.658	10483.2	1	1215.9	26.7	2	K.GGISNILEELVVQPLLVSVSALTLATETVR.S
*	HsFLAG-ARP6_Ti_1	2.6919	0.1683	932.19	932.021	4674.5	9	854.2	85.7	1	K.IDDVVNTR.-
gi|12408675|r	14	289	62.30%	154	16648	6.6	prefoldin 2 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.2928	0.4131	2050.73	2051.224	7438.8	1	410.4	35.7	1	K.SSGSGAGKGAVSAEQVIAGFNR.L
*	HsFLAG-UTX1_Ti_2	4.4992	0.3474	1419.3	1419.58	6761.9	1	1595.6	76.9	47	K.GAVSAEQVIAGFNR.L
*	HsFlag-FLJ20643_Ti	3.853	0.3697	1419.74	1419.58	3067.1	1	311.9	65.4	10	K.GAVSAEQVIAGFNR.L
*	HsFlag-NUFIP_Ti_1	4.8872	0.3537	2156.6	2156.456	5994.4	1	1333.8	41.7	27	K.AAELEMELNEHSLVIDTLK.E
*	HsFlag-NUFIP_Ti_11	6.1162	0.3371	2159.08	2156.456	10952.9	1	2677.8	66.7	131	K.AAELEMELNEHSLVIDTLK.E
*	HsFLAG-p53-DNA-D	3.2629	0.1535	960.27	960.18	4014.2	9	836.9	93.8	2	R.MVGGVLVER.T
*	HsFLAG-RPB5MP_2	2.3626	0.1359	1126.38	1127.283	4142.8	5	387.5	72.2	1	K.EVLPALENNK.E
*	HsFLAG-p53-DNA-D	2.8893	0.108	1127.23	1127.283	3481.5	6	476.4	72.2	2	K.EVLPALENNK.E
*	HsFLAG-p53-DNA-D	3.8966	0.3191	1753.28	1753.993	5843.5	1	822.9	67.9	2	K.EVLPALENNKEQIQK.I
*	HsFLAG-RPB5MP_2	5.4604	0.301	1385.72	1386.632	6395.6	1	1550.5	86.4	47	K.IIETLTQQLQAK.G
*	HsFlag-FLJ20643_Ti	3.4351	0.2079	1386.72	1386.632	7519	1	703	63.6	9	K.IIETLTQQLQAK.G
*	HsFLAG-p53-DNA-D	2.5704	0.1215	993.42	993.108	4959.1	3	829.5	85.7	1	K.GKELNEFR.E
*	HsFlag-FLJ20643_Ti	2.9176	0.1316	1188.66	1189.369	6777.5	3	649	65	2	R.LMGEDEKPAAK.E
*	HsFlag-FLJ20643_Ti	3.118	0.2452	1191.96	1189.369	6751.6	6	1057.9	80	7	R.LMGEDEKPAAK.E
gi|4506687|re	8	76	62.10%	145	17040	10.4	ribosomal protein S15 [Homo sapiens]				
	HsFlag-NUFIP_Ti_1	6.1589	0.4628	2589.35	2589.938	10695.7	1	2366.1	57.1	16	R.GVDLDQLLDMSYEQLMQLYSAR.Q
	HsFlag-NUFIP_Ti_1	2.7211	0.2618	1354.52	1354.604	3224.4	4	304.1	68.2	1	K.EAPPMEKPEVVK.T
	HsFlag-NUFIP_Ti_1	6.144	0.5298	2054.21	2054.486	5835.1	1	1863.2	75	8	R.DMIILPEMVGSMVGVYNGK.T
	HsFlag-FLJ90652_2	2.639	0.2531	2844.87	2846.27	5615.2	1	285.5	32.6	1	K.TFNQVEIKPEMIGHYLGEFSITYK.P
	HsFlag-NUFIP_Ti_11	5.7685	0.2634	2846.18	2846.27	9571.2	1	1382.1	34.8	21	K.TFNQVEIKPEMIGHYLGEFSITYK.P
	HsFLAG-ARP6_Ti_1	6.9746	0.4562	3170.81	3170.694	8379.4	1	1089.1	30.8	25	K.TFNQVEIKPEMIGHYLGEFSITYKPVK.H
	HsFlag-NUFIP_Ti_1	2.3809	0.2428	982.51	983.072	4937.5	1	331.4	66.7	1	R.PGIGATHSSR.F
	HsFlag-NUFIP_Ti_1	2.9849	0.3096	984.43	983.072	6628.2	1	917.8	83.3	3	R.PGIGATHSSR.F
gi|4505293|re	29	54	62.00%	700	78764	6.9	MYB-related protein B [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.7115	0.4625	2722.35	2722.761	7215.4	1	1241.9	54.8	1	R.TRCEDLDELHYQDTDSDVPEQR.D
*	HsFLAG-Lin9_Ti_20	5.9805	0.3774	2722.38	2722.761	7894.9	1	1754.4	40.5	2	R.TRCEDLDELHYQDTDSDVPEQR.D
*	HsFLAG-Lin9_Ti_20	5.2878	0.3111	2467.22	2465.469	8638.4	1	1353.4	57.9	1	R.CEDLDELHYQDTDSDVPEQR.D
*	HsFLAG-Lin9_Ti_20	2.8784	0.1935	1343.28	1343.395	5511.5	1	1004.4	88.9	1	K.WTHEEDEQLR.A
*	HsFLAG-Lin9_Ti_20	2.8541	0.2049	1090.3	1089.242	7772.4	2	888.3	75	2	K.FLASHFPNR.T
	HsFLAG-Lin9_Ti_20	3.2949	0.204	1274.15	1274.425	7167.9	1	997.5	77.8	2	R.WHNHLNPEVK.K
*	HsFLAG-Lin9_Ti_20	3.7341	0.3821	1832.63	1833.098	3208.6	1	704	75	3	K.DCKPPVYLLLELEDK.D
*	HsFLAG-Lin9_Ti_20	4.8699	0.1252	1832.78	1833.098	7704.2	2	2371.4	55.4	2	K.DCKPPVYLLLELEDK.D
*	HsFLAG-Lin9_Ti_20	4.0084	0.1473	4542.79	4542.865	5664.2	1	516.2	20.2	1	TTSK.E
*	HsFLAG-Lin9_Ti_20	3.5522	0.4046	3001.49	3002.261	9278.1	3	287.9	28	1	R.TPEPLEEFPKREDQEGSPPETSLPYK.W
*	HsFLAG-Lin9_Ti_20	4.118	0.3299	3003.46	3002.261	9072.3	1	920.5	29	1	R.TPEPLEEFPKREDQEGSPPETSLPYK.W
*	HsFLAG-Lin9_Ti_20	3.7866	0.2034	3885.35	3886.311	5394.7	1	505.9	22.9	1	K.WVVEAANLLIPAVGSSLSEALDLIESDPDAWCDLSK.F

*	HsFLAG-Lin9_Ti_20	3.7993	0.2577	3587.97	3588.913	3731.7	1	414	25.8	2	K.FDLPEEPSAEDSINNSLVQLQASHQQQVLPPR.Q
*	HsFLAG-Lin9_Ti_20	3.0154	0.2858	1213.45	1214.321	6502.7	1	1072.6	85	2	R.LDGHTISDLSR.S
*	HsFLAG-Lin9_Ti_20	3.8431	0.2312	2725.78	2724.084	6909.2	1	1190.6	30.6	1	R.SSRGELIPISPSTEVGGSGIGTPPSVLK.R
*	HsFLAG-Lin9_Ti_20	4.1956	0.2152	2392.7	2393.74	7052	1	1161.4	50	4	R.GELIPISPSTEVGGSGIGTPPSVLK.R
*	HsFLAG-Lin9_Ti_20	4.3249	0.4118	2667.7	2668.924	6671.7	1	668.6	41.7	5	R.VALSPVTENSTSLSFLDSCNSLTPK.S
*	HsFLAG-Lin9_Ti_20	3.4455	0.2349	1825.9	1827.092	3495.7	1	430	67.9	4	K.TLPFSPSQFLNFWNK.Q
*	HsFLAG-Lin9_Ti_20	4.972	0.5058	2220.55	2221.389	6528.3	1	1135.5	60.5	2	K.QDTLELESPSLTSTPVCSQK.V
*	HsFLAG-Lin9_Ti_20	2.8045	0.0899	1021.82	1022.236	6878.7	7	733.7	75	1	K.VVVTTPLHR.D
*	HsFLAG-Lin9_Ti_20	3.0112	0.3062	1113.5	1114.246	7031.2	1	890.2	72.2	2	K.HAAFVTPDQK.Y
*	HsFLAG-Lin9_Ti_20	3.9645	0.373	1114.18	1114.246	6958	1	1202.6	83.3	1	K.HAAFVTPDQK.Y
*	HsFLAG-Lin9_Ti_20	3.1442	0.3467	1635.43	1636.819	8737.2	1	762.5	57.7	1	K.YSMDNTPHTPTPFK.N
*	HsFLAG-Lin9_Ti_20	3.683	0.3304	2075.53	2076.4	4143.7	1	594.4	61.8	1	K.YGPLKPLPQTPHLEEDLK.E
*	HsFLAG-Lin9_Ti_20	3.4792	0.1922	1927.36	1928.147	10132.8	5	740.6	46.9	2	R.SEAGIELIIEDDIRPEK.Q
*	HsFLAG-Lin9_Ti_20	4.2366	0.2462	1317.34	1317.479	6518.2	1	1726.2	86.4	3	K.SLALDIVDEDVK.L
*	HsFLAG-Lin9_Ti_20	3.1335	0.3423	2064.91	2062.325	4119.1	1	343.4	45	2	K.SLSLPTTAPSNSSSLTLSGIK.E
*	HsFLAG-Lin9_Ti_20	3.6591	0.3086	1932.13	1932.141	8493.5	3	724.2	50	1	K.EDNSLLNQGFLQAKPEK.A
*	HsFLAG-Lin9_Ti_20	3.1659	0.1601	1547.58	1548.756	4835.6	2	621.4	57.7	2	R.SHFTTPAPMSSAWK.T
gi|7657162|re	10	234	62.00%	129	14583	8.9	HLA class II region expressed gene KE2 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	2.2777	0.1107	930.48	931.077	6132.4	3	529.8	71.4	1	K.KLQGEVEK.Y
*	HsFlag-NUFIP_Ti_1	5.2555	0.3291	3145.86	3144.593	9240.8	1	926.9	26.9	47	R.QKLEAQLTENNIVKEELALLDGSNVVFK.L
*	HsFlag-NUFIP_Ti_11	5.0319	0.268	2889.36	2888.288	6274.5	1	1287.6	35	13	K.LEAQLTENNIVKEELALLDGSNVVFK.L
*	HsFlag-NUFIP_Ti_1	5.5031	0.3872	2889.38	2888.288	9809.8	1	1531.2	46	30	K.LEAQLTENNIVKEELALLDGSNVVFK.L
*	HsFlag-FLJ20643_Ti	4.4865	0.3479	1536.61	1534.75	7146.3	1	1127.3	73.1	6	K.EELALLDGSNVVFK.L
*	HsFLAG-RPB5MP_2	4.5048	0.3988	1622.59	1622.949	7101.3	1	1355.1	75	5	K.LLGPVLVKQELGEAR.A
*	HsFLAG-BC014022_	3.6841	0.2974	1220.73	1222.427	4052.5	1	760.9	83.3	78	K.RLDYITAEIK.R
*	HsFLAG-p53-DNA-D	3.2173	0.1306	952.42	952.058	8058.4	2	1312.4	100	8	K.RYESQLR.D
*	HsFLAG-p53-DNA-D	2.7824	0.2024	1490.76	1491.644	2521.2	1	137.6	59.1	2	R.ETLAQLQQEFQR.A
*	HsFLAG-RPB5MP_2	4.5543	0.3949	1491.24	1491.644	8232.9	1	1413.1	77.3	44	R.ETLAQLQQEFQR.A
gi|6005814|re	40	1059	61.90%	465	54190	7.2	serine/threonine kinase 38 [Homo sapiens]				
*	HsFlag-ZnF-HIT2_Ti_	2.7246	0.1218	865.26	865.036	6051.2	7	762.3	91.7	1	K.ERVTMTK.V
*	HsARP6-FLAG_Ti_1	4.5685	0.2601	2064.4	2064.262	5185.8	1	1315.7	53.1	39	K.VTLENFYSNLIAQHEER.E
*	HsFLAG-ARP6_Ti_1	5.5446	0.4512	2064.75	2064.262	7373.3	1	1439.8	68.8	115	K.VTLENFYSNLIAQHEER.E
*	HsFLAG-ARP8_Ti_1	2.0129	0.1323	934.23	935.08	8371.7	7	637.4	71.4	1	K.VMEEEGLK.D
*	HsFlag-VPS71_Ti_1	3.2089	0.2189	1435.49	1436.574	5820.6	1	535.2	59.1	1	K.VMEEEGLKDEEK.R
*	HsFlag-ZnF-HIT2_Ti_	4.38	0.2646	1436.52	1436.574	8186.8	1	1767	86.4	20	K.VMEEEGLKDEEK.R
*	HsMRGBP-FLAG_Ti_	4.3603	0.3035	1592.74	1592.761	9172.4	1	2375	87.5	6	K.VMEEEGLKDEEKR.L
*	HsFLAG-RPB5MP_2	2.9113	0.1535	1408.44	1408.594	7692.4	5	652	54.5	1	R.TRLGLEDFESLK.V
*	HsFLAG-p53-DNA-D	2.8647	0.1979	1150.52	1151.302	8712	1	903.6	72.2	19	R.LGLEDFESLK.V
*	HsFlag-FLJ90652_2	3.7875	0.1378	1150.65	1151.302	5873.8	1	1233.8	88.9	50	R.LGLEDFESLK.V
*	HsFLAG-ARP5_Ti_1	2.269	0.2903	1149.5	1150.338	4615	1	400.1	55.6	1	K.KDTGHVYAMK.I
*	HsFLAG-ARP5_Ti_1	3.5662	0.333	1150.3	1150.338	7912	1	1455.6	88.9	5	K.KDTGHVYAMK.I
*	HsFlag-VPS71_Ti_1	2.5808	0.2872	1021.43	1022.164	5424.5	2	711.5	68.8	15	K.DTGHVYAMK.I
*	HsARP6-FLAG_Ti_1	5.4478	0.1938	1488.81	1487.736	6264	1	1839	87.5	56	R.DILVEADSLWVVK.M

	HsFLAG-ARP6_Ti_1	2.2059	0.115	1065.34	1066.216	6161.4	5	554.4	71.4	2	K.MFYSFQDK.L
*	HsFlag-FLJ90652_2	9.3978	0.2522	3619.35	3620.053	10716.6	1	3073.1	35.8	30	K.KDTLTEEETQFYIAETVLAIDSIHQLGFIHR.D
*	HsFLAG-ARP6_Ti_1	7.3167	0.4073	3490.93	3491.879	7001.9	1	1196.6	32.8	45	K.DTLTEEETQFYIAETVLAIDSIHQLGFIHR.D
*	HsFLAG-ARP8_Ti_2	2.7648	0.2017	1371.67	1371.574	6021.6	1	546.4	59.1	6	R.DIKPDNLLLDSK.G
*	HsFLAG-UTX1_Ti_2	3.5199	0.1874	1371.7	1371.574	3051.3	1	631.2	77.3	50	R.DIKPDNLLLDSK.G
	HsFlag-FLJ90652_2	2.8592	0.2419	1210.54	1211.367	4516.1	1	485.6	65	28	K.LSDFGLCTGLK.K
	HsFlag-FLJ90652_2	4.2329	0.2928	1211.36	1211.367	6417.2	1	1697.6	90	38	K.LSDFGLCTGLK.K
	HsFLAG-ARP6_Ti_1	3.4297	0.2592	1339.36	1339.541	6565.3	1	1017.5	77.3	7	K.LSDFGLCTGLKK.A
*	HsFlag-NUFIP_Ti_2	5.4955	0.3255	2094.72	2095.294	10620.5	1	1852.3	44.1	31	R.NLNHSLPSDFTFQNMNSK.R
*	HsFlag-VPS71_Ti_1	5.4843	0.378	2094.78	2095.294	4193.8	1	837.2	64.7	78	R.NLNHSLPSDFTFQNMNSK.R
*	HsFLAG-ARP6_Ti_1	5.0336	0.312	2933.79	2935.324	6800	1	990.4	33	3	R.RQLAFSTVGTPDYIAPEVFMQTGYNK.L
*	HsFlag-VPS71_Ti_1	4.8257	0.5003	2934.94	2935.324	6427.8	1	849.1	42	2	R.RQLAFSTVGTPDYIAPEVFMQTGYNK.L
*	HsFlag-NUFIP_Ti_1	3.8324	0.4498	2777.84	2779.136	4826.6	1	424.7	39.6	7	R.QLAFSTVGTPDYIAPEVFMQTGYNK.L
*	HsFlag-VPS71_Ti_1	5.2229	0.3686	2779.25	2779.136	8765.6	1	1493.1	35.4	6	R.QLAFSTVGTPDYIAPEVFMQTGYNK.L
*	HsFlag-FLJ90652_2	2.6181	0.2415	1586.87	1587.81	3285.2	1	251.8	53.8	3	K.ETLTFPPEVPISEK.A
*	HsFlag-ZnF-HIT2_Ti	3.4366	0.338	1587.63	1587.81	3042.7	1	684.9	80.8	32	K.ETLTFPPEVPISEK.A
*	HsFlag-FLJ90652_2	2.1546	0.2229	1223.32	1224.25	4214.9	5	236.3	64.3	3	R.FCCEWEHR.I
*	HsFlag-NUFIP_Ti_2	3.2432	0.2657	1223.77	1224.25	5748.6	1	1058.4	92.9	27	R.FCCEWEHR.I
*	HsFLAG-Lin9_Ti_20	2.4715	0.1856	1012.47	1013.179	4784.9	1	577.3	66.7	25	R.IGAPGVEEIK.S
*	Hs293Flag-Ies2_Ti_1	3.3037	0.2662	1012.53	1013.179	3507.8	1	844.7	88.9	36	R.IGAPGVEEIK.S
*	HsH2AZ-FLAG_293_	4.4022	0.4503	1722.94	1723.842	6310.2	1	1416.5	76.9	105	K.SNSFFEGVDWEHIR.E
*	HsFLAG-ARP8_Ti_2	3.5686	0.2308	1723.26	1723.842	6563.6	1	1092.6	48.1	2	K.SNSFFEGVDWEHIR.E
*	HsFlag-NUFIP_Ti_2	3.5186	0.2869	1227.22	1227.447	6664.5	1	1154.5	85	16	R.ERPAAISIEIK.S
*	HsFLAG-ARP6_Ti_1	6.3235	0.4817	3615.28	3614.812	8339.2	1	1298.4	29.8	85	K.SIDDTSNFDEFPESDILKPTVATSNHPETDYK.N
*	HsFLAG-p53-DNA-D	4.5027	0.3631	1591.45	1591.806	6205.4	1	1332.2	81.8	6	K.NKDWVFINYTYK.R
*	HsFlag-NUFIP_Ti_1	3.545	0.1914	950.45	950.085	7967.8	2	1149.9	92.9	56	K.RFEGLTAR.G
gi|5729838|re	24	178	61.70%	227	26499	8.4	glioma-amplified sequence-41 [Homo sapiens]				
*	HsFLAG-TIP49b_Ti_	2.395	0.2261	1279.39	1280.401	3628.8	1	372.8	63.6	1	K.RMAEFGPDSGGR.V
*	HsFLAG-TIP49b_Ti_	3.7583	0.2809	1280.09	1280.401	5308	1	1127.7	81.8	17	K.RMAEFGPDSGGR.V
*	HsVPS71-FLAG_Ti_	3.4753	0.2625	1124.39	1124.213	4487.1	1	1001.4	80	2	R.MAEFGPDSGGR.V
*	HsMRGBP-FLAG_Ti	3.6431	0.2741	1586.87	1586.918	3643.9	1	334.7	60.7	8	K.GVTIVKPIVYGNVAR.Y
*	HsH2AZ-FLAG_293_	3.7206	0.2801	1587.32	1586.918	3826.5	1	633.2	71.4	22	K.GVTIVKPIVYGNVAR.Y
*	HsH2AZ-FLAG_293_	4.7684	0.338	1588.1	1586.918	7709	1	1984.9	53.6	7	K.GVTIVKPIVYGNVAR.Y
*	HsFlag-VPS71_Ti_1	1.8909	0.0918	988.6	989.162	5041.9	4	356.6	75	1	K.PIVYGNVAR.Y
*	HsFlag-VPS71_Ti_1	3.6492	0.3001	1474.81	1473.643	5630.4	1	1170.6	81.8	8	K.PYRNEDMSAYVK.K
*	HsH2AZ-FLAG_293_	2.9207	0.26	1057.15	1057.163	3968.6	1	878.5	87.5	1	R.NEDMSAYVK.K
*	HsYL1_Ti_101.1668.	2.451	0.1965	1057.49	1057.163	4098.5	1	374.8	68.8	5	R.NEDMSAYVK.K
*	HsH2AZ-FLAG_293_	3.298	0.2583	1185.46	1186.313	5472.9	1	696.9	77.8	25	K.LHESYGNPLR.V
*	HsH2AZ-FLAG_293_	3.2137	0.2536	1187.57	1186.313	5240	1	1376.5	94.4	12	K.LHESYGNPLR.V
*	HsSrcap_Ti_206.288	3.5766	0.2333	2215.97	2216.631	7038.1	1	606	52.9	3	K.IFFIDPNERPVTLYHLLK.L
*	HsTIP60_Ti_103.17	2.6262	0.2985	1324.42	1325.522	8436.5	1	541.5	59.1	2	K.LFQSDTNAMLGK.K
*	HsH2AZ-FLAG_293_	4.0134	0.3246	1325.08	1325.522	6884.1	2	1177.9	77.3	7	K.LFQSDTNAMLGK.K
*	HsFlag-VPS71_Ti_1	4.1761	0.4683	3182.13	3183.633	5452.4	1	537.2	38.5	8	K.TVVSEFYDEMIFQDPTAMMQQLLTTSR.Q

*	HsMRGBP-FLAG_Ti_	3.7863	0.2872	3184.83	3183.633	5747.2	1	629.2	28.8	2	K.TVVSEFYDEMIFQDPTAMMQQLLTTSR.Q
*	HsFlag-VPS71_Ti_1	3.006	0.2119	1331.53	1332.453	4520	6	515.7	65	6	K.HETEFAELEVK.T
*	HsH2AZ-FLAG_293_	4.2289	0.3704	1332.25	1332.453	5064.7	1	1152.8	90	21	K.HETEFAELEVK.T
*	HsH2AZ-FLAG_293_	3.5353	0.1947	1166.48	1166.36	4611.8	1	1085.9	88.9	8	K.KTSFEIAELK.E
*	HsMRGBP-FLAG_Ti_	2.4748	0.1455	1037.69	1038.186	6913.7	4	695	75	1	K.TSFEIAELK.E
*	HsTIP60_Ti_103.200	3.3179	0.2428	1037.92	1038.186	4225.9	1	935	93.8	7	K.TSFEIAELK.E
*	HsTIP60_Ti_106.229	3.269	0.2602	1323.39	1323.489	6003.2	1	862.6	75	3	K.TSFEIAELKER.L
*	HsYL1_Ti_103.0679.	2.89	0.1785	1304.56	1304.397	5074.5	1	1220.5	90	1	R.KLEEDDQAKDI.-
gi|11415030|r	13	93	61.20%	103	11367	11.4	H4 histone family, member E [Homo sapiens]				
gi|89066445|r	13	93	61.20%	103	11367	11.4	PREDICTED: similar to germinal histone H4 gene isoform 4 [Homo sapiens]				
gi|89066443|r	13	93	61.20%	103	11367	11.4	PREDICTED: similar to germinal histone H4 gene isoform 3 [Homo sapiens]				
gi|89066441|r	13	93	61.20%	103	11367	11.4	PREDICTED: similar to germinal histone H4 gene isoform 2 [Homo sapiens]				
gi|89066439|r	13	93	61.20%	103	11367	11.4	PREDICTED: similar to germinal histone H4 gene isoform 1 [Homo sapiens]				
gi|4504323|re	13	93	61.20%	103	11367	11.4	histone 2, H4 [Homo sapiens]				
gi|4504321|re	13	93	61.20%	103	11367	11.4	H4 histone family, member M [Homo sapiens]				
gi|4504317|re	13	93	61.20%	103	11367	11.4	H4 histone family, member K [Homo sapiens]				
gi|4504315|re	13	93	61.20%	103	11367	11.4	H4 histone family, member J [Homo sapiens]				
gi|4504313|re	13	93	61.20%	103	11367	11.4	H4 histone family, member I [Homo sapiens]				
gi|4504311|re	13	93	61.20%	103	11367	11.4	H4 histone family, member H [Homo sapiens]				
gi|4504309|re	13	93	61.20%	103	11367	11.4	H4 histone family, member G [Homo sapiens]				
gi|4504307|re	13	93	61.20%	103	11367	11.4	H4 histone family, member D [Homo sapiens]				
gi|4504305|re	13	93	61.20%	103	11367	11.4	H4 histone family, member C [Homo sapiens]				
gi|4504303|re	13	93	61.20%	103	11367	11.4	H4 histone family, member B [Homo sapiens]				
gi|4504301|re	13	93	61.20%	103	11367	11.4	H4 histone family, member A [Homo sapiens]				
gi|28173560|r	13	93	61.20%	103	11367	11.4	histone H4 [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.0145	0.2922	1325.57	1326.539	3834	3	369.8	68.2	3	R.DNIQGITKPAIR.R
	HsFlag-NUFIP_Ti_20	4.0131	0.1701	1326.46	1326.539	8422.1	3	1090.6	72.7	18	R.DNIQGITKPAIR.R
	HsFLAG-ARP6_Ti_1	3.6067	0.2995	1337.36	1337.519	4896.1	1	1171.3	90	19	K.RISGLIYEETR.G
	HsFLAG-ARP8_Ti_2	3.4126	0.1563	1181.26	1181.331	5753.2	1	1221.9	94.4	2	R.ISGLIYEETR.G
	HsFLAG-ARP8_Ti_2	3.438	0.1052	990.08	990.191	3690.6	4	724.1	92.9	1	K.VFLENVIR.D
	HsFLAG-p53-DNA-D	3.1131	0.3479	1134.43	1135.219	4958.1	1	547	72.2	4	R.DAVTYTEHAK.R
	HsH2AZ-FLAG_293_	3.2692	0.2089	1135.49	1135.219	3844.6	2	765.2	88.9	9	R.DAVTYTEHAK.R
	HsFLAG-p53-DNA-D	2.8927	0.2581	1291.62	1291.406	7360.3	1	982.2	75	2	R.DAVTYTEHAKR.K
	HsFLAG-p53-DNA-D	4.0605	0.3019	1439.34	1439.753	7918.2	1	1802.1	83.3	3	R.KTVTAMDVVYALK.R
	HsFLAG-p53-DNA-D	2.218	0.2332	1310.57	1311.579	8668.9	7	452.4	54.5	1	K.TVTAMDVVYALK.R
	HsFLAG-ARP8_Ti_2	3.9675	0.3764	1311.12	1311.579	4993.7	1	1080.2	86.4	19	K.TVTAMDVVYALK.R
	HsFLAG-p53-DNA-D	3.5812	0.2851	1467.43	1467.767	9472.1	1	1549.8	75	9	K.TVTAMDVVYALKR.Q
	HsH2AZ-FLAG_293_	2.0919	0.0943	714.4	714.796	4050.5	1	414.5	75	3	R.TLYGFGG.-
gi|14589951|r	11	223	61.00%	210	24611	6	PolII_Rpb5 {DNA directed RNA polymerase II polypeptide E; polymerase (RNA) II (DNA directed) polypeptide				
*	HsFLAG-UTX1_Ti_2	2.6605	0.1319	1175.3	1174.326	5777.7	1	706.6	81.2	2	K.TIMQLCHDR.G
*	HsFlag-NUFIP_Ti_10	6.3309	0.4955	2028.84	2029.208	8545.4	1	2603.1	78.1	70	R.GYLVTQDELDQTLEEFK.A
*	HsFLAG-p53-DNA-D	4.63	0.3275	3456.79	3455.762	7924.9	1	765.6	25.9	4	R.GYLVTQDELDQTLEEFKAQFGDKPSEGRPR.R
*	HsFLAG-BC014022_	2.8155	0.2105	1445.29	1445.578	6933.2	1	547.3	62.5	4	K.AQFGDKPSEGRPR.R

*	HsFlag-NUFIP_Ti_10	6.9793	0.4802	3162.37	3163.529	10303.9	1	2838.6	40.4	80	R.RTDLTVLVAHNDDPTDQMFVFFPEEPK.V
*	HsFlag-NUFIP_Ti_10	3.5774	0.399	3163.06	3163.529	6979.7	1	469.8	34.6	2	R.RTDLTVLVAHNDDPTDQMFVFFPEEPK.V
*	HsFLAG-p53-DNA-D	3.4875	0.3275	1442.64	1443.745	6369	1	548.3	61.5	7	R.ALIVVQQGMTPSAK.Q
*	HsFLAG-p53-DNA-D	4.5992	0.4515	1443.42	1443.745	7058.8	1	1550.8	73.1	18	R.ALIVVQQGMTPSAK.Q
*	HsFlag-NUFIP_Ti_11	7.2163	0.38	3509.22	3509.098	8045.6	1	1411.7	33	9	K.YILEQFLQQELLINITEHELVPEHVVMTK.E
*	HsFLAG-p53-DNA-D	2.6607	0.2128	1060.35	1060.192	7138.7	1	1412.6	93.8	2	K.EEVTELLAR.Y
*	HsFLAG-p53-DNA-D	3.2621	0.1127	1100.54	1100.263	5708.4	3	746	77.8	25	K.IIRPSETAGR.Y
gi|13123776|r	43	431	60.80%	467	52993	9.5	DNA methyltransferase 1-associated protein 1 [Homo sapiens]				
*	HsTIP60_Ti_103.011	5.9542	0.4978	1831.31	1830.987	5869.4	1	1590.3	72.2	26	R.DILELGGPEGDAASGTISK.K
*	HsH2AZ-FLAG_293_	5.0563	0.3958	1957.72	1959.161	5941.1	1	1108.4	63.2	14	R.DILELGGPEGDAASGTISKK.D
*	HsYL1_Ti_103.1338.	2.3417	0.1813	1040.52	1041.189	4160.8	1	448.6	68.8	1	K.KSSETLTFK.R
*	HsH2AZ-FLAG_293_	2.889	0.2756	913.51	913.015	3660	2	704.9	92.9	2	K.SSETLTFK.R
*	HsH2AZ-FLAG_293_	3.2408	0.2388	1201.32	1201.362	5732.6	1	988.8	88.9	2	R.EVYALLYSDK.K
*	HsFlag-VPS71_Ti_10	3.4131	0.2291	1201.57	1201.362	4529.5	1	471.5	72.2	6	R.EVYALLYSDK.K
*	HsH2AZ-FLAG_293_	3.7437	0.2871	1329.3	1329.536	7700.7	1	1688	90	14	R.EVYALLYSDKK.D
*	HsVPS71-FLAG_Ti_	3.496	0.2583	1329.84	1329.536	4618.7	1	420.4	65	7	R.EVYALLYSDKK.D
*	HsFLAG-TIP49b_Ti_	4.2508	0.2536	1715.43	1715.903	4016.2	1	716.5	66.7	16	K.KDAPPLLPSDTGQGYR.T
*	HsYL1-FLAG_Ti_202	2.668	0.1939	1587.8	1587.729	3159.1	7	442.8	60.7	1	K.DAPPLLPSDTGQGYR.T
*	HsFLAG-TIP49b_Ti_	2.3451	0.2527	1166.38	1167.33	2819.9	6	299.2	68.8	1	K.DGAMFFHWR.R
*	HsFLAG-TIP49b_Ti_	3.1737	0.3716	1167.31	1167.33	6958.9	1	1508.8	93.8	9	K.DGAMFFHWR.R
*	HsH2AZ-FLAG_293_	3.8835	0.3638	1510.6	1510.649	4083.7	2	766.4	79.2	3	R.RAAEEGKDYPFAR.F
*	HsFlag-VPS71_Ti_10	2.3496	0.2597	1353.67	1354.462	3922.5	5	252.6	50	2	R.AAEEGKDYPFAR.F
*	HsH2AZ-FLAG_293_	3.4599	0.4151	1354.38	1354.462	5072	1	1045.2	81.8	8	R.AAEEGKDYPFAR.F
*	HsH2AZ-FLAG_293_	4.8987	0.4085	2813.4	2814.08	8388.7	1	1239.4	47.7	30	K.TVQVPVYSEQEYQLYLHDDAWTK.A
*	HsVPS71-FLAG_Ti_	2.8626	0.4052	1304.63	1304.402	3159.9	1	343.3	65	10	K.AETDHLFDLSR.R
*	HsYL1_Ti_102.1739.	4.0094	0.2213	1304.71	1304.402	6352.5	1	1454.3	85	15	K.AETDHLFDLSR.R
*	HsFLAG-TIP49a_Ti_	2.5315	0.16	886.76	886.041	3832.1	1	678.7	91.7	2	R.FVVIHDR.Y
*	HsMRGBP-FLAG_Ti_	4.0804	0.3622	1833.84	1833.059	4958	1	736.2	69.2	10	R.FVVIHDRYDHQQFK.K
*	HsFLAG-TIP49b_Ti_	2.1464	0.2194	1239.55	1240.37	3210.5	5	274.3	68.8	2	K.ERYYHICAK.L
*	HsFLAG-TIP49b_Ti_	3.0693	0.3113	1240.22	1240.37	9310.1	1	1321.4	87.5	6	K.ERYYHICAK.L
*	HsH2AZ-FLAG_293_	2.018	0.1471	954.36	955.067	5061	9	459.4	66.7	1	R.YYHICAK.L
*	HsYL1_Ti_104.1311.	2.5246	0.1943	956.47	955.067	3746.9	1	535.3	91.7	3	R.YYHICAK.L
*	HsMRGBP-FLAG_Ti_	2.5941	0.1575	1355.21	1354.592	4463	6	571.9	62.5	1	K.LANVRAVPGTDLK.I
*	HsFlag-VPS71_Ti_10	2.2028	0.158	1140.69	1141.272	5057.1	8	419.5	61.1	2	K.IPVFDAGHER.R
*	HsH2AZ-FLAG_293_	2.8401	0.1706	1140.79	1141.272	5478.1	2	829.1	83.3	12	K.IPVFDAGHER.R
*	HsH2AZ-FLAG_293_	5.7935	0.4452	2494.38	2494.764	9390.8	1	1915.1	63.2	37	R.LYNRTPEQVAEEEYLLQELR.K
*	HsH2AZ-FLAG_293_	3.8307	0.1264	2494.47	2494.764	6381.8	2	1050.4	36.8	1	R.LYNRTPEQVAEEEYLLQELR.K
*	HsFlag-VPS71_Ti_10	6.3195	0.3734	1947.77	1948.137	6528.7	1	2179.3	83.3	47	R.TPEQVAEEEYLLQELR.K
*	HsH2AZ-FLAG_293_	4.3324	0.212	1947.79	1948.137	7929.3	1	1920.7	50	6	R.TPEQVAEEEYLLQELR.K
*	HsH2AZ-FLAG_293_	3.0188	0.3483	1289.43	1290.416	4186.6	1	418.8	68.2	7	K.LITAADTTAEQR.R
*	HsTIP60_Ti_102.138	4.6747	0.3276	1289.62	1290.416	9400.7	1	2158.8	86.4	24	K.LITAADTTAEQR.R
*	HsTIP60_Ti_103.141	3.2023	0.2348	1440.21	1440.637	3240.3	3	415.4	65.4	7	K.EAEKPAVPETAGIK.F
*	HsFLAG-TIP49b_Ti_	2.1996	0.2979	982.44	983.153	4600.6	1	452	66.7	5	K.PAVPETAGIK.F

*	HsFLAG-TIP49a_Ti_	2.9961	0.2087	1192.46	1193.426	7057.5	6	566.6	61.1	13	R.SDLVLLYELK.Q
*	HsYL1_Ti_102.2384.	4.1433	0.1751	1193.78	1193.426	4547.6	3	1037.4	83.3	33	R.SDLVLLYELK.Q
*	HsYL1_Ti_102.1788.	4.38	0.3015	1788.13	1786.93	7668.5	1	976.6	65.4	5	K.QACANCEYELQMLR.H
*	HsFlag-VPS71_Ti_1	2.6543	0.1302	991.67	990.113	5997.2	1	944.1	85.7	2	R.HRHEALAR.A
*	HsTIP60_Ti_106.233	4.9121	0.4223	2923.1	2924.237	6922.2	1	657.5	35.9	19	R.AGVLGGPATPASGPGPASAEPAVTEPGLGPDPK.D
*	HsH2AZ-FLAG_293_	5.1334	0.2515	2925.54	2924.237	8403.6	1	898.3	26.6	4	R.AGVLGGPATPASGPGPASAEPAVTEPGLGPDPK.D
*	HsMRGBP-FLAG_Ti_	5.4943	0.3311	4574.54	4574.101	5688.9	1	441.7	18.2	10	GAPLTPNSR.K
*	HsH2AZ-FLAG_293_	4.069	0.2976	1669.72	1668.888	4980.6	1	974.3	66.7	5	K.DTIIDVVGAPLTPNSR.K
gi|5032027|re	15	69	60.70%	425	47656	4.9	retinoblastoma binding protein 4 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	5.1583	0.3722	3827.41	3828.377	9597.6	1	1610.2	28.9	8	K.NTPFLYDLVMTHALEWPSLTAQWLPDVTRPEGK.D
*	HsFLAG-Lin9_Ti_20	6.5992	0.4144	4097.55	4096.37	8584.8	1	925	24.3	4	R.LVLGTHTSDEQNHLVIASVQLPNDDAQFDASHYDSEK.G
	HsFLAG-Lin9_Ti_20	2.2237	0.2484	1128.44	1129.214	6381	1	554.5	63.6	2	K.GEFGGFGSVSGK.I
	HsFLAG-Lin9_Ti_20	3.6625	0.2615	1129.2	1129.214	7271.5	1	1515.5	81.8	2	K.GEFGGFGSVSGK.I
	HsSrcap_Ti_203.235	3.002	0.3428	1472.37	1472.635	4836.8	1	486.8	62.5	7	K.TPSSDVLVFDYTK.H
	HsFLAG-Lin9_Ti_20	4.3366	0.3815	1473.5	1472.635	7851	1	1516.2	75	9	K.TPSSDVLVFDYTK.H
	HsFLAG-Lin9_Ti_20	2.7647	0.2874	1808.45	1806.896	6894.7	1	438.3	50	1	K.HPSKPDPSGECNPDLR.L
*	HsSrcap_Ti_203.371	4.0791	0.2734	3756.03	3755.101	9077.9	2	547.4	19.7	6	K.EGYGLSWNPNLSGHLLSASDDHTICLWDISAVPK.E
*	HsFLAG-Lin9_Ti_20	5.8192	0.5307	3439.33	3440.794	9811.4	1	1920.6	33.3	9	K.TIFTGHTAVVEDVSWHLLHESLFGSVADDQK.L
*	HsFLAG-Lin9_Ti_20	5.925	0.2998	4099.24	4098.352	9916.8	1	992.7	23	9	R.SNNTSKPSHSVDAHTAEVNCLSFNPYSEFILATGSADK.T
	HsFLAG-Lin9_Ti_20	2.7344	0.0828	973.28	974.148	3249.6	3	701.2	85.7	1	K.TVALWDLR.N
	HsSrcap_Ti_205.221	2.7488	0.1048	1131.52	1131.32	4440.3	3	625	81.2	1	R.RLNVWDLSK.I
	HsFLAG-Lin9_Ti_20	2.8604	0.1205	975.25	975.133	4581	5	882.6	92.9	1	R.LNVWDLSK.I
*	HsFLAG-Lin9_Ti_20	3.745	0.3865	2874.48	2875.078	4534.9	1	341.7	36.5	3	K.IGEEQSPEDAEDGPPELLFIHGGHTAK.I
*	HsFLAG-Lin9_Ti_20	4.7938	0.2719	2875.13	2875.078	5244.8	2	644.4	30.8	6	K.IGEEQSPEDAEDGPPELLFIHGGHTAK.I
gi|23346420|r	76	402	60.40%	1324	141860	9	nuclear factor related to kappaB binding protein [Homo sapiens]				
*	HsFlag-FLJ90652_2	4.0767	0.1647	1264.71	1265.433	6995.3	5	1399.9	85	1	R.IMEDCLLGGTR.V
*	HsFLAG-FLJ20309_	6.8053	0.4374	3694.42	3695.071	9882.7	1	1747.2	30.6	14	R.VSLPEDLLEDPEIFFDVVSLSTWQEVLSDSQR.E
*	HsFLAG-TCF3_Ti_1	5.6199	0.5147	3775.07	3777.141	10044.3	1	1066.1	25	29	R.EHLQQFLPQFPEDSAEQQNELILALFSGENFR.F
*	Hs293Flag-Ies2_Ti_1	3.386	0.2737	1125.05	1125.316	4661.2	1	952.3	83.3	11	R.FGNPLHIAQK.L
*	HsFLAG-FLJ20309_	2.8138	0.091	1125.57	1125.316	5956.6	1	814.7	72.2	3	R.FGNPLHIAQK.L
*	HsFLAG-TCF3_Ti_1	2.7406	0.1394	1141.46	1142.257	6458.1	7	788.7	66.7	1	R.DGHFNPEVVK.Y
*	HsFLAG-TCF3_Ti_1	3.6441	0.2373	1640.08	1640.801	7208.4	1	629.2	63.6	4	K.RYLNSQQQYFHR.L
*	HsFLAG-TCF3_Ti_1	4.1275	0.2862	1486.52	1484.614	9117.3	1	1798.4	85	17	R.YLNSQQQYFHR.L
*	HsFlag-FLJ90652_2	2.9851	0.1978	935.17	935.083	5384.4	1	1043	92.9	1	R.SDLLEMAR.R
*	HsFLAG-TCF3_Ti_1	3.1806	0.2516	1001.51	1001.176	5725.2	3	647	81.2	8	R.RSGPALPFR.Q
*	HsFLAG-FLJ20309_	2.2748	0.0993	844.45	844.989	5311.1	1	442.7	78.6	1	R.SGPALPFR.Q
*	HsFLAG-TCF3_Ti_1	1.9236	0.1104	923.61	924.088	4212	9	246.5	62.5	1	R.SPSPAVPLR.V
*	HsFLAG-TCF3_Ti_1	2.3183	0.2465	1191.53	1192.413	4864.9	1	382.1	65	2	R.VVPTLSTTDMK.T
*	HsFLAG-ARP5_Ti_1	3.8193	0.2653	1391.29	1391.518	7807.9	2	1328.4	70.8	4	K.TADKVELGDSDLK.I
*	HsFlag-FLJ90652_2	2.2276	0.1694	975.42	976.072	5559.6	1	648.1	75	1	K.VELGDSDLK.I
*	HsFLAG-TIP49a_Ti_	5.9145	0.4697	2403.06	2403.672	8149.5	1	2200.2	46.2	4	K.HQPDHPDLLTGDLTLNDIMTR.V
*	HsFLAG-TIP49a_Ti_	4.0448	0.2484	2403.9	2403.672	7395.7	2	596.9	42.5	4	K.HQPDHPDLLTGDLTLNDIMTR.V
*	HsFLAG-ARP8_Ti_2	4.7903	0.3465	1462.26	1462.773	9937.7	1	2380.3	80.8	5	R.KGSLAALYDLAVLK.K

*	HsFLAG-ARP8_Ti_2	2.3015	0.2026	1334.31	1334.599	9294.5	1	790	58.3	1	K.GSLAALYDLAVLK.K
*	HsFLAG-FLJ20309_	5.0626	0.4236	1334.52	1334.599	6129.9	1	1751.8	83.3	16	K.GSLAALYDLAVLK.K
*	HsFLAG-TCF3_Ti_1	3.4558	0.2421	1463.81	1462.773	7999.8	1	1312.9	69.2	1	K.GSLAALYDLAVLKK.K
*	HsFLAG-FLJ20309_	2.9485	0.2549	1441.94	1442.654	2556.4	1	258.2	66.7	1	R.AVPSSFSPFVEFK.E
*	HsFLAG-TCF3_Ti_1	3.3353	0.3651	1699.51	1699.944	3771.6	1	539.7	71.4	3	R.AVPSSFSPFVEFKEK.T
*	HsFLAG-TCF3_Ti_1	2.9901	0.1981	1132.33	1132.216	4467.8	1	752.2	88.9	2	K.LLGQSQDNEK.E
*	HsFLAG-ARP5_Ti_1	4.1099	0.295	2675.84	2676.042	9170.8	1	967	28.4	2	K.LLGQSQDNEKELAALFQLWLETK.D
*	HsFLAG-FLJ20309_	5.3395	0.425	1562.48	1562.849	7260.8	1	1935.8	87.5	19	K.ELAALFQLWLETK.D
*	Hs293Flag-Ies2_Ti_1	4.207	0.3548	2397.08	2396.452	9460.7	1	1243.2	52.5	1	K.DQAFCKQENEDSSDATTPVPR.V
*	HsFLAG-FLJ20309_	4.739	0.3872	1646.08	1646.665	8664.5	1	1281.1	67.9	4	K.QENEDSSDATTPVPR.V
*	HsFLAG-TIP49b_Ti_	2.9361	0.0954	1736.51	1736.922	4672.8	8	334.2	50	1	R.VRTDYVVRPSTGEEK.R
*	HsFLAG-FLJ20309_	3.6862	0.268	1481.61	1481.602	7617.9	1	1229.1	75	4	R.TDYVVRPSTGEEK.R
*	HsFLAG-TCF3_Ti_1	3.2044	0.0819	1092.04	1092.2	6738.8	2	1117.6	92.9	2	K.RVFQEQER.Y
*	HsFLAG-TIP49a_Ti_	3.2777	0.3628	1286.34	1287.519	5657.1	1	937.4	72.7	12	R.MHGFESVVGPVK.G
*	HsFLAG-ARP5_Ti_1	3.9031	0.408	1287.35	1287.519	4512.6	1	753.9	77.3	10	R.MHGFESVVGPVK.G
*	HsFLAG-ARP5_Ti_1	4.2565	0.3668	1590.5	1590.863	5629.2	1	1027.4	73.1	18	R.SDRPAYVTILSLVR.D
*	HsFLAG-FLJ20309_	5.8306	0.451	2521.86	2521.744	5903.2	1	1200.7	58.7	23	K.DSQFLAPDVTSTQVNTVVSGALDR.L
*	HsFLAG-TCF3_Ti_1	3.575	0.2496	3193.3	3192.51	2890.7	4	199.9	24.1	1	K.DSQFLAPDVTSTQVNTVVSGALDRLHYEK.D
*	HsFLAG-ARP5_Ti_1	2.7675	0.1791	1289.34	1289.44	5111.2	1	804.5	77.8	2	R.LHYEKDPCVK.Y
*	HsFlag-FLJ90652_2	2.6819	0.126	1001.1	1001.219	4207.5	5	673.9	91.7	1	K.LWIYLHR.D
*	HsFLAG-ARP5_Ti_1	3.1866	0.1979	1197.04	1197.203	5626	1	784.5	87.5	6	R.DRSEEEFER.I
*	HsFLAG-FLJ20309_	2.6847	0.269	1009.84	1009.153	4981.4	1	596.5	72.2	5	R.IHQAQAAAAK.A
*	HsFLAG-FLJ20309_	2.8936	0.1239	1221.68	1222.473	5823.9	1	675	70	1	K.ALQQKPKPPSK.V
*	HsFLAG-FLJ20309_	3.299	0.1144	1222.5	1222.473	5390.6	2	601.6	70	4	K.ALQQKPKPPSK.V
*	HsFLAG-ARP8_Ti_2	3.8392	0.2087	3516.06	3513.963	6214.2	1	747.6	25	1	K.SSSGVLLVSSPTMPHLGTMLSPASSQTAPSSQAAAR.V
*	HsFLAG-FLJ20309_	3.8081	0.4099	1383.6	1384.535	5257.3	1	580.1	65.4	16	R.VVSHSGSAGLSQVR.V
*	HsFLAG-TCF3_Ti_1	4.0602	0.4457	1384.86	1384.535	6715.3	1	1542.2	80.8	25	R.VVSHSGSAGLSQVR.V
*	HsFlag-FLJ90652_2	3.8598	0.4232	3122.25	3122.613	6764.9	1	678.9	38.3	3	R.VVAQPSLPAVPQQSGGPAQTLPQMPAGPQIR.V
*	HsFLAG-FLJ20309_	3.2803	0.3867	1368.82	1369.706	3548.5	1	485.5	70.8	2	K.VVPQTVMATVPVK.A
*	HsFLAG-TCF3_Ti_1	3.6667	0.4434	3094.13	3095.48	8020.5	1	373	27.4	1	K.AQTTAATVQRPGPGQTGLTVTSLPATASPVSK.P
*	HsFLAG-FLJ20309_	5.5008	0.436	3096.31	3095.48	7117.1	1	757.3	25.8	3	K.AQTTAATVQRPGPGQTGLTVTSLPATASPVSK.P
*	HsFLAG-FLJ20309_	2.5443	0.1046	2064.53	2067.347	7117.1	2	303.2	35.7	1	R.PGPGQTGLTVTSLPATASPVSK.P
*	HsFlag-FLJ90652_2	4.6744	0.3726	2770.67	2770.069	7754.7	1	871.2	41.1	2	K.PATSSPGTSAPSASTAAVIQNVTGQNIIK.Q
*	HsFLAG-TCF3_Ti_1	3.2625	0.2512	2712.2	2713.109	4961.8	1	233.8	32	4	K.QVAITGQLGVKPQTGNSIPLTATNFR.I
*	Hs293Flag-Ies2_Ti_1	4.7991	0.3806	2714.44	2713.109	6676.8	1	1422.9	36	4	K.QVAITGQLGVKPQTGNSIPLTATNFR.I
*	HsFlag-FLJ90652_2	4.4432	0.4358	1617.48	1617.802	4725.6	1	810.5	75	2	K.PQTGNSIPLTATNFR.I
*	HsFLAG-TCF3_Ti_1	2.848	0.2635	1129.38	1130.283	5895.9	1	597.7	65	2	R.LPPSSITTDAK.G
*	HsFLAG-FLJ20309_	4.1198	0.3536	1510.22	1510.644	6209.6	1	1128.7	71.4	2	K.LTQDLFGTGGNTTGK.G
*	HsFlag-FLJ90652_2	4.7835	0.3756	2073.68	2074.301	8836.1	1	1443.4	55	5	K.GISATLHVTSNPVHAADSPAK.A
*	HsFLAG-TCF3_Ti_1	3.2945	0.2744	1648.99	1649.795	3648.7	3	404.6	52.9	4	K.ASSASAPSSTPTGTTVVK.V
*	HsFlag-FLJ90652_2	3.3033	0.3318	1329.29	1329.598	5056	1	915.2	79.2	1	R.LMPALGVSVADQK.G
*	HsYL1_Ti_103.1226.	3.9083	0.3419	1489.95	1489.669	4402.4	1	845.6	71.4	9	K.STVASSEAKPAATIR.I
*	HsFlag-FLJ90652_2	3.1621	0.3546	1197.78	1198.365	4551.9	1	562.3	72.7	5	K.AGQTITVATHAK.Q

*	HsFLAG-ARP5_Ti_1	3.6193	0.2441	1198.3	1198.365	5704.6	1	1187.7	81.8	14	K.AGQTITVATHAK.Q
*	HsYL1-FLAG_Ti_202	3.7159	0.3495	2115.65	2115.392	6352.2	1	733.3	50	2	K.TVAVASGAASTPISISTGAPTVR.Q
*	HsFLAG-FLJ20309_	2.4678	0.3314	1588.62	1589.786	2325.7	3	95	43.3	1	R.QVPVSTTVVSTSQAGK.L
*	HsYL1_Ti_104.1552.	4.3386	0.3852	2056.91	2057.355	5204.9	1	682.5	57.9	2	R.QVPVSTTVVSTSQAGKLPTR.I
*	HsYL1_Ti_103.2124.	2.1539	0.2615	1412.64	1413.759	7396.2	1	600.1	58.3	1	R.ITVPLSVISQPMK.G
*	HsFLAG-FLJ20309_	3.4614	0.3053	1413.64	1413.759	4437.6	1	677.5	75	2	R.ITVPLSVISQPMK.G
*	HsFLAG-ARP5_Ti_1	2.8462	0.2744	1128.25	1129.261	5623	8	523.7	68.2	1	K.GNLGANLSGLGR.N
*	HsFLAG-TCF3_Ti_1	2.7528	0.1957	1259.59	1260.535	6230.3	1	558.7	63.6	2	R.NIILTTMPAGTK.L
*	HsFlag-FLJ90652_2	2.5695	0.1281	1260.57	1260.535	9011.4	5	1007.6	63.6	1	R.NIILTTMPAGTK.L
*	HsFLAG-TCF3_Ti_1	4.9774	0.3688	3194.21	3195.649	8829.5	1	1053.9	39.3	4	K.LIAGNKPVSFLTAQQLQQLQQQGQATQVR.I
*	HsFLAG-TCF3_Ti_1	6.0555	0.3485	3196.9	3195.649	11147.7	1	2302.5	33	3	K.LIAGNKPVSFLTAQQLQQLQQQGQATQVR.I
*	HsFLAG-TCF3_Ti_1	6.0368	0.3475	2597.76	2598.922	11385.9	1	1881.5	52.3	7	K.PVSFLTAQQLQQLQQQGQATQVR.I
*	HsFLAG-TCF3_Ti_1	4.3994	0.4919	1897.81	1898.083	4312.8	1	630.9	58.3	14	R.IQTVPASHLQQGTASGSSK.A
*	HsFLAG-FLJ20309_	2.2419	0.3433	1356.63	1357.59	8111.6	4	327.8	46.2	1	K.AVSTVVVTTAPSPK.Q
*	HsFLAG-FLJ20309_	4.4655	0.289	1357.39	1357.59	6599.5	1	1301.7	73.1	4	K.AVSTVVVTTAPSPK.Q
gi|18079254|r	13	314	60.20%	133	15511	6	p53 and DNA damage-regulated protein [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	6.6793	0.4116	1849.67	1850.073	8362.1	1	3512.2	86.7	197	R.YLVEVEELAEEVLADK.R
*	HsFLAG-RPB5MP_2	4.9731	0.2275	1851.02	1850.073	9598.3	1	1981	48.3	1	R.YLVEVEELAEEVLADK.R
*	HsFLAG-p53-DNA-D	5.9224	0.4017	2005.11	2006.26	8312.3	1	2925.9	81.2	14	R.YLVEVEELAEEVLADKR.Q
*	HsFLAG-RPB5MP_2	4.4327	0.3064	2007.21	2006.26	3188.7	1	779.5	48.4	4	R.YLVEVEELAEEVLADKR.Q
*	HsFLAG-p53-DNA-D	3.2924	0.1475	1088.24	1088.249	3469.3	3	710.5	93.8	5	K.RQIVDLDTK.R
*	HsFLAG-p53-DNA-D	3.3887	0.1972	1244.66	1244.437	5175.9	1	948	83.3	2	K.RQIVDLDTKR.N
*	HsFLAG-p53-DNA-D	5.4343	0.4676	2106.85	2106.423	6462.3	1	1219.6	61.8	16	K.DLSLSEDVMVCFGNMFIK.M
*	HsFLAG-p53-DNA-D	3.035	0.2726	1500.53	1501.651	3907.2	1	349.5	59.1	2	K.EMIEKDQDHLDK.E
*	HsFLAG-p53-DNA-D	3.543	0.1137	1501.48	1501.651	10315.4	3	1192	72.7	2	K.EMIEKDQDHLDK.E
*	HsFLAG-p53-DNA-D	3.445	0.1257	1259.67	1260.476	6728.1	2	968.6	75	11	R.LFEAQGKPELK.G
*	HsFlag-NUFIP_Ti_1	3.8902	0.1457	1260.3	1260.476	6368.9	1	1618.9	85	41	R.LFEAQGKPELK.G
*	HsFLAG-p53-DNA-D	3.5101	0.2803	1501.66	1502.667	7512.8	1	536.9	54.2	1	K.GFNLNPLNQDELK.A
*	HsFLAG-p53-DNA-D	4.2756	0.2277	1502.63	1502.667	4021.3	1	913.7	83.3	18	K.GFNLNPLNQDELK.A
gi|5729877|re	43	647	60.10%	646	70898	5.5	heat shock 70kDa protein 8 isoform 1 [Homo sapiens]				
	HsFlag-FLJ90652_2	6.1368	0.2388	2264.47	2264.509	7961.4	1	1281.9	57.1	25	K.GPAVGIDLGTTYSCVGVFQHGK.V
	HsFLAG-ARP6_Ti_1	4.8475	0.294	2266.77	2264.509	3889.5	1	746.3	36.9	13	K.GPAVGIDLGTTYSCVGVFQHGK.V
	HsFlag-FLJ90652_2	3.6517	0.3726	1487.89	1488.594	3812.9	1	610.4	75	34	R.TTPSYVAFTDTER.L
	Hs293Flag-Ies2_Ti_1	3.2174	0.4318	1488.58	1488.594	3710.2	1	167.1	54.2	6	R.TTPSYVAFTDTER.L
	HsFLAG-ARP6_Ti_1	5.2019	0.4065	1650.56	1650.847	5678.5	1	1596.9	82.1	13	K.NQVAMNPTNTVFDAK.R
	HsFlag-FLJ90652_2	4.0513	0.3251	1411.44	1411.573	5518.4	1	1586.9	90.9	14	R.RFDDAVVQSDMK.H
	HsFLAG-p53-DNA-D	3.3929	0.3724	1654.52	1654.93	4523.5	1	590	65.4	15	K.HWPFMVVNDAGRPK.V
	HsFlag-NUFIP_Ti_11	4.4408	0.3172	1655.16	1654.93	5908.1	1	1389.3	53.8	8	K.HWPFMVVNDAGRPK.V
	HsYL1_Ti_103.1140.	2.546	0.195	1180.57	1181.331	4585.1	2	464.2	66.7	2	K.VQVEYKGETK.S
	HsFLAG-ARP6_Ti_1	3.2097	0.268	1181.78	1181.331	4772.1	4	814.9	83.3	12	K.VQVEYKGETK.S
	HsFlag-ZnF-HIT2_Ti_	3.7928	0.387	1617.93	1617.854	4953.5	1	1057.1	80.8	6	K.SFYPEEVSSMVLTK.M
	HsFLAG-TCF3_Ti_1	2.6624	0.1335	994.58	994.133	3857.7	1	319.8	68.8	4	K.EIAEAYLGK.T
	HsFlag-FLJ90652_2	4.3129	0.3232	1982.21	1983.188	8554.8	1	1356	44.1	3	K.TVTNAVVTVPAYFNDSQR.Q

	HsFlag-VPS71_Ti_1(	3.8212	0.2319	1983.81	1983.188	4124.5	4	391	52.9	12	K.TVTNAVVTVPAYFNDSQR.Q
	HsFLAG-Lin9_Ti_20	5.2508	0.4465	1660.49	1660.908	5331.5	1	1768.4	80	50	R.IINEPTAAAIAYGLDK.K
	HsFLAG-ARP5_Ti_1	3.8699	0.1778	1788.62	1789.082	4190.7	1	571.2	59.4	2	R.IINEPTAAAIAYGLDKK.V
	HsFLAG-TCF3_Ti_1(	2.6522	0.2646	1235.34	1236.474	6278.3	1	602.7	66.7	8	R.MVNHFIAEFK.R
	HsFLAG-TCF3_Ti_1(	3.9739	0.3248	1237.36	1236.474	8017.1	1	1623.2	88.9	27	R.MVNHFIAEFK.R
	HsFlag-NUFIP_Ti_1(	2.6943	0.3096	2999.39	2999.255	8382.7	1	292.9	25	1	R.TLSSSTQASIEIDSLYEGIDFYTSITR.A
	HsFlag-FLJ90652_2(	2.0904	0.2727	1480.7	1481.651	2330.8	4	142.3	59.1	1	R.ARFEELNADLFR.G
	HsFLAG-ARP6_Ti_1	4.2068	0.2215	1481.81	1481.651	6808.7	1	1830.4	59.1	3	R.ARFEELNADLFR.G
	HsYL1_Ti_103.1942.	4.6423	0.2622	1483.93	1481.651	4875.6	1	1115	86.4	58	R.ARFEELNADLFR.G
	HsFlag-FLJ90652_2(	3.6003	0.2919	1254.46	1254.385	7777.4	2	1585.6	88.9	3	R.FEELNADLFR.G
	HsFLAG-ARP5_Ti_1	4.479	0.2769	1838.53	1839.102	7962.7	1	1490.9	62.5	6	K.LDKSQIHDIVLVGGSTR.I
	HsFLAG-ARP6_Ti_1	4.2922	0.4754	1481.45	1482.68	4719.5	1	870.9	69.2	10	K.SQIHDIVLVGGSTR.I
	HsFLAG-Lin9_Ti_20	5.0441	0.3533	1483.74	1482.68	8431.4	1	2557.7	84.6	72	K.SQIHDIVLVGGSTR.I
	HsTIP60_Ti_105.226	2.8115	0.2224	1082.24	1082.244	4474.4	5	672.9	87.5	2	K.LLQDFFNGK.E
	HsFLAG-FLJ20729_	6.6243	0.4729	2260.41	2261.494	10653	1	2432.9	39.8	26	K.SINPDEAVAYGAAVQAAILSGDK.S
	HsFlag-NUFIP_Ti_1(	6.472	0.4678	2261.89	2261.494	8798.4	1	1804.1	56.8	148	K.SINPDEAVAYGAAVQAAILSGDK.S
	HsFlag-FLJ90652_2(	6.0047	0.467	3242.05	3240.821	10030	1	1685	30.8	3	K.SENVQDLLLLDVTPLSLGIETAGGVMTVLIK.R
	HsFlag-FLJ90652_2(	2.5343	0.1365	931.17	931.08	5013.8	4	875.8	100	1	K.RNTTIPTK.Q
	HsFLAG-ARP6_Ti_1	4.7632	0.3753	2775.1	2775.989	5899.5	1	578	43.5	4	K.QTQTFTTYSDNQPGVLIQVYEGER.A
*	HsFlag-NUFIP_Ti_11	2.9131	0.178	2515.83	2515.823	8219.3	1	560.9	34.8	1	R.GVPQIEVTFDIDANGILNVSAVDK.S
*	HsFLAG-ARP6_Ti_1	2.0968	0.1104	989.31	990.101	3569.2	7	337.3	78.6	1	R.LSKEDIER.M
*	HsYL1_Ti_103.1207.	2.8106	0.1017	990.54	990.101	4889.7	1	753.6	92.9	2	R.LSKEDIER.M
*	HsFLAG-ARP5_Ti_1	4.5401	0.2682	1982.14	1983.204	6226.5	1	1085.3	46.7	3	R.MVQEAEKYKAEDEKQR.D
*	HsFLAG-ARP5_Ti_1	4.0934	0.3341	1982.65	1983.204	7790.9	1	1091	56.7	1	R.MVQEAEKYKAEDEKQR.D
*	HsFLAG-ARP8_Ti_2	3.2683	0.2359	1303.54	1304.46	5286.2	1	413.3	65	5	K.NSLESYAFNMK.A
*	HsFlag-FLJ90652_2(	3.9575	0.3541	1304.43	1304.46	7369.1	2	1477.2	85	10	K.NSLESYAFNMK.A
*	HsFLAG-TCF3_Ti_1(	2.5191	0.1459	1304.54	1305.439	4201.9	1	290.3	66.7	1	K.CNEIINWLDK.N
*	HsFlag-FLJ90652_2(	4.0012	0.1542	1305.38	1305.439	6819.6	4	1419.3	88.9	10	K.CNEIINWLDK.N
*	HsFLAG-p53-DNA-D	4.884	0.2504	1746.59	1746.831	9904	1	1987.6	73.1	20	K.NQTAEKEEFEHQQK.E
*	HsFlag-FLJ90652_2(	3.8403	0.2562	1747.86	1746.831	5867.2	1	1288.9	53.8	1	K.NQTAEKEEFEHQQK.E
gi|5901926|re		9	36	59.50%	227	26227	8.8	cleavage and polyadenylation specific factor 5 [Homo sapiens]			
*	HsFlag-VPS71_Ti_1(	3.2132	0.0962	1490.76	1490.743	5512.3	2	1097.9	81.8	6	K.YIQQTKPLTLER.T
*	HsFLAG-p53-DNA-D	3.3439	0.2419	1748.67	1747.001	3845.4	5	269.8	50	4	R.TINLYPLTNYTFGTK.E
*	HsFLAG-Lin9_Ti_20	4.5531	0.3681	1727.58	1728.131	7843.1	1	2187.8	82.1	2	R.LPHVLLLQLGTTFFK.L
*	HsFLAG-FLJ20729_	4.8971	0.4118	1753.7	1753.904	4309.2	1	1101.2	75	11	K.LPGGELNPGEDEVEGLK.R
*	HsFLAG-Lin9_Ti_20	2.5508	0.0985	1090.32	1089.342	4844.7	1	446.6	81.2	1	K.RLMTEILGR.Q
*	HsFlag-VPS71_Ti_1(	4.3011	0.3699	2376.65	2376.556	6454.3	1	685.8	50	4	R.QDGVLQDWVIDDCIGNWWR.P
*	HsFLAG-FLJ20729_	4.5688	0.2614	2239.24	2238.594	4064.6	1	770.4	44.4	1	R.PNFEPPQYPYIPAHITKPK.E
*	HsFLAG-Lin9_Ti_20	3.6045	0.3462	3115.33	3116.627	5496.7	1	477	35.7	4	K.LVAAPLFELYDNAPGYGPIISSLPQLLSR.F
*	HsFLAG-Lin9_Ti_20	5.6914	0.4486	3118.02	3116.627	8279.6	1	2061.6	35.7	3	K.LVAAPLFELYDNAPGYGPIISSLPQLLSR.F
gi|4557343|re		21	46	59.10%	511	55366	6.9	antiquitin [Homo sapiens]			
	HsFLAG-TCF3_Ti_1(	3.3565	0.1918	1906.5	1906.069	6073.6	1	736.4	56.2	1	R.GEVITTYCPANNEPIAR.V
	HsFLAG-TCF3_Ti_1(	2.9498	0.1128	1340.5	1340.43	5708.5	2	583.2	72.7	1	R.QASVADYEETVK.K

	HsFLAG-TCF3_Ti_1	4.0738	0.3709	1474.6	1474.799	7171.1	1	1483.2	76.9	2	K.IQVLGSLVSLEMGK.I
	HsFLAG-TCF3_Ti_1	3.2581	0.2411	2683.11	2684.969	11249.5	1	757.8	37	3	K.ILVEGVGEVQEYVDICDYAVGLSR.M
	HsFLAG-TCF3_Ti_1	2.758	0.2282	1169.5	1170.412	6139.2	6	420.2	60	1	R.MIGGPILPSER.S
	HsFLAG-TCF3_Ti_1	3.5036	0.1533	1171.58	1170.412	5588.2	1	1294.9	90	2	R.MIGGPILPSER.S
	HsFLAG-TCF3_Ti_1	3.3907	0.3712	1346.25	1345.579	5735.3	1	938.7	73.1	2	K.GAPTTSLISVAVTK.I
	HsFLAG-TCF3_Ti_1	4.9525	0.4131	1451.44	1451.663	6761	1	1797.9	80.8	4	R.VNLLSFTGSTQVGK.Q
	HsFLAG-TCF3_Ti_1	2.4456	0.2649	1451.68	1451.663	5804	2	340.4	53.8	2	R.VNLLSFTGSTQVGK.Q
	HsFLAG-TCF3_Ti_1	6.0133	0.3744	3702.96	3702.199	8230.4	1	1491.9	28.5	2	R.SLLELGGNNAIIAFEDADLSLVVPSALFAAVGTAGQR.C
	HsFLAG-TCF3_Ti_1	4.147	0.3895	1708.59	1708.914	7913.3	1	1445.3	73.1	2	R.LFIHESIHDEVVNR.L
	HsFLAG-TCF3_Ti_1	4.082	0.3784	1906.93	1908.167	4233.2	1	629.4	59.4	5	R.VGNPWDPNVLYGPLHTK.Q
	HsFLAG-TCF3_Ti_1	4.9239	0.1905	1910.1	1908.167	4979.1	1	888.1	46.9	2	R.VGNPWDPNVLYGPLHTK.Q
	HsFLAG-TCF3_Ti_1	3.592	0.3662	1609.66	1608.893	8205.4	1	1025.3	60.7	2	K.QAVSMFLGAVEEAKK.E
	HsFLAG-TCF3_Ti_1	4.9047	0.4476	4060.88	4061.645	9390.5	1	803.7	22.2	2	K.VMDRPGNYVEPTIVTGLGHDASIAHTETFAPILYVFK.F
	HsFLAG-TCF3_Ti_1	4.7824	0.3366	1883.53	1884.055	7410.5	1	1612.5	75	2	K.FKNEEEVFAWNNEVK.Q
	HsFLAG-TCF3_Ti_1	5.2927	0.3629	2508.2	2507.683	4319.9	1	673.9	50	5	K.GSDCGIVNVNIPTSGAEIGGAFGGEK.H
*	HsFLAG-TCF3_Ti_1	3.0291	0.3368	1445.56	1445.491	6762.2	1	938.8	73.1	2	K.HTGGGRESGSDAWK.Q
*	HsFLAG-TCF3_Ti_1	3.1249	0.1242	1231.69	1230.329	8341.3	2	1042.1	77.8	1	R.RSTCTINYSK.D
*	HsFLAG-TCF3_Ti_1	3.8281	0.4411	2284.11	2285.568	9403.2	1	644.1	44.7	2	R.STCTINYSKDLPLAQGIKFQ.-
*	HsFLAG-TCF3_Ti_1	3.7695	0.2562	2287.43	2285.568	9653.2	1	1042.5	32.9	1	R.STCTINYSKDLPLAQGIKFQ.-
gi|7019371|re	21	376	58.50%	253	28278	5.2	TCF3 (E2A) fusion partner (in childhood Leukemia) [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	3.4634	0.292	1234.58	1234.222	6335.4	1	889.7	83.3	1	R.ERDEEEEAAR.G
*	HsFLAG-TCF3_Ti_1	2.7813	0.0935	836.52	835.982	3698.9	5	543.3	91.7	1	R.KYQALGR.R
*	HsFLAG-TCF3_Ti_1	3.9852	0.2636	1333.43	1333.41	8728.2	1	1334.6	83.3	13	R.CREIEQVNER.V
*	HsFLAG-FLJ20309_	2.7736	0.2976	1202.51	1203.251	3097.7	2	299.2	66.7	1	R.VLDSYGDDYR.A
*	HsFLAG-TCF3_Ti_1	3.7899	0.3031	1203.69	1203.251	4935.7	1	1072.4	88.9	2	R.VLDSYGDDYR.A
*	HsFLAG-TCF3_Ti_1	5.7915	0.4536	3231.55	3230.38	8248	1	1886.2	35	5	R.ASQFTIVLEDEGSQGTDAPTPGNAENEPPEK.E
*	HsFLAG-TCF3_Ti_1	5.2672	0.392	4008.64	4011.259	9087.3	1	867	23.6	12	R.ASQFTIVLEDEGSQGTDAPTPGNAENEPPEKETLSPPR.R
*	HsFLAG-ARP5_Ti_1	4.7266	0.4764	1914.27	1915.073	7448.7	1	1637.1	68.4	20	R.RTPAPPEPGSPAPGEGPSGR.K
*	HsFLAG-ARP5_Ti_1	5.3731	0.372	1915.68	1915.073	6768.6	1	1461.4	43.4	9	R.RTPAPPEPGSPAPGEGPSGR.K
*	HsFLAG-FLJ20309_	4.0473	0.4443	1758.64	1758.885	4112.2	1	652	58.3	19	R.TPAPPEPGSPAPGEGPSGR.K
*	HsFLAG-TCF3_Ti_1	3.739	0.2305	1759.16	1758.885	6391.9	2	1240.5	43.1	1	R.TPAPPEPGSPAPGEGPSGR.K
*	HsFLAG-FLJ20309_	4.3356	0.2958	1678.92	1678.972	5303.1	1	830.6	60	9	R.RAGNALTPELAPVQIK.V
*	HsFLAG-TCF3_Ti_1	5.7557	0.2586	3948.86	3949.323	11940.7	1	1166.7	23.6	15	R.RAGNALTPELAPVQIKVEEDFGFEADEALDSSWVSR.G
*	HsFLAG-TCF3_Ti_1	2.5248	0.3432	1521.68	1522.785	7629.8	1	536.8	50	2	R.AGNALTPELAPVQIK.V
*	HsFLAG-TCF3_Ti_1	3.9043	0.307	1523.82	1522.785	4342.7	1	619.4	64.3	20	R.AGNALTPELAPVQIK.V
*	HsFLAG-TCF3_Ti_1	6.3445	0.3936	3794.32	3793.135	4377.8	1	545.8	26.5	66	R.AGNALTPELAPVQIKVEEDFGFEADEALDSSWVSR.G
*	HsFLAG-TCF3_Ti_1	6.1006	0.5228	2290.02	2289.373	9886.9	1	2609.9	65.8	156	K.VEEDFGFEADEALDSSWVSR.G
*	HsFLAG-TCF3_Ti_1	5.3355	0.4539	2290.45	2289.373	11223.2	1	2461.5	43.4	17	K.VEEDFGFEADEALDSSWVSR.G
*	HsFLAG-TCF3_Ti_1	3.2538	0.3062	2686.67	2686.805	8409.9	1	400.5	32.6	3	K.VEEDFGFEADEALDSSWVSRGPDK.L
*	HsFLAG-TCF3_Ti_1	4.4127	0.3364	2686.93	2686.805	5377.2	1	654.9	33.7	1	K.VEEDFGFEADEALDSSWVSRGPDK.L
*	HsFLAG-TCF3_Ti_1	4.0266	0.3099	1347.42	1345.535	5406.4	1	1174.6	79.2	3	K.LLPYPTLASPASD.-
gi|29788768|r	27	622	58.00%	445	49953	4.9	tubulin, beta polypeptide paralog [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	4.2213	0.2479	1617.4	1616.87	4265.9	1	1041.3	78.6	14	R.AILVDLEPGTMDSVR.S

	HsFLAG-ARP6_Ti_1	5.3305	0.4496	2798.59	2800.065	6948.6	1	1444.6	52	59	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-ARP6_Ti_1	7.0292	0.3487	2802.51	2800.065	7956.6	1	2098.3	39	59	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G
	HsFLAG-TCF3_Ti_1(	7.1819	0.4728	1959.62	1960.151	9139.8	1	3610.1	82.4	73	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-ARP6_Ti_1	4.9251	0.2887	1959.94	1960.151	7005.8	1	1288.7	41.2	34	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-TIP49b_Ti_	5.684	0.3213	2087.63	2088.325	8116.7	1	2259	51.4	39	K.GHYTEGAELVDSVLDVVRK.E
	HsSrcap_Ti_206.286	6.4593	0.361	2087.84	2088.325	9352.8	1	2739.4	72.2	25	K.GHYTEGAELVDSVLDVVRK.E
	HsYL1_Ti_103.1035.	2.9392	0.1782	1078.13	1078.17	3062.5	4	568.7	85.7	4	K.IREEYPDR.I
	HsFLAG-ARP6_Ti_1	4.2407	0.3299	1352.9	1352.65	7307.1	1	1886.4	90.9	4	R.IMNTFSVMPSPK.V
	HsFLAG-ARP6_Ti_1	6.4706	0.4855	4594.76	4595.903	4988.3	1	541.4	23.7	83	K.VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR.T
	HsFLAG-ARP6_Ti_1	4.7805	0.3574	2709.73	2710.041	10385.7	1	1165	31.2	30	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsFLAG-ARP6_Ti_1	5.4731	0.383	2710.22	2710.041	8352.5	1	1412.5	47.9	39	K.LTTPTYGDLNHLVSATMSGVTTCLR.F
	HsFLAG-ARP6_Ti_1	2.1817	0.2119	1130.19	1131.277	3484.6	1	331.1	72.2	1	R.FPGQLNADLR.K
	HsFLAG-ARP6_Ti_1	3.1035	0.1934	1133.31	1131.277	4537.1	1	968.3	94.4	20	R.FPGQLNADLR.K
	HsFLAG-ARP6_Ti_1	2.7216	0.2275	1259.45	1259.451	6377.3	1	1130.1	85	3	R.FPGQLNADLRK.L
	Hs293Flag-Ies2_Ti_1	4.1115	0.2404	1271.88	1272.594	7432.2	1	1437.4	85	9	R.KLAVNMVPFPR.L
	HsFLAG-Lin9_Ti_202	3.7432	0.2947	1144.31	1144.42	4934.2	1	1119.4	94.4	37	K.LAVNMVPFPR.L
	HsFLAG-ARP6_Ti_1	3.784	0.2563	1621.62	1621.94	4747.2	1	1118	76.9	9	R.LHFFMPGFAPLTSR.G
	HsFLAG-TCF3_Ti_1(	3.8701	0.3677	1709.52	1708.967	3488.3	1	695.7	75	2	R.ALTVPELTQQMFDSK.N
	HsFLAG-ARP6_Ti_1	3.1514	0.3044	1065.99	1066.201	5998.7	1	1325.1	87.5	4	K.NMMAACDPR.H
	HsFLAG-ARP6_Ti_1	3.1252	0.3693	1054.29	1054.277	4338.1	1	916.8	93.8	2	R.YLTVAAIFR.G
	Hs293Flag-Ies2_Ti_1	4.5214	0.2599	1447.29	1447.603	7900.2	2	1960.1	86.4	10	K.EVDEQMLNVQNK.N
	HsScrap_Ti_102.174	3.2133	0.1712	1447.35	1447.603	3682	1	435.8	72.7	4	K.EVDEQMLNVQNK.N
	HsFLAG-ARP6_Ti_1	4.0978	0.3327	1699.12	1697.888	5299.1	1	715	61.5	39	K.NSSYFVEWIPNNVK.T
	HsFLAG-TCF3_Ti_1(	2.8997	0.2395	1029.45	1029.147	6481.9	1	1559.4	93.8	2	K.TAVCDIPPR.G
	HsFLAG-ARP6_Ti_1	4.1879	0.3996	1386.16	1386.612	7897.9	1	1417.6	85	10	K.RISEQFTAMFR.R
	HsFLAG-ARP6_Ti_1	3.7061	0.3498	1229.27	1230.424	8240.8	1	1542.7	88.9	7	R.ISEQFTAMFR.R
gi|13775202|r	17	108	58.00%	343	37218	9.4	high mobility group AT-hook 1-like 4 [Homo sapiens]				
*	Hs293Flag-Ies2_Ti_1	4.572	0.3997	2196.68	2196.384	9970.9	1	1536.2	57.9	24	K.HHQEEDAGPTQPSPAKPQLK.L
*	HsFLAG-ARP8_Ti_2	5.5666	0.3423	2196.68	2196.384	6746.2	1	1200.9	43.4	13	K.HHQEEDAGPTQPSPAKPQLK.L
*	Hs293Flag-Ies2_Ti_1	2.1007	0.0817	872.38	873.04	4532.6	1	318.4	68.8	1	K.LGGQVLGTK.S
*	HsFlag-FLJ90652_2!	3.4624	0.1566	873.15	873.04	5001.7	2	985	87.5	4	K.LGGQVLGTK.S
*	Hs293Flag-Ies2_Ti_1	4.243	0.4846	2745.94	2747.064	7675.8	1	1157.5	47.8	2	R.SPSPLMVVDNEEEPMEGVPLEQYR.A
*	Hs293Flag-Ies2_Ti_1	4.1299	0.2103	1700.63	1700.845	7323	1	1694.4	78.6	7	R.AWLDEDSNLSPSPLR.D
*	Hs293Flag-Ies2_Ti_1	5.2296	0.4059	1733.32	1733.743	9574.5	1	2371.4	76.7	17	R.DLSGGLGGQEEEEEQR.W
*	HsFLAG-ARP5_Ti_1	5.1758	0.4056	2059.38	2060.268	9693.8	1	1858.9	64.7	6	R.WLDALEKGELDDNGDLKK.E
*	HsFLAG-ARP5_Ti_1	4.8154	0.2184	2060.2	2060.268	5579.2	1	726.9	41.2	3	R.WLDALEKGELDDNGDLKK.E
*	HsFLAG-FLJ20309_	3.387	0.1759	1204.34	1204.279	8751	1	1514.8	85	7	K.GELDDNGDLKK.E
*	HsFlag-FLJ90652_2!	3.8321	0.3315	2904.86	2904.416	6614	1	832.5	42.3	4	R.SQPSPMLPLPVAEGCPPPALTEEMLLK.R
*	HsFLAG-ARP5_Ti_1	3.8764	0.3858	3410.25	3409.749	6484.5	1	878	27.3	1	R.YCSGAQGSTLSFPPGVPAPTAVSQRPSPSGPPPR.C
*	HsFLAG-FLJ20309_	1.9778	0.0929	1166.62	1167.242	4337.9	5	235.3	61.1	1	R.CSVPGCPHPR.R
*	Hs293Flag-Ies2_Ti_1	3.2103	0.1835	1167.3	1167.242	3449	6	477.4	77.8	6	R.CSVPGCPHPR.R
*	Hs293Flag-Ies2_Ti_1	2.9053	0.2227	1456.24	1457.559	3081.4	2	125.9	54.5	2	R.TGQALCSLQCYR.I
*	Hs293Flag-Ies2_Ti_1	4.1214	0.236	1457.05	1457.559	7626.5	1	1447.6	77.3	1	R.TGQALCSLQCYR.I

*	Hs293Flag-Ies2_Ti_1	2.8237	0.2971	1266.41	1266.437	6317.3	1	462.3	46.2	9	R.LGGPEGPGSPLLAT.-
gi|36287069|r	26	129	57.50%	546	61798	8.6	HIV-1 Tat interactive protein, 60kDa isoform 1 [Homo sapiens]				
*	HsH2AZ-FLAG_293_	5.1271	0.2402	2449.24	2447.72	8155.3	1	1782.9	38	5	R.ARGPPVADPGVALSPQGEIIEGCR.L
*	HsYL1-FLAG_Ti_203	3.8472	0.3345	2220.87	2220.453	6116.7	1	723.7	47.6	1	R.GPPVADPGVALSPQGEIIEGCR.L
	HsFLAG-TIP49b_Ti_	4.0613	0.2809	2157.52	2157.345	6935.8	1	1343.2	61.8	8	R.RNQDNEDEWPLAEILSVK.D
	HsFLAG-TIP49a_Ti_	5.9002	0.39	2002.07	2001.157	4146.4	1	1108.3	75	25	R.NQDNEDEWPLAEILSVK.D
	HsFLAG-TIP49b_Ti_	3.931	0.2443	1459.19	1459.687	7907.7	1	1982.1	85	9	K.LFYVHYIDFNK.R
	HsMRGBP-FLAG_Ti_	3.6649	0.2151	1342.17	1341.469	7315.5	5	1058.4	77.8	8	K.RLDEWVTHER.L
	HsMRGBP-FLAG_Ti_	4.1964	0.4581	2762.29	2762.919	8168.9	1	636.6	29.2	1	K.EREAIPGGEPDQPLSSSSCLQPNHR.S
	HsMRGBP-FLAG_Ti_	2.7358	0.1335	2964.16	2964.351	8125.2	3	239.8	25	1	K.RKVEVVSPATPVPSETAPASVFPQNGAAR.R
	HsMRGBP-FLAG_Ti_	4.8721	0.2082	2964.31	2964.351	5782.1	1	938.8	33	6	K.RKVEVVSPATPVPSETAPASVFPQNGAAR.R
	HsFLAG-TIP49b_Ti_	4.4035	0.5383	2806.95	2808.164	5689.3	1	846.6	46.3	2	R.KVEVVSPATPVPSETAPASVFPQNGAAR.R
	HsMRGBP-FLAG_Ti_	4.4889	0.4004	2808.88	2808.164	7299	2	529.5	26.9	2	R.KVEVVSPATPVPSETAPASVFPQNGAAR.R
	HsMRGBP-FLAG_Ti_	5.2622	0.4905	2309.84	2309.285	4808	1	697.7	54.8	5	K.SNCLGTDEDSQDSSDGIPSAPR.M
	HsTIP60_Ti_103.173	3.4038	0.1375	1104.19	1104.215	4889.7	1	1005	87.5	2	K.NIECIELGR.H
	HsMRGBP-FLAG_Ti_	4.31	0.3745	3164.78	3166.616	4332.8	1	428.6	39.6	3	K.PWYFSPYPQELTTLPVLYLCEFCLK.Y
	HsFLAG-TIP49b_Ti_	2.2903	0.2	1082.46	1083.192	4368.2	1	328.9	68.8	2	R.HPPGNEIYR.K
	HsYL1_Ti_104.1972.	4.1175	0.3944	1370.97	1370.548	5278.6	1	1020.5	77.3	1	R.KGTISFFEIDGR.K
	HsTIP60_Ti_106.267	3.8881	0.4063	1241.66	1242.374	6385	1	1105.6	80	1	K.GTISFFEIDGR.K
	HsMRGBP-FLAG_Ti_	3.3832	0.2357	1298.1	1297.46	6746.3	1	1070.4	80	3	K.SYSQNLCLLAK.C
	HsFLAG-TIP49b_Ti_	2.7789	0.2234	1154.44	1155.342	6289.7	1	805.7	72.2	2	K.GFHIVGYFSK.E
	HsH2AZ-FLAG_293_	3.7784	0.3531	2270.61	2270.467	4716.2	2	474.2	52.8	3	K.ESTEDYNVACILTLPPYQR.R
	HsMRGBP-FLAG_Ti_	3.903	0.3855	1848.89	1848.106	3367.8	1	697.9	65.6	10	K.TGTPEKPLSDLGLLSYR.S
	HsMRGBP-FLAG_Ti_	4.5772	0.3751	2332.09	2332.57	8518.1	1	689.7	42.5	5	K.SESGERPQITINEISEITSIK.K
	HsFLAG-TIP49b_Ti_	6.2028	0.3682	2219.45	2218.555	7082.8	1	2777.8	79.4	9	K.KEDVISTLQYLNLINYYK.G
	HsH2AZ-FLAG_293_	3.453	0.3001	2090.21	2090.381	8527.1	1	900.2	53.1	5	K.EDVISTLQYLNLINYYK.G
	HsMRGBP-FLAG_Ti_	4.6615	0.4477	1947.48	1946.124	5764	1	1125.5	68.8	9	K.GQYILTLSEDIVDGHER.A
	HsFLAG-TIP49b_Ti_	1.8752	0.2315	902.31	903.035	4604.6	5	312	66.7	1	K.CLHFTPK.D
gi|41152056|r	51	265	57.30%	972	109478	5	U5 snRNP-specific protein, 116 kD [Homo sapiens]				
*	HsFlag-ZnF-HIT2_Ti_	6.0183	0.4027	3667.97	3669.618	9118.9	1	1536.2	29.8	4	K.DLDEMDDDDDDDVGDHDDDHPGMEVVLHEDK.K
*	HsFlag-ZnF-HIT2_Ti_	4.9853	0.3828	3710.71	3711.111	7469.2	1	1204.2	29.8	4	K.KYYPTAEEVYGPEVETIVQEEDTQPLTEPIIK.P
*	HsFlag-ZnF-HIT2_Ti_	7.8508	0.5141	4035.77	4035.534	8731.1	1	1827.4	32.4	11	K.KYYPTAEEVYGPEVETIVQEEDTQPLTEPIIKPVK.T
*	HsFlag-ZnF-HIT2_Ti_	3.9217	0.3451	3905.36	3907.36	5873.4	1	444.1	22	2	K.YYPTAEEVYGPEVETIVQEEDTQPLTEPIIKPVK.T
*	HsFlag-ZnF-HIT2_Ti_	4.3993	0.3634	2018.71	2019.194	8296.5	1	1304.4	66.7	9	K.TCFVDCLIEQTHPEIR.K
*	HsFlag-ZnF-HIT2_Ti_	3.9045	0.3616	2018.75	2019.194	4005.4	1	830.3	50	1	K.TCFVDCLIEQTHPEIR.K
*	HsFlag-ZnF-HIT2_Ti_	5.1535	0.3633	2366.88	2366.512	6617.2	1	1672.1	70.6	9	K.RYDQDLCYTDILFTEQER.G
*	HsFlag-ZnF-HIT2_Ti_	5.454	0.3042	2368.84	2366.512	8388.2	1	1741.1	45.6	6	K.RYDQDLCYTDILFTEQER.G
*	HsFlag-ZnF-HIT2_Ti_	2.504	0.1439	1256.63	1257.47	9355.7	1	643.3	59.1	1	K.STPVTVVLPDTK.G
*	HsFlag-ZnF-HIT2_Ti_	6.0262	0.5047	2683.37	2684.983	6179.5	1	832.9	45.7	2	K.SYLFNIMDTPGHVNFSDEVTAGLR.I
*	HsFlag-ZnF-HIT2_Ti_	4.1033	0.3895	2684.95	2684.983	7434.9	1	1260	35.9	1	K.SYLFNIMDTPGHVNFSDEVTAGLR.I
*	HsFlag-ZnF-HIT2_Ti_	6.6237	0.4057	2250.06	2250.572	9004.8	1	1771.9	41.2	4	R.ISDGVVLFIDAAEGVMLNTER.L
*	HsFlag-ZnF-HIT2_Ti_	5.7383	0.5188	2250.9	2250.572	11187.9	1	2354.4	60	10	R.ISDGVVLFIDAAEGVMLNTER.L
*	HsFlag-ZnF-HIT2_Ti_	2.0106	0.1862	1017.71	1018.208	8547.8	4	633.8	68.8	1	R.LAVTVCINK.I

*	HsFlag-ZnF-HIT2_Ti_	5.8906	0.4936	1895.93	1896.063	5458.4	1	1765.3	80	2	K.IYADTFGDINYQEFAK.R
*	HsFlag-ZnF-HIT2_Ti_	3.7425	0.1965	1408.8	1409.63	5084.4	1	918.6	80	4	K.RLWGDIYFNPK.T
*	HsFlag-ZnF-HIT2_Ti_	3.3667	0.213	1485.58	1485.763	6359.9	3	683.4	63.6	4	R.SFVEFILEPLYK.I
*	HsFlag-ZnF-HIT2_Ti_	4.4383	0.2638	1486.58	1485.763	6960.2	1	1682.2	86.4	24	R.SFVEFILEPLYK.I
*	HsFlag-ZnF-HIT2_Ti_	5.5231	0.4644	1583.73	1583.825	6572.6	1	1709.3	78.6	2	K.ILAQVVGDVDTSLPR.T
*	HsFlag-ZnF-HIT2_Ti_	4.0292	0.326	1240.47	1240.442	6324.7	1	1394.8	85	3	R.TLDELGIHLTK.E
*	HsFlag-ZnF-HIT2_Ti_	4.6784	0.4257	1739.13	1740.007	8431.9	1	2011.5	78.6	5	R.TLDELGIHLTKEELK.L
*	HsFlag-ZnF-HIT2_Ti_	4.5925	0.4374	1731.01	1731.88	6923.2	1	1371.2	71.4	4	K.MYSTDDGVQFHAFGR.V
*	HsFlag-ZnF-HIT2_Ti_	2.7558	0.2758	1306.7	1307.536	4617.1	1	551.2	58.3	6	R.VLSGTIHAGQPVK.V
*	HsFlag-ZnF-HIT2_Ti_	4.0089	0.3284	1307.38	1307.536	7682.6	1	1363	75	14	R.VLSGTIHAGQPVK.V
*	HsFlag-ZnF-HIT2_Ti_	5.4798	0.3363	2429.98	2428.535	8838.3	1	1924.8	60	2	K.VLGENYTLEDEEDSQICTVGR.L
*	HsFlag-ZnF-HIT2_Ti_	5.2382	0.2818	2846.34	2847.29	7780.9	1	1421.1	50	1	R.YHIEVNRVPAGNWVLIEGVDQPIVK.T
*	HsFlag-ZnF-HIT2_Ti_	6.7659	0.3992	2846.91	2847.29	9298.4	1	2504.8	40.6	2	R.YHIEVNRVPAGNWVLIEGVDQPIVK.T
*	HsFlag-ZnF-HIT2_Ti_	5.3051	0.4351	1934.49	1935.274	8651.3	1	1994.5	70.6	3	R.VPAGNWVLIEGVDQPIVK.T
*	HsFlag-ZnF-HIT2_Ti_	3.6474	0.2017	1402.42	1402.593	7338.1	1	1258.6	77.3	4	R.GNEEAQIFRPLK.F
*	HsFlag-ZnF-HIT2_Ti_	3.3819	0.2708	1393.49	1393.623	3890.8	3	574.4	70.8	3	K.IAVEPVNPSELPK.M
*	HsFlag-ZnF-HIT2_Ti_	5.9214	0.3127	3749.46	3751.166	10323.4	1	1543.4	28.9	1	K.SYPSLTTKVEESGEHVILGTGELYLDCVMHDLR.K
*	HsFlag-ZnF-HIT2_Ti_	5.1652	0.4633	2873.02	2873.173	9286	1	2284.6	39.6	2	K.VEESGEHVILGTGELYLDCVMHDLR.K
*	HsFlag-ZnF-HIT2_Ti_	6.5275	0.4103	3000.89	3001.347	9989.3	1	1850.5	36	4	K.VEESGEHVILGTGELYLDCVMHDLRK.M
*	HsFlag-ZnF-HIT2_Ti_	3.5341	0.4275	2081.7	2082.322	5652.9	1	676.6	50	3	K.VADPVVTFCETVVETSSLK.C
*	HsFlag-ZnF-HIT2_Ti_	2.1648	0.1829	967.54	967.033	3289.7	1	260.6	78.6	1	K.CFAETPNK.K
*	HsFlag-ZnF-HIT2_Ti_	1.8358	0.1216	1094.5	1095.207	2876.2	3	139.9	62.5	1	K.CFAETPNKK.N
*	HsFlag-ZnF-HIT2_Ti_	2.681	0.243	1096.88	1095.207	6324.7	1	673.1	75	1	K.CFAETPNKK.N
*	HsFlag-ZnF-HIT2_Ti_	2.9652	0.2543	1144.59	1145.4	4915.4	1	590.8	72.2	2	K.ITMIAEPLEK.G
*	HsFlag-ZnF-HIT2_Ti_	3.9498	0.1413	1986.91	1987.177	8676.3	1	1266.2	42.2	2	K.GLAEDIENEVVQITWNR.K
*	HsFlag-ZnF-HIT2_Ti_	5.0191	0.281	1987.73	1987.177	8510.2	1	1586.8	65.6	18	K.GLAEDIENEVVQITWNR.K
*	HsFlag-ZnF-HIT2_Ti_	2.8654	0.0997	1098.34	1098.287	4516	3	794.8	87.5	2	K.KLGEFFQTK.Y
*	HsFlag-ZnF-HIT2_Ti_	4.3367	0.1799	2759.05	2759.042	6779	1	671.2	40	9	R.SIWAFGPDATGPNILVDDTLPSEVDK.A
*	HsFlag-ZnF-HIT2_Ti_	4.4637	0.4222	1394.51	1394.53	6425.7	1	1417.8	81.8	3	K.DSIVQGFQWGTR.E
*	HsFlag-ZnF-HIT2_Ti_	2.5653	0.2086	1460.87	1461.704	3550	9	209.1	45.8	1	K.ILDAVVAQEPLHR.G
*	HsFlag-ZnF-HIT2_Ti_	4.0873	0.3856	1461.57	1461.704	6991.8	1	1435.9	79.2	14	K.ILDAVVAQEPLHR.G
*	HsFlag-ZnF-HIT2_Ti_	4.1197	0.2457	2994.01	2993.41	5112.8	1	420.4	36	2	R.LMEPYYFVEVQAPADCVSAVYTVLAR.R
*	HsFlag-ZnF-HIT2_Ti_	4.6168	0.4262	2050.72	2051.353	5207.4	1	747.6	61.1	5	R.RGHVTQDAPIPGSPLYTIK.A
*	HsFlag-ZnF-HIT2_Ti_	4.2365	0.241	2051.43	2051.353	5323.8	1	1178.4	47.2	1	R.RGHVTQDAPIPGSPLYTIK.A
*	HsFlag-ZnF-HIT2_Ti_	5.4344	0.3348	1894.64	1895.166	5326.2	1	2128	82.4	22	R.GHVTQDAPIPGSPLYTIK.A
*	HsFlag-ZnF-HIT2_Ti_	4.4254	0.4208	1800.88	1800.021	5182.6	1	982.6	70	20	K.AFIPAIDSFGFETDLR.T
*	HsFLAG-p53-DNA-D	3.5175	0.2766	1439.3	1439.709	6093.8	1	1215.3	81.8	3	K.FFDDPMLLELAK.Q
gi|11036646|r	10	142	57.10%	126	13944	10.4	H2B histone family, member S [Homo sapiens]				
gi|18105048|r	10	142	57.10%	126	13890	10.3	H2B histone family, member T [Homo sapiens]				
	HsH2AZ-FLAG_293_	2.9916	0.2187	1265.44	1266.436	4983.9	1	594.3	66.7	15	R.KESYSVYVYK.V
	HsFLAG-p53-DNA-D	3.6871	0.2815	1266.22	1266.436	5282.1	1	943	83.3	19	R.KESYSVYVYK.V
	HsFLAG-p53-DNA-D	2.1092	0.1853	1137.53	1138.262	5401.3	4	300.5	68.8	3	K.ESYSVYVYK.V
	HsYL1_Ti_106.1903.	2.8877	0.1799	1509.99	1509.746	5149.6	1	638.4	53.8	1	K.VLKQVHPDTGISSK.A

	HsFLAG-ARP8_Ti_2	2.2788	0.2719	1169.93	1169.28	2245.9	4	158.6	65	2	K.QVHPDTGISSK.A
	HsFLAG-ARP8_Ti_2	2.763	0.201	1171.27	1169.28	4157.9	1	655.4	80	1	K.QVHPDTGISSK.A
	HsFlag-VPS71_Ti_1	5.3194	0.4845	1744.79	1745.021	7989.3	1	1617.2	75	97	K.AMGIMNSFVNDIFER.I
	HsYL1_Ti_104.2355.	3.3611	0.173	1752.76	1752.107	3644.4	1	813.1	73.3	1	R.EIQTAVRLLLPGELAK.H
	HsYL1_Ti_106.2215.	3.3096	0.3494	1763.68	1764.075	4726.2	1	785	65.6	2	R.LLLPGELAKHAVSEGTK.A
	HsYL1_Ti_106.1936.	2.8482	0.4352	1779.64	1779.003	6772.3	1	611.5	53.1	1	K.HAVSEGTKAVTKYTSAK.-
gi|20336754|r	9	116	57.10%	126	13904	10.3	H2B histone family, member R [Homo sapiens]				
	HsYL1_Ti_104.1550.	2.8197	0.2773	1279.58	1280.463	4592	1	597.6	66.7	8	R.KESYSIYVYK.V
	HsFLAG-p53-DNA-D	3.5477	0.291	1280.44	1280.463	5752.7	1	1177.4	88.9	3	R.KESYSIYVYK.V
	HsYL1_Ti_106.1903.	2.8877	0.1799	1509.99	1509.746	5149.6	1	638.4	53.8	1	K.VLKQVHPDTGISSK.A
	HsFLAG-ARP8_Ti_2	2.2788	0.2719	1169.93	1169.28	2245.9	4	158.6	65	2	K.QVHPDTGISSK.A
	HsFLAG-ARP8_Ti_2	2.763	0.201	1171.27	1169.28	4157.9	1	655.4	80	1	K.QVHPDTGISSK.A
	HsFlag-VPS71_Ti_1	5.3194	0.4845	1744.79	1745.021	7989.3	1	1617.2	75	97	K.AMGIMNSFVNDIFER.I
	HsYL1_Ti_104.2355.	3.3611	0.173	1752.76	1752.107	3644.4	1	813.1	73.3	1	R.EIQTAVRLLLPGELAK.H
	HsYL1_Ti_106.2215.	3.3096	0.3494	1763.68	1764.075	4726.2	1	785	65.6	2	R.LLLPGELAKHAVSEGTK.A
	HsYL1_Ti_106.1936.	2.8482	0.4352	1779.64	1779.003	6772.3	1	611.5	53.1	1	K.HAVSEGTKAVTKYTSAK.-
gi|4506693|re	8	123	57.00%	135	15550	9.8	ribosomal protein S17 [Homo sapiens]				
	HsFlag-NUFIP_Ti_1	3.4626	0.1594	1047.49	1046.128	8531.8	3	1166.9	87.5	7	R.LGNDFHTNK.R
*	HsFlag-NUFIP_Ti_1	3.4712	0.1998	1415.71	1415.639	3337.3	7	534.5	77.3	2	K.RVCEEIAIIPSK.K
*	HsFlag-NUFIP_Ti_1	3.4456	0.0902	1543.59	1543.813	3666.5	5	517.5	66.7	3	K.RVCEEIAIIPSKK.L
	HsFlag-NUFIP_Ti_11	2.052	0.0995	1132.49	1133.394	5080.7	8	508.8	66.7	1	K.IAGYVTHLMK.R
	HsFlag-NUFIP_Ti_1	3.3813	0.2869	1133.44	1133.394	6665.6	1	1229.4	88.9	14	K.IAGYVTHLMK.R
	HsFlag-NUFIP_Ti_1	4.3814	0.3551	2646.69	2646.868	7985.9	1	767.2	45.5	8	R.RDNYVPEVSALDQEIIEVDPDTK.E
	HsFlag-NUFIP_Ti_1	5.5254	0.383	2489.85	2490.68	6238.8	1	1233.3	57.1	57	R.DNYVPEVSALDQEIIEVDPDTK.E
	HsFlag-NUFIP_Ti_1	5.2327	0.4244	2410.33	2410.791	6750	1	1117.6	54.8	31	K.LLDFGSLSNLQVTQPTVGMNFK.T
gi|58761486|r	28	109	56.80%	544	60463	6.5	chaperonin containing TCP1, subunit 3 isoform b [Homo sapiens]				
gi|63162572|r	28	109	56.70%	545	60534	6.5	chaperonin containing TCP1, subunit 3 isoform a [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	5.5292	0.4272	2132.07	2132.559	6925.4	1	2173.6	71.1	4	K.MLLDPMGGIVMTNDGNAILR.E
	HsFLAG-ARP6_Ti_1	3.0068	0.092	1120.35	1121.282	5851.1	2	742.5	83.3	6	R.EIQVQHPAAK.S
	HsFLAG-p53-DNA-D	3.0572	0.1797	1120.48	1121.282	4764.2	1	512.5	72.2	7	R.EIQVQHPAAK.S
	HsFLAG-ARP5_Ti_1	4.1173	0.2849	1362.93	1363.656	9133.6	1	1806.6	81.8	3	R.KALDDMISTLKK.I
	HsFLAG-ARP6_Ti_1	1.8829	0.0945	1106.26	1107.307	8193.8	1	517.6	61.1	1	K.ALDDMISTLK.K
	HsFLAG-ARP6_Ti_1	3.5108	0.2162	2737.33	2737.196	9500.1	1	968	29.2	1	K.KISIPVDISDSDMMLNIINSSITTK.A
	HsFLAG-ARP6_Ti_1	2.861	0.3269	2608.08	2609.022	7599.6	1	473.1	37	1	K.ISIPVDISDSDMMLNIINSSITTK.A
	HsFLAG-ARP6_Ti_1	4.8274	0.3265	1548.68	1548.745	6054.4	1	1797.2	84.6	4	R.WSSLACNIALDAVK.M
	HsFLAG-ARP6_Ti_1	2.8361	0.085	1237.68	1238.404	7126.4	3	1253.8	83.3	1	K.MVQFEENGRK.E
	HsFLAG-ARP6_Ti_1	4.0507	0.2486	1430.82	1429.623	6396.9	1	1700.8	87.5	4	K.IPGGIIEDSCVLR.G
	HsFLAG-ARP6_Ti_1	2.1911	0.09	1279.22	1280.504	7034.7	1	798.1	65	1	R.IVLLDSSLEYK.K
	HsFLAG-ARP6_Ti_1	3.4373	0.2031	1280.17	1280.504	4311.4	2	996.9	80	4	R.IVLLDSSLEYK.K
	HsFLAG-ARP5_Ti_1	2.7195	0.1848	2154.32	2155.283	6478.4	1	376.1	44.1	1	K.KGESQTDIEITREEDFTR.I
	HsFLAG-ARP5_Ti_1	5.7198	0.4228	3418.4	3419.919	10536.5	1	1523.9	30.6	5	R.ILQMEEEYIQQLCEDIIQLKPDVVITEK.G
	HsFLAG-ARP6_Ti_1	4.1627	0.3574	1404.25	1404.627	7147.8	1	1539.3	81.8	10	K.GISDLAQHYLMR.A
	HsFLAG-ARP6_Ti_1	4.0942	0.2996	2497.79	2497.808	6695.8	1	354.7	36.4	3	R.IVSRPEELREDDVGTGAGLLEIK.K

	HsFLAG-ARP5_Ti_1	4.9631	0.3494	2497.95	2497.808	5122.2	1	847.6	36.4	7	R.IVSRPEELREDDVGTGAGLLEIK.K
	HsFLAG-ARP6_Ti_1	5.1371	0.4526	1738.21	1737.913	6394.6	1	1921.2	84.6	15	K.KIGDEYFTFITDCK.D
	HsFLAG-ARP6_Ti_1	2.1714	0.1041	974.53	975.087	2572.9	5	190.7	78.6	1	K.EILSEVER.N
	HsFLAG-ARP5_Ti_1	3.5163	0.1969	2619.85	2619.008	6146.5	5	597.9	27	1	R.NVLLDPQLVPGGGASEMAVAHALTEK.S
	HsFLAG-ARP6_Ti_1	3.592	0.3418	1339.76	1338.524	7991.8	1	1254	80	4	K.AMTGVEQWPYR.A
	HsFLAG-ARP6_Ti_1	4.3318	0.3091	1168.29	1167.394	6408.7	2	1690.9	90	5	R.AVAQALEVIPR.T
	HsFLAG-ARP6_Ti_1	3.479	0.2957	1334.08	1334.481	7277.1	1	1601.1	86.4	2	R.TLIQNCGASTIR.L
	HsFLAG-ARP6_Ti_1	3.4608	0.2446	1255.6	1255.5	3427	2	739.9	85	2	K.ELGIWEPLAVK.L
	HsFLAG-ARP6_Ti_1	2.1967	0.1012	1185.67	1186.437	3759.1	1	351.4	70	1	K.TAVETAVLLLR.I
	HsFLAG-ARP6_Ti_1	4.4816	0.2995	1186.47	1186.437	7872	1	2535.5	95	12	K.TAVETAVLLLR.I
	HsFLAG-ARP6_Ti_1	2.0616	0.2394	983.34	984.097	4823.8	1	530.6	75	2	R.IDDIVSGHK.K
	HsFLAG-ARP5_Ti_1	2.8124	0.1249	1112.15	1112.271	6570.4	5	770.6	77.8	1	R.IDDIVSGHKK.K
gi|5730065|re	14	58	56.70%	247	28152	6	spindlin [Homo sapiens]				
*	HsFlag-FLJ20643_Ti	2.8941	0.3002	1327.39	1326.495	3889.8	1	418.1	62.5	4	R.SSVGPSKPVSQPR.R
*	HsFLAG-p53-DNA-D	4.4782	0.3632	1856.4	1857.2	3704.2	1	718	68.8	12	K.GTVLDQVPVNPSLYLIK.Y
*	HsFLAG-FLJ20729_	4.4059	0.3221	1856.92	1857.2	6652.5	1	1685.8	51.6	1	K.GTVLDQVPVNPSLYLIK.Y
*	HsFLAG-FLJ20729_	5.258	0.495	1693.27	1693.816	6606.5	1	2370.4	92.3	5	K.YDGFDCVYGLELNK.D
*	HsFLAG-FLJ20729_	4.694	0.3536	1373.36	1372.579	8526.5	1	1942.9	79.2	3	R.ISDAHLADTMIGK.A
*	HsFLAG-ARP5_Ti_1	4.7692	0.4268	2066.61	2067.194	8449.8	1	1477.7	65.6	2	K.AVEHMFETEDGSKDEWR.G
*	HsFLAG-FLJ20729_	4.2206	0.0812	1763.17	1764.049	8190.2	1	955.1	61.5	1	R.APVMNTWFYITYEK.D
	HsFLAG-FLJ20729_	5.2623	0.3813	1777.42	1777.042	6048	1	2196.4	84.6	6	K.DPVLYMYQLLDDYK.E
	HsFLAG-Lin9_Ti_20	2.7729	0.244	2346.47	2347.645	10325.5	3	474.4	36.1	1	K.DPVLYMYQLLDDYKEGDLR.I
*	HsFLAG-FLJ20729_	3.3527	0.1475	1371.45	1369.625	7551.5	1	1442.9	81.8	4	K.RTGMVIHQVEAK.P
*	HsFLAG-FLJ20729_	4.4105	0.3913	2203.43	2204.638	5837.5	1	810	55.6	2	K.RTGMVIHQVEAKPSVYFIK.F
*	HsFLAG-FLJ20729_	5.5168	0.3699	2204.28	2204.638	7492.4	1	1548.4	44.4	1	K.RTGMVIHQVEAKPSVYFIK.F
*	HsFLAG-FLJ20729_	4.4359	0.2894	2049.18	2048.451	9500.9	1	1174.3	52.9	2	R.TGMVIHQVEAKPSVYFIK.F
	HsFLAG-FLJ20729_	5.3702	0.4789	1791.37	1789.982	7785.7	1	1835.1	76.9	14	K.FDDDFHIYVYDLVK.T
gi|29294624|r	9	72	55.90%	118	13527	9.9	small nuclear ribonucleoprotein polypeptide D2 [Homo sapiens]				
gi|4759158|re	9	72	55.90%	118	13527	9.9	small nuclear ribonucleoprotein polypeptide D2 [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.3461	0.1316	3337.92	3337.68	7294	1	853.6	27.7	4	K.SEMTPEELQKREEEEFNTGPLSVLTQSVK.N
	HsFLAG-ARP6_Ti_1	5.1758	0.3938	2163.35	2164.377	9638.6	1	1297.9	38.9	6	K.REEEEFNTGPLSVLTQSVK.N
	HsFLAG-Lin9_Ti_20	6.4651	0.4694	2164.57	2164.377	11398.5	1	2515.9	66.7	19	K.REEEEFNTGPLSVLTQSVK.N
	HsFLAG-ARP6_Ti_2	4.3144	0.4691	2008.13	2008.19	5467.1	1	1095.2	64.7	5	R.EEEEFNTGPLSVLTQSVK.N
	HsFLAG-ARP6_Ti_1	3.785	0.2586	1232.28	1232.348	7949.9	1	1537.1	88.9	3	K.NNTQVLINCR.N
	HsFLAG-ARP6_Ti_1	2.5356	0.1438	1243.3	1244.417	4820.5	1	560.6	72.2	1	R.HCNMVLENVK.E
	HsFLAG-ARP6_Ti_1	4.1711	0.3512	1244.21	1244.417	7134.8	1	1564.3	88.9	16	R.HCNMVLENVK.E
	HsFLAG-ARP6_Ti_1	3.1179	0.1141	1329.29	1329.603	4750.7	3	738.1	72.2	4	K.DRYISKMFLR.G
	HsFLAG-p53-DNA-D	2.5562	0.1004	712.45	712.867	4071.3	4	499.9	83.3	14	R.NPLIAGK.-
gi|19924159|r	40	631	55.70%	535	59832	5	RPB5-mediating protein isoform a [Homo sapiens]				
gi|19924161|r	40	631	60.20%	495	55584	5.2	RPB5-mediating protein isoform b [Homo sapiens]				
	HsFlag-ZnF-HIT2_Ti_	2.5913	0.083	1207.57	1208.316	4944.5	1	605	77.8	5	K.KVDNDYNALR.E
	HsFLAG-p53-DNA-D	4.0338	0.2188	1208.46	1208.316	5440.9	1	1266	94.4	15	K.KVDNDYNALR.E
	HsFlag-NUFIP_Ti_10	4.3596	0.2955	2017.72	2017.454	3686.8	1	475.8	55.9	14	K.LSYNIMVPFGPFAFMPGK.L

	HsFLAG-p53-DNA-D	4.7265	0.2031	2056.48	2057.357	4691.5	7	810.9	41.2	29	K.LVHTNEVTVLLGDNWFAK.C
	HsFLAG-UTX1_Ti_2(	6.6072	0.4799	2057.43	2057.357	8346.1	1	2477	76.5	69	K.LVHTNEVTVLLGDNWFAK.C
	HsFlag-NUFIP_Ti_1(	1.9445	0.2043	1008.63	1009.153	2166.9	6	98.6	68.8	1	K.QAVGLVEHR.K
	HsFlag-NUFIP_Ti_1(	3.136	0.1761	1009.26	1009.153	2683.3	2	310	81.2	17	K.QAVGLVEHR.K
	HsFlag-FLJ20643_Ti	2.2579	0.2127	1108.55	1109.221	7687.9	7	585.9	68.8	1	R.VEFTEDLQK.M
	HsFlag-FLJ20643_Ti	2.986	0.2233	1110.89	1109.221	3707.4	2	624.6	87.5	1	R.VEFTEDLQK.M
	HsFLAG-p53-DNA-D	4.2521	0.3569	1263.16	1263.408	7584.7	1	2234.5	90.9	2	K.MSDAAGDIVDIR.E
	HsFLAG-p53-DNA-D	5.0434	0.3953	1762.01	1762.973	8797.5	1	1923	73.3	15	K.MSDAAGDIVDIREEIK.C
	HsFLAG-RPB5MP_2	2.5082	0.1891	1345.37	1345.458	5736.3	1	687.8	77.8	1	R.EEIKCDFEFK.A
	HsFLAG-p53-DNA-D	4.0559	0.3696	1537.45	1538.651	7296.2	1	994.5	65.4	8	K.TSDIFEADIANDVK.S
	HsFlag-NUFIP_Ti_1(	5.2947	0.3499	1538.36	1538.651	6987.8	1	1776.4	80.8	120	K.TSDIFEADIANDVK.S
	HsFlag-NUFIP_Ti_1(	6.06	0.3875	4334	4335.544	5926.7	1	1426.6	29.1	12	R.LEELERQEELLGELDSKPDTVIANGEDTTSSEEEKEDR.N
	HsFLAG-TIP49a_Ti_	4.8873	0.4327	2191.49	2192.337	6655.2	1	1412.7	63.9	14	R.NTNVNAMHQVTDSHTPCHK.D
	HsFlag-ZnF-HIT2_Ti_	4.6103	0.1818	2192.22	2192.337	8178.9	1	1489.2	41.7	14	R.NTNVNAMHQVTDSHTPCHK.D
	HsFLAG-BC014022_	4.419	0.3201	1784.4	1783.939	10806.4	1	2042	62.5	2	R.KNSTGSGHSAQELPTIR.T
	HsFlag-FLJ20643_Ti	4.733	0.4376	1656.1	1655.765	8175.7	1	1654.1	66.7	31	K.NSTGSGHSAQELPTIR.T
	HsFLAG-RPB5MP_2	3.6021	0.2717	1656.7	1655.765	5184.7	2	763	40	2	K.NSTGSGHSAQELPTIR.T
	HsFLAG-p53-DNA-D	2.3308	0.1551	835.56	835.935	2189	6	143	75	1	R.TPADIYR.A
	HsFlag-FLJ20643_Ti	2.5176	0.1795	837.56	835.935	4602.2	7	661.8	91.7	1	R.TPADIYR.A
	HsFLAG-p53-DNA-D	4.8479	0.2938	1464.77	1465.649	7170.4	1	1963.2	83.3	43	R.AFVDVVNGEYVPR.K
	HsFLAG-p53-DNA-D	2.9424	0.2027	1465.69	1465.649	3505.1	9	274.7	54.2	2	R.AFVDVVNGEYVPR.K
	HsFlag-FLJ20643_Ti	3.0431	0.1934	1594.8	1593.823	9256.4	1	891.9	61.5	1	R.AFVDVVNGEYVPRK.S
	HsFLAG-TIP49a_Ti_	5.0555	0.4593	2350.57	2350.294	4387.2	1	773.9	60	15	R.SRENSVCSDTSESSAAEFDDR.R
	HsFlag-FLJ20643_Ti	4.8374	0.4046	2350.63	2350.294	8840.8	1	1352.8	36.2	4	R.SRENSVCSDTSESSAAEFDDR.R
	HsFlag-FLJ20643_Ti	3.7523	0.3386	2507.77	2506.482	6700.5	6	528.6	29.8	2	R.SRENSVCSDTSESSAAEFDDRR.G
	HsFlag-NUFIP_Ti_1(	5.3945	0.5477	2106.57	2107.028	10810.9	1	2097.9	61.1	22	R.ENSVCSDTSESSAAEFDDR.R
	HsFlag-NUFIP_Ti_1(	5.0862	0.434	3002.07	3002.012	8747	1	1443.4	46	34	R.SISCEEATCSDTSESILEEEPQENQK.K
	HsFlag-FLJ20643_Ti	5.9306	0.2663	3002.4	3002.012	7050.1	1	818.5	31	9	R.SISCEEATCSDTSESILEEEPQENQK.K
	HsFlag-FLJ20643_Ti	3.6281	0.3039	3129.97	3130.186	5902.6	1	790.9	29.8	1	R.SISCEEATCSDTSESILEEEPQENQKK.L
	HsFLAG-p53-DNA-D	5.5797	0.4128	2029.25	2030.412	5996.5	1	1604.6	72.2	39	K.KLLPLSVTPEAFSGTVIEK.E
	HsFlag-NUFIP_Ti_1(	6.2192	0.3748	2030.07	2030.412	8184.3	1	2747.3	51.4	17	K.KLLPLSVTPEAFSGTVIEK.E
	HsFlag-NUFIP_Ti_1(	4.1309	0.3716	1903.32	1902.238	4721	1	501.9	55.9	23	K.LLPLSVTPEAFSGTVIEK.E
	HsFLAG-RPB5MP_2	4.528	0.3561	1903.44	1902.238	8724.6	1	1861.6	45.6	3	K.LLPLSVTPEAFSGTVIEK.E
	HsFlag-NUFIP_Ti_11	4.9289	0.4402	2537.62	2538.949	5044.5	1	719.6	33.7	6	K.EFVSPSLTPPPAIAHPALPTIPER.K
	HsFlag-NUFIP_Ti_11	4.1478	0.356	2538.11	2538.949	4462.9	1	334	39.1	5	K.EFVSPSLTPPPAIAHPALPTIPER.K
	HsFLAG-RPB5MP_2	3.3038	0.2821	1304.34	1305.425	4030.4	1	431.8	68.2	3	K.EVLLEASEETGK.R
	HsFlag-NUFIP_Ti_1(	4.1917	0.2487	1305.56	1305.425	6814	1	1262.5	81.8	27	K.EVLLEASEETGK.R
gi|7706753|re	15	62	55.60%	329	37607	5.3	ubiquitin C-terminal hydrolase UCH37 [Homo sapiens]				
	HsFLAG-ARP8_Ti_2	2.8672	0.2732	2587.71	2586.9	6951.5	1	615.1	38.6	1	-.MTGNAGEWCLMESDPGVFTELIK.G
	HsFLAG-TCF3_Ti_1(	4.7238	0.2691	2006.7	2006.176	6493.1	1	882.5	59.4	15	R.GAQVEEIWSLEPENFEK.L
*	HsFLAG-TCF3_Ti_1(	4.5253	0.3769	3809.9	3812.204	6996.4	1	666.9	24.2	7	K.QVINNACATQAIVSVLLNCTHQDVHLGETLSEFK.E
	HsFLAG-ARP5_Ti_1	2.5752	0.1322	1145.06	1145.301	7084.9	5	688	70	1	K.GLALSNSDVIR.Q
	HsFLAG-TCF3_Ti_1(	2.1377	0.1934	1145.59	1145.301	3437.5	7	133.6	55	1	K.GLALSNSDVIR.Q

	HsFlag-FLJ90652_29	2.2147	0.0991	1172.51	1174.314	2957.7	2	213.4	62.5	1	R.QQMFEFDTK.T
	HsFLAG-TCF3_Ti_10	5.2147	0.4942	2253.75	2254.464	6435.8	1	1179.6	57.9	2	K.TSAKEEDAFHFVSYVPVNGR.L
	HsFLAG-FLJ20309_T	3.8171	0.3131	1867.35	1867.028	8062.6	1	1270.4	60	3	K.EEDAFHFVSYVPVNGR.L
	HsFLAG-TCF3_Ti_10	2.2815	0.1374	978.65	979.121	5029.1	4	448	78.6	1	R.LYELDGLR.E
	HsFlag-FLJ90652_29	4.5321	0.2868	3643.51	3644.042	9538.5	1	908.9	25.8	2	R.LYELDGLREGPIDLGACNQDDWISAVRPVIEK.R
	HsFLAG-ARP8_Ti_2	4.1462	0.3228	2682.72	2683.944	8090.7	1	720.8	39.1	5	R.EGPIDLGACNQDDWISAVRPVIEK.R
	HsFLAG-TIP49a_Ti_	3.9048	0.2374	2684.52	2683.944	4078.8	1	730.6	35.9	2	R.EGPIDLGACNQDDWISAVRPVIEK.R
	HsFLAG-TCF3_Ti_10	3.3052	0.1958	1294.59	1294.555	7963.6	1	1509.7	80	4	R.FNLMAIVSDRK.M
	HsFLAG-TCF3_Ti_10	4.0582	0.3438	1519.59	1518.857	5513.5	1	1143.6	81.8	10	K.HNYLPFIMELLK.T
	HsFlag-FLJ90652_29	4.1525	0.1294	1619.39	1619.902	4913.1	1	869.3	73.1	7	K.TLAEHQQLIPLVEK.A
gi|24638446|r	6	92	55.00%	129	13988	10.9	H2A histone family, member Q [Homo sapiens]				
gi|88943487|r	6	92	54.60%	130	14095	10.9	PREDICTED: similar to Histone H2A.o (H2A/o) (H2A.2) (H2a-615) [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.1573	0.1473	944.77	945.109	5816.4	2	976.3	87.5	4	R.AGLQFPVGR.V
	HsFLAG-Lin9_Ti_207	4.9776	0.3338	2934.24	2935.408	10020.2	1	1226.7	30.4	6	R.VGAGAPVYMAAVLEYLTAEILELAGNAAR.D
	HsFLAG-ARP8_Ti_2	5.5206	0.2936	2935.44	2935.408	7841.9	1	1343.7	42.9	5	R.VGAGAPVYMAAVLEYLTAEILELAGNAAR.D
	HsFLAG-ARP6_Ti_1	4.029	0.2972	1693.82	1693.9	8806.2	2	1211.8	69.2	9	R.HLQLAIRNDEELNK.L
	HsFlag-NUFIP_Ti_10	5.3135	0.4282	1931.78	1932.357	4289.2	1	956.2	66.7	62	K.VTIAQGGVLPNIQAVLLPK.K
	HsFLAG-Lin9_Ti_202	5.2747	0.3488	1931.88	1932.357	8773.2	1	2498.1	50	6	K.VTIAQGGVLPNIQAVLLPK.K
gi|4506439|re	14	43	54.80%	425	47820	5	retinoblastoma binding protein 7 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	5.3976	0.4159	3839.8	3841.46	7901.1	1	751.8	24.2	1	K.NTPFLYDLVMTHALQWPSLTVQWLPEVTKPEGK.D
*	HsFLAG-Lin9_Ti_201	3.3002	0.2334	1143.12	1143.241	8818.1	1	1157.9	72.7	1	K.GEFGGFGSVTGK.I
*	HsFlag-NUFIP_Ti_20	2.744	0.2028	1413.53	1413.678	5332.3	1	517	68.2	2	R.YMPQNPHIIATK.T
	HsSrcap_Ti_203.235	3.002	0.3428	1472.37	1472.635	4836.8	1	486.8	62.5	7	K.TPSSDVLVFDYTK.H
	HsFLAG-Lin9_Ti_202	4.3366	0.3815	1473.5	1472.635	7851	1	1516.2	75	9	K.TPSSDVLVFDYTK.H
*	HsFLAG-Lin9_Ti_205	2.7812	0.2549	1789.97	1790.896	6775.9	1	422.9	46.7	2	K.HPAKPDPSGECNPDLR.L
*	HsFlag-VPS71_Ti_10	4.5965	0.3634	3715.39	3715.981	10285.4	1	1093.2	25	3	K.EGYGLSWNSNLSGHLLSASDDHTVCLWDINAGPK.E
*	HsSrcap_Ti_206.319	7.0758	0.5566	3380.87	3380.741	8604.6	1	1575.8	32.5	3	K.AIFTGHSAVVEDVAWHLLHESLFGSVADDQK.L
*	HsSrcap_Ti_205.325	5.6947	0.4984	4111.79	4111.434	8370.4	1	1223.1	25	4	R.SNTTSKPSHLVDAHTAEVNCLSFNPYSEFILATGSADK.T
	HsFLAG-Lin9_Ti_201	2.7344	0.0828	973.28	974.148	3249.6	3	701.2	85.7	1	K.TVALWDLR.N
	HsSrcap_Ti_205.221	2.7488	0.1048	1131.52	1131.32	4440.3	3	625	81.2	1	R.RLNVWDLSK.I
	HsFLAG-Lin9_Ti_201	2.8604	0.1205	975.25	975.133	4581	5	882.6	92.9	1	R.LNVWDLSK.I
*	HsSrcap_Ti_203.225	5.2256	0.3197	2848.85	2849.04	8887.2	1	1737.3	33.7	6	K.IGEEQSAEDAEDGPPELLFIHGGHTAK.I
*	HsFlag-VPS71_Ti_10	4.4434	0.3821	2848.92	2849.04	4160.8	1	520	42.3	2	K.IGEEQSAEDAEDGPPELLFIHGGHTAK.I
gi|10800130|r	6	89	54.60%	130	14107	10.9	histone 1, H2ad [Homo sapiens]				
gi|4504243|re	6	89	54.60%	130	14091	10.9	H2A histone family, member I [Homo sapiens]				
gi|4504241|re	6	89	54.60%	130	14091	10.9	H2A histone family, member D [Homo sapiens]				
gi|4504239|re	6	89	54.60%	130	14091	10.9	H2A histone family, member C [Homo sapiens]				
gi|29553970|r	6	89	55.00%	129	14019	10.9	H2A histone family, member J isoform 2 [Homo sapiens]				
gi|18105045|r	6	89	55.50%	128	13906	10.9	H2A histone family member [Homo sapiens]				
gi|10800144|r	6	89	55.50%	128	13936	10.9	H2A histone family, member E [Homo sapiens]				
gi|10800132|r	6	89	54.60%	130	14091	10.9	H2A histone family, member P [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.1573	0.1473	944.77	945.109	5816.4	2	976.3	87.5	4	R.AGLQFPVGR.V
	HsFLAG-Lin9_Ti_207	5.4913	0.4094	2916.83	2917.375	9478.7	1	1610.8	32.1	3	R.VGAGAPVYLAAVLEYLTAEILELAGNAAR.D

	HsFLAG-Lin9_Ti_20	5.6884	0.3714	2917.12	2917.375	9129.3	1	1489.7	42.9	5	R.VGAGAPVYLAAVLEYLTAEILELAGNAAR.D
	HsFLAG-ARP6_Ti_1	4.029	0.2972	1693.82	1693.9	8806.2	2	1211.8	69.2	9	R.HLQLAIRNDEELNK.L
	HsFlag-NUFIP_Ti_1	5.3135	0.4282	1931.78	1932.357	4289.2	1	956.2	66.7	62	K.VTIAQGGVLPNIQAVLLPK.K
	HsFLAG-Lin9_Ti_20	5.2747	0.3488	1931.88	1932.357	8773.2	1	2498.1	50	6	K.VTIAQGGVLPNIQAVLLPK.K
gi|5902102|re	8	175	54.60%	119	13282	11.6	small nuclear ribonucleoprotein D1 polypeptide 16kDa [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	2.5117	0.1204	1269.6	1270.469	6351	8	641.6	65	1	K.LSHETVTIELK.N
*	HsFLAG-Lin9_Ti_20	3.2154	0.2776	1270.26	1270.469	5667	1	682.3	75	3	K.LSHETVTIELK.N
*	HsFlag-NUFIP_Ti_1	3.9711	0.373	2210.03	2210.47	9044.3	1	1213.2	52.5	6	K.NGTQVHGTITGVDVSMNTHLK.A
*	HsFlag-NUFIP_Ti_1	5.0796	0.3573	2211.47	2210.47	6656.6	1	1103.3	38.8	6	K.NGTQVHGTITGVDVSMNTHLK.A
*	HsFlag-ZnF-HIT2_Ti_	4.4214	0.3546	1555.71	1555.775	6171.3	1	1358.4	83.3	40	K.NREPVQLETLSIR.G
*	HsFlag-NUFIP_Ti_1	5.1129	0.2958	1556.15	1555.775	8925.8	1	2112.1	56.2	10	K.NREPVQLETLSIR.G
*	HsFlag-NUFIP_Ti_1	5.1195	0.3716	2289.17	2288.686	4438.5	1	1027.9	65.8	99	R.YFILPDSLPLDTLLVDVEPK.V
*	HsFlag-VPS71_Ti_1	6.1435	0.4091	2289.38	2288.686	6737.1	1	1628.8	44.7	10	R.YFILPDSLPLDTLLVDVEPK.V
gi|5803225|re	14	78	54.50%	255	29174	4.7	tyrosine 3/tryptophan 5 -monooxygenase activation protein, epsilon polypeptide [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.8503	0.3213	1929.29	1930.155	8610.2	1	1274.8	60	1	K.LAEQAERYDEMVESMK.K
	HsFlag-FLJ90652_2	3.101	0.3096	1417.73	1418.587	7329.8	2	830.2	72.7	2	R.IISSIEQKEENK.G
*	HsFLAG-ARP6_Ti_1	3.6955	0.318	1237.5	1238.386	4414.5	1	831.7	77.3	7	K.HLIPAANTGESK.V
*	HsFLAG-p53-DNA-D	3.2679	0.2547	1238.42	1238.386	3579.2	1	1017	86.4	16	K.HLIPAANTGESK.V
	HsFLAG-ARP6_Ti_1	3.4271	0.2191	1386.02	1385.519	7928.6	1	1148.7	72.7	2	R.YLAEFATGNDRK.E
*	HsFLAG-p53-DNA-D	2.4105	0.1077	1194.4	1195.315	5001.9	4	328.3	65	1	K.EAAENSLVAYK.A
*	HsFlag-FLJ90652_2	3.2196	0.2421	1195.09	1195.315	6866.9	1	839	75	1	K.EAAENSLVAYK.A
*	HsFLAG-ARP6_Ti_1	4.6759	0.4057	1821.34	1821.102	4163.6	1	668.5	62.5	10	K.AASDIAMTELPPTHPIR.L
*	HsFLAG-ARP6_Ti_2	5.3451	0.4823	2088.55	2089.217	6348.7	1	1865.5	72.2	29	K.AAFDDAIAELDTLSEESYK.D
*	HsFLAG-ARP6_Ti_1	4.6625	0.4355	2089.85	2089.217	6451.8	1	1311.3	45.8	1	K.AAFDDAIAELDTLSEESYK.D
	HsFLAG-FLJ20729_	3.7624	0.1371	1189.5	1190.444	6163.6	5	1616.1	88.9	2	K.DSTLIMQLLR.D
	HsMRGBP-FLAG_Ti_	4.1108	0.4192	2181.97	2182.28	7316.2	1	1521.9	63.9	4	R.DNLTLWTSDMQGDGEEQNK.E
*	HsFLAG-p53-DNA-D	3.1464	0.1944	1289.37	1290.283	9428.4	2	892.3	65	1	K.EALQDVEDENQ.-
*	HsFLAG-ARP6_Ti_1	2.6871	0.0972	1291.13	1290.283	4381.8	2	444.9	70	1	K.EALQDVEDENQ.-
gi|4506597|re	8	27	54.50%	165	17819	9.4	ribosomal protein L12 [Homo sapiens]				
	HsFLAG-TCF3_Ti_1	2.2908	0.2739	1418.45	1419.541	3634.9	1	222.4	50	1	R.CTGGEVGATSALAPK.I
	HsFLAG-TCF3_Ti_1	4.2628	0.3386	1421.46	1419.541	5559	1	1385.8	78.6	1	R.CTGGEVGATSALAPK.I
	HsFLAG-ARP6_Ti_1	2.9745	0.223	882.05	882.091	3638.3	9	553.6	81.2	4	K.IGPLGLSPK.K
	HsFLAG-TCF3_Ti_1	3.8996	0.1691	1667.64	1667.987	5306.7	8	570	60	1	R.QAQIEVVPSASALIIK.A
*	HsFLAG-ARP6_Ti_1	4.141	0.1386	1686.02	1686.865	7437.1	2	1436	46.4	2	K.HSGNITFDEIVNIAR.Q
*	HsFLAG-TCF3_Ti_1	5.2958	0.4736	1687.08	1686.865	7111.1	1	2078.3	85.7	12	K.HSGNITFDEIVNIAR.Q
	HsFLAG-Lin9_Ti_20	3.7379	0.4533	1676.49	1676.79	6346.9	1	1179.6	70	4	K.EILGTAQSVGCNVDGR.H
	HsFLAG-ARP6_Ti_1	4.759	0.4884	2046.53	2048.139	6633.9	1	1161.9	61.1	2	R.HPHDIIDDINSGAVECPAS.-
gi|31542947|r	27	130	54.10%	573	61055	5.9	chaperonin [Homo sapiens]				
gi|41399285|r	27	130	54.10%	573	61055	5.9	chaperonin [Homo sapiens]				
	HsFLAG-p53-DNA-D	5.5338	0.4996	2113.48	2114.567	10660.5	1	1523.5	55	8	R.ALMLQGVDLLADAVAVTMGPK.G
	HsFLAG-ARP6_Ti_1	5.391	0.4548	2114.33	2114.567	9059.4	1	2358.5	43.8	6	R.ALMLQGVDLLADAVAVTMGPK.G
	HsFlag-NUFIP_Ti_1	6.1214	0.3765	2561.08	2561.722	8966	1	1820.6	54.2	4	K.LVQDVANNTNEEAGDGTTTATVLAR.S
	HsFLAG-ARP5_Ti_1	3.6681	0.1764	1585.75	1585.946	8117.6	2	1043.3	60.7	3	R.RGVMLAVDAVIAELK.K

	HsFLAG-ARP6_Ti_1	4.3822	0.4648	2384.79	2385.634	6086.1	1	549.6	43.2	2	K.QSKPVTTPEEIAQVATISANGDK.E
	HsFLAG-ARP6_Ti_1	4.446	0.2934	1505.12	1505.724	7336.5	1	1719.1	79.2	5	K.TLNDELEIIEGMK.F
	HsFLAG-ARP6_Ti_1	2.955	0.2332	1389.99	1390.579	5399.6	1	934.5	72.7	1	R.GYISPYFINTSK.G
	HsFLAG-TCF3_Ti_1	3.0129	0.253	1390.53	1390.579	5715.8	1	465	59.1	1	R.GYISPYFINTSK.G
	HsFLAG-ARP6_Ti_1	4.7779	0.4626	1602.37	1602.747	6952	1	1624	79.2	6	K.CEFQDAYVLLSEK.K
	HsFlag-NUFIP_Ti_11	6.3387	0.4166	2048.6	2048.393	7295.1	1	1867.2	48.6	4	K.KISSIQSIVPALEIANAHR.K
	HsFLAG-ARP6_Ti_1	5.8646	0.4263	2048.6	2048.393	4692.3	1	1375.4	75	7	K.KISSIQSIVPALEIANAHR.K
	HsFLAG-ARP6_Ti_1	4.7559	0.4779	1920.15	1920.219	3775.1	1	755.6	64.7	3	K.ISSIQSIVPALEIANAHR.K
	HsFLAG-p53-DNA-D	4.4083	0.3058	1921.07	1920.219	6857.7	1	1290.5	44.1	4	K.ISSIQSIVPALEIANAHR.K
	HsFLAG-ARP6_Ti_1	3.924	0.2068	2366.53	2366.761	11581.3	2	1250.7	32.1	6	R.KPLVIIAEDVDGEALSTLVLNR.L
	HsFLAG-ARP6_Ti_1	6.6853	0.5385	2367.1	2366.761	6873.3	1	2390.4	69	4	R.KPLVIIAEDVDGEALSTLVLNR.L
	HsFLAG-p53-DNA-D	2.2311	0.1462	912.56	913.148	6590.4	6	527.8	68.8	1	K.VGLQVVAVK.A
	HsFLAG-p53-DNA-D	2.769	0.13	962.29	962.053	7646.4	1	799.3	81.2	2	K.APGFGDNRK.N
	HsFLAG-TCF3_Ti_1	2.0758	0.1639	844.48	845.027	8364.9	4	683	78.6	3	K.VGEVIVTK.D
	HsFLAG-ARP6_Ti_1	4.3579	0.2713	1633.24	1631.968	6391.5	1	1478.3	75	2	K.VGEVIVTKDDAMLLK.G
	HsFLAG-ARP6_Ti_1	4.1842	0.445	2194.02	2195.431	8786.1	1	746	47.1	6	K.RIQEIIEQLDVTTSEYEK.E
	HsFLAG-ARP6_Ti_1	4.1095	0.3238	2195.95	2195.431	9109.3	1	1744.8	41.2	4	K.RIQEIIEQLDVTTSEYEK.E
	HsH2AZ-FLAG_293_	3.5566	0.3636	1234	1234.306	6514.6	1	1079.5	77.3	7	K.VGGTSDVEVNEK.K
	HsFLAG-p53-DNA-D	4.2411	0.3519	1685.82	1685.927	8740.4	1	1960.6	68.8	1	R.AAVEEGIVLGGGCALLR.C
	HsFLAG-ARP6_Ti_2	3.9088	0.3224	1773.36	1772.916	6085.9	1	985.8	66.7	3	R.CIPALDSLTPANEDQK.I
	HsFLAG-ARP6_Ti_1	5.6067	0.5819	2508.57	2509.823	6917.3	1	1522	56.8	2	K.IMQSSSEVGYDAMAGDFVNMVEK.G
	HsFLAG-Lin9_Ti_20	6.2836	0.3962	2870.29	2870.31	5700.5	1	1443.2	38.9	29	R.TALLDAAGVASLLTTAEVVVTEIPKEEK.D
	HsFLAG-ARP6_Ti_1	4.5396	0.3634	2870.67	2870.31	8357	1	925.8	37	6	R.TALLDAAGVASLLTTAEVVVTEIPKEEK.D
gi|4502643|re	25	135	53.90%	531	58024	6.7	chaperonin containing TCP1, subunit 6A isoform a [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.0397	0.3034	2315.39	2316.681	10158.4	1	999.4	47.5	3	K.DGNVLLHEMQIQHPTASLIAK.V
*	HsFLAG-ARP6_Ti_1	5.4597	0.3552	2316.08	2316.681	7053.2	1	1273.5	38.8	7	K.DGNVLLHEMQIQHPTASLIAK.V
*	HsFLAG-ARP6_Ti_1	5.9	0.4955	2544.15	2545.847	7588.3	1	1762.9	56.2	17	K.VATAQDDITGDGTTSNVLIIGELLK.Q
	HsFLAG-ARP6_Ti_1	3.7343	0.4002	1499.92	1499.666	6308.5	1	943.2	75	4	K.QADLYISEGLHPR.I
	HsFLAG-ARP6_Ti_1	1.9682	0.1405	1078.3	1079.238	7763.1	8	553.1	61.1	1	R.IITEGFEAAK.E
	HsFLAG-ARP6_Ti_1	2.8823	0.1664	1078.39	1079.238	2862.6	2	591.7	88.9	1	R.IITEGFEAAK.E
	HsFLAG-ARP5_Ti_1	2.8343	0.1002	1336.36	1336.528	6423.4	1	834.4	68.2	2	R.IITEGFEAAKEK.A
	HsFLAG-ARP6_Ti_1	3.3487	0.1038	1077.59	1077.266	5573.2	2	907.3	81.2	1	K.ALQFLEEVK.V
	HsFLAG-ARP6_Ti_1	2.9696	0.2692	1448.75	1448.634	5842.5	1	872.3	77.3	2	R.EMDRETLIDVAR.T
	HsFLAG-ARP5_Ti_1	6.3446	0.5346	2435.86	2436.852	8694.7	1	2660.2	65.9	2	R.TKVHAELADVLTEAVVDSILAIK.K
	HsFLAG-ARP5_Ti_1	4.8342	0.2882	2436.84	2436.852	8341.7	1	1494.1	36.4	4	R.TKVHAELADVLTEAVVDSILAIK.K
	HsFLAG-ARP5_Ti_1	7.6471	0.5783	2206.64	2207.572	8752	1	3403.7	75	13	K.VHAELADVLTEAVVDSILAIK.K
	HsFlag-FLJ90652_2	4.7128	0.3449	2206.73	2207.572	7305.3	1	1410.9	40	4	K.VHAELADVLTEAVVDSILAIK.K
	HsFLAG-ARP6_Ti_1	4.8275	0.4556	2110.32	2111.534	5992.6	1	1469.2	71.9	8	K.KQDEPIDLFMIEIMEMK.H
	HsFLAG-ARP5_Ti_1	2.7313	0.2003	937.89	938.074	5439	8	1126.8	87.5	1	R.GLVLDHGAR.H
	HsFLAG-ARP6_Ti_1	5.519	0.4344	2203.14	2203.42	8598.2	1	1933.9	67.6	8	K.RVEDAYILTCNVSLEYEK.T
	HsFLAG-ARP6_Ti_1	3.5106	0.3082	2203.21	2203.42	9087.7	1	1117.4	36.8	1	K.RVEDAYILTCNVSLEYEK.T
	HsFLAG-ARP6_Ti_1	3.4526	0.2115	1192.52	1192.313	4731.4	5	825.4	83.3	1	K.TEVNSGFFYK.S
	HsFLAG-ARP6_Ti_1	3.1888	0.1069	1264.48	1263.433	4938	1	1009.5	77.3	2	K.GIDPFSLDALSK.E

	HsFLAG-ARP6_Ti_1	7.1509	0.5181	3885.64	3887.221	6718.3	1	1314.8	28.6	9	R.LTLACGGVALNSFDDLSPDCLGHAGLVYEYTLGEEK.F
	HsFLAG-ARP5_Ti_1	3.1407	0.3284	1282.61	1282.486	5310	1	733.7	80	1	K.HTLTQIKDAVR.D
	HsFLAG-ARP6_Ti_1	4.6203	0.2911	2471.47	2471.794	6517.8	1	1740.5	39.6	1	K.NAIDDGCVVPGAGAVEVAMAEALIK.H
	HsFLAG-ARP6_Ti_1	4.3445	0.2152	2474.4	2471.794	2984.9	1	713.7	54.2	7	K.NAIDDGCVVPGAGAVEVAMAEALIK.H
	HsFLAG-ARP6_Ti_1	4.6701	0.2341	1768.42	1769.137	6717	1	1399.5	65.6	29	R.AQLGVQAFADALLIIPK.V
	HsFLAG-ARP6_Ti_1	4.8912	0.4372	1761.75	1763.001	7799.7	1	2103.6	80	6	K.VLAQNSGFDLQETLVK.I
gi|15718687|r	15	143	53.90%	243	26688	9.7	ribosomal protein S3 [Homo sapiens]				
*	HsFLAG-ARP8_Ti_2	1.9781	0.1022	896.47	897.062	8093.3	9	639.2	71.4	2	K.FVADGIFK.A
*	HsFlag-NUFIP_Ti_10	4.4139	0.4158	1423.66	1424.507	7334.9	1	2188.9	87.5	9	R.ELAEDGYSGVEVR.V
*	HsFlag-NUFIP_Ti_10	3.7172	0.1719	1030.53	1030.253	7810.6	2	1884.5	93.8	35	R.TEIIILATR.T
*	HsFLAG-ARP6_Ti_1	2.8445	0.0947	1157.49	1157.399	5164.6	1	987	83.3	3	R.IRELTAVVQK.R
*	HsFlag-NUFIP_Ti_10	4.2958	0.3545	1729.5	1729.93	8183.8	1	1661.6	75	8	K.RFGFPEGSVELYAEK.V
*	HsFlag-NUFIP_Ti_10	4.1674	0.2938	1290.6	1289.441	6768.3	1	1505.5	81.8	4	R.GLCAIAQAESLR.Y
*	HsFlag-NUFIP_Ti_10	5.1309	0.3436	2468.86	2469.774	6437.1	1	1533.8	59.5	14	K.FVDGLMIHSGDPVNYYVDTAVR.H
*	HsFlag-NUFIP_Ti_10	5.0199	0.2285	2469.07	2469.774	9502.6	6	1057.7	32.1	3	K.FVDGLMIHSGDPVNYYVDTAVR.H
*	HsFlag-NUFIP_Ti_11	2.4634	0.3074	1458.66	1459.729	5097.4	6	439.8	54.2	4	K.KPLPDHVSIVEPK.D
*	HsFlag-NUFIP_Ti_11	4.2433	0.379	1459.12	1459.729	6007.8	1	1564.5	87.5	8	K.KPLPDHVSIVEPK.D
*	HsFlag-NUFIP_Ti_11	4.5983	0.3078	1459.94	1459.729	6227.7	5	1194	54.2	2	K.KPLPDHVSIVEPK.D
*	HsFlag-NUFIP_Ti_11	5.6127	0.3552	2911.57	2912.353	6118.2	1	1002.9	36	18	K.KPLPDHVSIVEPKDEILPTTPISEQK.G
*	HsFlag-NUFIP_Ti_10	3.243	0.1752	1471.39	1471.648	3445.3	1	581.7	70.8	2	K.DEILPTTPISEQK.G
*	HsFLAG-TCF3_Ti_1	3.263	0.3808	1573.38	1574.835	5732.5	1	677.7	56.7	10	K.GGKPEPPAMPQPVPTA.-
*	HsFlag-NUFIP_Ti_10	3.8216	0.2734	1575.58	1574.835	4494.7	1	507.6	56.7	21	K.GGKPEPPAMPQPVPTA.-
gi|4504255|re	9	185	53.90%	128	13553	10.6	H2A histone family, member Z [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.1573	0.1473	944.77	945.109	5816.4	2	976.3	87.5	4	R.AGLQFPVGR.I
	HsFLAG-ARP6_Ti_1	5.0088	0.2203	2896.64	2897.295	7081.8	1	768.2	37.5	10	R.VGATAAVYSAAILEYLTAEVLELAGNASK.D
	HsFLAG-p53-DNA-D	6.921	0.5122	2897.68	2897.295	9973.9	1	2207.8	33.9	34	R.VGATAAVYSAAILEYLTAEVLELAGNASK.D
	HsFlag-VPS71_Ti_1	3.9541	0.3703	1952.08	1951.23	5907.3	1	963.2	43.8	18	R.HLQLAIRGDEELDSLIK.A
	HsFlag-VPS71_Ti_1	4.5407	0.3286	1952.4	1951.23	7387	1	1319.1	68.8	84	R.HLQLAIRGDEELDSLIK.A
	HsYL1_Ti_101.2142.	2.8377	0.2463	1118.51	1119.214	5405.5	3	537.2	66.7	7	R.GDEELDSLIK.A
	HsYL1_Ti_101.2175.	3.6642	0.2321	1118.57	1119.214	5769.5	1	1206.6	83.3	6	R.GDEELDSLIK.A
	HsFLAG-TIP49a_Ti_	2.8651	0.19	1371.53	1371.625	4630.4	2	508.2	53.8	3	K.ATIAGGGVIPHIHK.S
	HsFLAG-ARP6_Ti_1	4.3316	0.2618	1372.57	1371.625	6908.8	1	1554	76.9	19	K.ATIAGGGVIPHIHK.S
gi|14165435|r	24	411	53.60%	463	50976	5.5	heterogeneous nuclear ribonucleoprotein K isoform b [Homo sapiens]				
gi|14165439|r	24	411	53.40%	464	51028	5.3	heterogeneous nuclear ribonucleoprotein K isoform a [Homo sapiens]				
gi|14165437|r	24	411	53.40%	464	51028	5.3	heterogeneous nuclear ribonucleoprotein K isoform a [Homo sapiens]				
	HsFlag-DPCD_Ti_20	4.4594	0.3903	1580.41	1580.709	8750.7	1	1614.6	79.2	6	K.RPAEDMEEEQAFK.R
	HsFLAG-p53-DNA-D	4.2225	0.4525	1735.84	1736.897	7303.3	1	1413.5	76.9	1	K.RPAEDMEEEQAFKR.S
	HsFlag-VPS71_Ti_1	2.0636	0.0937	729.55	729.855	4751.3	5	414.1	71.4	1	K.NAGAVIGK.G
	HsFLAG-FLJ20729_	3.684	0.236	1784.14	1781.83	4270.2	1	432.9	56.2	13	R.TDYNASVSVPDSSGPER.I
	HsFLAG-Lin9_Ti_20	5.4288	0.2928	1715.29	1716.025	8143.2	1	2154.5	76.7	90	R.ILSISADIETIGEILK.K
	HsFLAG-p53-DNA-D	4.3681	0.3647	1844.7	1844.199	10272.9	1	1356.2	59.4	11	R.ILSISADIETIGEILKK.I
	HsFlag-NUFIP_Ti_10	6.5926	0.4129	4185.69	4185.684	7498.7	1	1073.2	26.4	14	K.KIIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYK.G
	HsFLAG-UTX1_Ti_2	5.32	0.2271	4056.59	4057.51	5435	1	600.8	25	2	K.IIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYK.G

	HsFlag-VPS71_Ti_1	3.1261	0.2606	1099.29	1099.108	4459.9	5	727	81.2	2	K.GSDFDCELR.L
	HsFlag-NUFIP_Ti_2	4.6696	0.3998	1517.57	1519.871	7205.9	1	1602.6	75	5	R.LLIHQSLAGGIIGVK.G
	HsFlag-NUFIP_Ti_11	3.6738	0.1203	1518.9	1519.871	5994.2	1	1076.9	67.9	6	R.LLIHQSLAGGIIGVK.G
	HsFlag-VPS71_Ti_1	2.976	0.1126	1333.59	1333.484	6995.3	1	634.1	75	2	K.ELRENTQTTIK.L
	HsFLAG-p53-DNA-D	4.1596	0.2946	1550.03	1550.6	7686.2	1	1290.3	72.7	33	K.LFQECCPHSTDR.V
	HsFlag-VPS71_Ti_1	4.2103	0.2343	2585.19	2585.855	9169.4	1	1170.6	31	2	K.LFQECCPHSTDRVVLIGGKPDR.V
	HsFLAG-FLJ20729_	3.274	0.2561	1053.74	1054.278	6148.7	2	1111.9	83.3	22	R.VVLIGGKPDR.V
	HsFlag-NUFIP_Ti_2	4.8394	0.2806	1341.43	1341.631	8445.6	1	1884.7	81.8	36	K.IILDLISESPIK.G
	HsFLAG-p53-DNA-D	3.3999	0.1928	1341.82	1341.631	7956.6	1	710.1	63.6	10	K.IILDLISESPIK.G
	HsFlag-VPS71_Ti_1	3.2249	0.4284	3059.28	3060.249	4550.9	1	370.3	37.5	1	R.AQPYDPNFYDETYDYGGFTMMFDDR.R
	HsFLAG-ARP6_Ti_1	5.3093	0.3956	1917.12	1918.197	6253.6	1	1088.8	61.1	37	R.GSYGDLGGPIITTQVTIPK.D
	HsFLAG-p53-DNA-D	1.9309	0.1591	873.53	874.025	8213.5	1	728.1	75	1	K.DLAGSIIGK.G
	HsFLAG-p53-DNA-D	3.8613	0.3227	1259.91	1260.3	4944.5	1	1238.7	90	9	K.IDEPLEGSEDR.I
	HsFLAG-Lin9_Ti_20	6.3425	0.3952	3831.32	3832.213	9179	1	1133.7	25.8	3	K.IDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVK.Q
	HsFLAG-FLJ20309_	5.8294	0.3973	2590.9	2590.937	8461.4	1	1983.1	59.1	59	R.IITITGTQDQIQNAQYLLQNSVK.Q
	HsFlag-VPS71_Ti_1	6.7891	0.3569	2591.57	2590.937	11336.8	1	2038.3	35.2	45	R.IITITGTQDQIQNAQYLLQNSVK.Q
gi|16933546|r	13	54	53.60%	317	34274	6	ribosomal protein P0 [Homo sapiens]				
gi|4506667|re	13	54	53.60%	317	34274	6	ribosomal protein P0 [Homo sapiens]				
	HsFLAG-TCF3_Ti_1	2.8544	0.1604	1217.55	1218.436	9270.4	8	867.6	72.2	1	K.IIQLLDDYPK.C
	HsFLAG-ARP6_Ti_1	3.7857	0.2935	1218.67	1218.436	6828.6	3	1473.1	88.9	2	K.IIQLLDDYPK.C
	HsFLAG-ARP6_Ti_1	1.9059	0.1948	717.42	717.945	7227.4	5	538.6	66.7	1	K.AVVLMGK.N
	HsFlag-Ies6_293_Ti_	2.7323	0.2491	1221.32	1222.343	5096.6	3	473.7	60	2	R.GHLENNPALEK.L
	HsFLAG-p53-DNA-D	3.6373	0.2817	1222.89	1222.343	5747.6	1	1149.9	85	6	R.GHLENNPALEK.L
	HsFLAG-TCF3_Ti_1	3.3324	0.3577	1825.71	1826.059	7910.1	1	881.1	56.7	1	R.GNVGFVFTKEDLTEIR.D
	HsFLAG-ARP6_Ti_1	3.8678	0.3706	2179.42	2181.417	3426	1	521	54.8	5	R.AGAIAPCEVTVPAQNTGLGPEK.T
	HsFLAG-ARP6_Ti_1	4.6061	0.3448	1314.29	1314.524	8266.8	1	2246.1	90.9	6	K.TSFFQALGITTK.I
	HsFLAG-ARP6_Ti_1	4.1133	0.2876	1430.21	1429.697	6219.9	4	870.5	66.7	7	R.GTIEILSDVQLIK.T
	HsFLAG-ARP6_Ti_1	4.9592	0.4238	2788.5	2789.17	7792.9	1	1174.3	31	4	R.NVASVCLQIGYPTVASVPHSIINGYK.R
	HsFLAG-ARP6_Ti_1	4.8884	0.4658	2053.19	2053.363	5594.2	1	1440	67.6	9	K.RVLALSVETDYTFPLAEK.V
	HsFLAG-TCF3_Ti_1	4.9384	0.5219	2753.49	2754.158	4976.7	1	931.4	46.7	2	K.AFLADPSAFVAAAPVAAATTAAPAAAAAPAK.V
	HsFLAG-ARP6_Ti_1	5.4288	0.2899	3180.94	3181.659	6767.8	1	1117.6	27.9	8	K.AFLADPSAFVAAAPVAAATTAAPAAAAAPAKVEAK.E
gi|17933772|r	4	16	53.40%	103	11801	6.8	S100 calcium binding protein A16 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.0377	0.2938	1295.74	1295.565	6598.9	1	1342.7	80	4	K.AVIVLVENFYK.Y
*	HsMRGBP-FLAG_Ti_	2.8714	0.3129	1515.58	1515.684	8755.5	1	796	58.3	3	K.ELNHMLSDTGNRK.A
*	HsFlag-VPS71_Ti_1	3.9606	0.2933	1366.7	1366.476	7820.8	1	1706	86.4	3	K.LIQNLDANHDGR.I
*	HsFlag-VPS71_Ti_1	4.9324	0.2565	2083.4	2082.404	6205.4	1	1098.4	58.3	6	R.ISFDEYWTLIGGITGPIAK.L
gi|20070220|r	26	224	53.10%	637	72684	6.3	SKB1 homolog [Homo sapiens]				
*	HsFLAG-ARP6_Ti_2	5.1946	0.4258	1787.13	1786.986	2751.9	1	578.7	68.8	11	R.DLNCVPEIADTLGAVAK.Q
*	HsFLAG-FLJ20729_	3.142	0.4346	1751.03	1752.009	7308	2	558.3	53.8	7	K.QGFDFLCMPVFHPR.F
*	HsFlag-NUFIP_Ti_11	3.6752	0.2986	1752.16	1752.009	6631.7	1	945.2	46.2	3	K.QGFDFLCMPVFHPR.F
*	HsFlag-VPS71_Ti_1	2.6178	0.1607	1118.6	1118.278	4121.7	3	700.5	87.5	1	K.REFIQEPAK.N
*	HsFlag-FLJ90652_2	2.6158	0.1054	1045.35	1046.211	5656.2	2	868.2	81.2	6	R.DWNTLIVGK.L
*	HsFlag-FLJ90652_2	6.4074	0.4439	3848.69	3850.338	7917.3	1	1751.8	32.4	6	R.NSEAAMLQELNFGAYLGLPAFLLPLNQEDNTNLAR.V

*	HsFlag-NUFIP_Ti_1	3.4275	0.264	1109.42	1109.311	6605.8	2	1071.5	83.3	16	R.VPLVAPEDLR.D
*	HsFlag-VPS71_Ti_1	5.0254	0.3991	2280.81	2279.333	5042.8	1	1043.1	60.5	13	R.DDIIENAPTTHTEEYSGEEK.T
*	HsFLAG-ARP6_Ti_1	2.692	0.1495	1364.32	1364.569	6505	1	1124.8	87.5	1	K.TWMWWHNFR.T
*	HsFlag-FLJ90652_2	3.6996	0.2411	2005.73	2004.294	8047.9	2	863.3	50	1	R.IAVALEIGADLPSNHVIDR.W
*	HsFlag-VPS71_Ti_1	2.5957	0.2375	1389.52	1389.678	6026	3	418.8	54.2	1	K.AAILPTSIFLTNK.K
*	HsFlag-VPS71_Ti_1	4.3077	0.4366	1389.66	1389.678	3138	1	848.4	83.3	24	K.AAILPTSIFLTNK.K
*	HsARP6-FLAG_Ti_1	3.1522	0.2594	1517.38	1517.852	4242.2	1	454.2	61.5	3	K.AAILPTSIFLTNKK.G
*	HsFLAG-ARP6_Ti_1	1.9027	0.1552	875.23	876.087	4239.2	5	463	71.4	1	K.KGFPVLSK.M
*	HsFLAG-ARP6_Ti_1	3.2311	0.0923	876.3	876.087	3289.3	2	852.6	100	2	K.KGFPVLSK.M
*	HsFlag-FLJ90652_2	5.6089	0.4636	3343.94	3342.698	9846.9	1	1039.8	27.9	23	K.EFCSYLQYLEYLSQNRPPPNAYELFAK.G
*	HsFLAG-p53-DNA-D	4.5541	0.3257	3692.6	3692.085	4916.7	1	445.8	25	1	K.GYEDYLQSPLQPLMDNLESQTYEVFEKDPIK.Y
*	HsFlag-VPS71_Ti_1	2.9186	0.1393	1291.54	1292.434	8771	1	842.1	72.2	4	K.YSQYQQAIYK.C
*	HsFLAG-FLJ20729_	3.738	0.2497	1294.2	1292.434	6430.7	1	1248.3	88.9	11	K.YSQYQQAIYK.C
*	HsFLAG-FLJ20729_	3.8105	0.1816	1388.37	1388.527	6978	4	1467.2	85	3	K.CLLDRVPEEEK.D
*	HsFlag-FLJ20643_Ti	2.1587	0.0909	927.67	927.092	3040.6	6	140.5	68.8	1	R.GPLVNASLR.A
*	HsFLAG-ARP6_Ti_1	3.0009	0.1917	928.41	927.092	4495.7	1	882.7	87.5	7	R.GPLVNASLR.A
*	HsFlag-VPS71_Ti_1	5.7245	0.2148	3290.53	3290.617	6905.6	1	1197	32.8	32	K.ADIIVSELLGSFADNELSPECLDGAQHFLK.D
*	HsFLAG-ARP6_Ti_1	4.4815	0.5053	2170.59	2171.365	2996.2	1	466.1	57.5	29	K.DDGVSIPGEYTSFLAPISSSK.L
*	HsFlag-VPS71_Ti_1	3.7445	0.3664	1854.67	1853.059	3927.3	1	572.2	67.9	6	K.DRDPEAQFEMPYVVR.L
*	HsFLAG-ARP6_Ti_1	4.5472	0.4432	2415.83	2415.679	5542.7	1	658	50	11	K.VWYEWAVTAPVCSAIHNPTGR.S
gi|4757756|re	14	36	52.80%	339	38604	7.8	annexin A2 isoform 2 [Homo sapiens]				
gi|50845388|r	14	36	50.10%	357	40411	8.4	annexin A2 isoform 1 [Homo sapiens]				
gi|50845386|r	14	36	52.80%	339	38604	7.8	annexin A2 isoform 2 [Homo sapiens]				
	HsFlag-VPS71_Ti_1	4.7006	0.4008	1845.64	1846.004	3999.8	1	675.1	58.8	2	K.LSLEGDHSTPPSAYGSVK.A
	HsFlag-VPS71_Ti_1	4.9755	0.3423	2156.9	2156.357	9527.1	1	1703	58.3	4	K.AYTNFDAERDALNIETAIK.T
	HsFlag-VPS71_Ti_1	4.6366	0.377	1545.79	1543.761	7825.3	2	1412.5	69.2	3	K.GVDEVTIVNILTNR.S
	HsFlag-VPS71_Ti_1	5.5143	0.3919	1652.07	1651.987	7690.6	1	1532.2	66.7	2	K.SALSGHLETVILGLLK.T
	HsFlag-VPS71_Ti_1	3.0298	0.2405	1222.55	1223.325	4699.9	2	364.5	65	2	K.TPAQYDASELK.A
	HsFlag-VPS71_Ti_1	4.5309	0.3381	1779.71	1778.92	8664.5	1	1505.3	66.7	4	K.GLGTDEDSLIEIICSR.T
	HsFlag-VPS71_Ti_1	3.784	0.1427	1245.48	1245.335	8893.2	5	1396.8	83.3	2	R.TNQELQEINR.V
	HsFlag-VPS71_Ti_1	3.5438	0.3613	1354.95	1354.459	6328.9	1	942.1	72.7	2	K.DIISDTSGDFRK.L
	HsFlag-VPS71_Ti_1	4.4071	0.2774	1911.65	1910.001	7202.7	1	1101.3	59.4	2	R.AEDGSVIDYELIDQDAR.D
	HsFlag-VPS71_Ti_1	3.7581	0.3363	1461.69	1461.629	6535.9	1	1194.4	81.8	2	K.SYSPYDMLESIR.K
	HsFlag-VPS71_Ti_1	5.4387	0.3657	1976.99	1977.191	8279.6	1	1920.1	68.8	5	K.GDLENAFLNLVQCIQNK.P
	HsFlag-VPS71_Ti_1	3.9033	0.3522	2840.16	2840.174	7230.3	1	554.5	37	2	K.GDLENAFLNLVQCIQNKPLYFADR.L
	HsFlag-VPS71_Ti_1	4.5102	0.3094	2841.4	2840.174	5634.5	2	683.5	31.5	3	K.GDLENAFLNLVQCIQNKPLYFADR.L
	HsFlag-VPS71_Ti_1	1.961	0.3259	1096.45	1097.176	7032.6	6	595.9	55.6	1	K.ALLYLCGGDD.-
gi|5453597|re	10	26	52.40%	286	32923	5.7	F-actin capping protein alpha-1 subunit [Homo sapiens]				
*	HsFlag-FLJ90652_2	5.0952	0.2311	2089.41	2090.302	5807.2	1	1687	50	5	K.FITHAPPGEFNEVFNDVR.L
*	HsFLAG-p53-DNA-D	3.4989	0.3539	2090.06	2090.302	3673.9	1	420.1	52.9	5	K.FITHAPPGEFNEVFNDVR.L
	HsFlag-FLJ90652_2	3.7224	0.1765	1199.09	1198.408	6513.5	1	1344.7	94.4	5	R.LLLNNDNLLR.E
*	HsFlag-FLJ90652_2	5.2782	0.4116	4354.19	4353.723	11358.5	1	1096.1	22.4	1	F
*	HsFlag-FLJ90652_2	3.1525	0.3068	1542.66	1543.584	4532.1	2	590.5	64.3	2	K.EASDPQPEEADGGLK.S

*	HsFlag-FLJ90652_2	3.5417	0.2973	2314.54	2315.554	8045.8	1	993.1	52.6	2	K.TIDGQQTIIACIESHQFQPK.N
*	HsFLAG-ARP6_Ti_1	3.7527	0.2252	2316.8	2315.554	2908.3	1	335.6	35.5	1	K.TIDGQQTIIACIESHQFQPK.N
*	HsFlag-FLJ90652_2	2.7952	0.2627	1572.51	1571.9	6265.8	1	390.8	46.4	1	K.FTITPPTAQVVGVLK.I
	HsFlag-FLJ90652_2	4.9973	0.4721	2029.62	2030.247	9558.4	1	2401.2	75	2	K.IQVHYYEDGNVQLVSHK.D
*	HsFLAG-ARP6_Ti_1	4.6486	0.3437	1706.18	1706.804	6726.8	1	1317.5	70	2	K.DVQDSLTVSNEAQTAK.E
gi|4504253|re	6	58	52.40%	143	15145	10.7	H2A histone family, member X [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.1573	0.1473	944.77	945.109	5816.4	2	976.3	87.5	4	R.AGLQFPVGR.V
	HsFLAG-Lin9_Ti_20	5.4913	0.4094	2916.83	2917.375	9478.7	1	1610.8	32.1	3	R.VGAGAPVYLAAVLEYLTAEILELAGNAAR.D
	HsFLAG-Lin9_Ti_20	5.6884	0.3714	2917.12	2917.375	9129.3	1	1489.7	42.9	5	R.VGAGAPVYLAAVLEYLTAEILELAGNAAR.D
	HsFLAG-ARP6_Ti_1	4.029	0.2972	1693.82	1693.9	8806.2	2	1211.8	69.2	9	R.HLQLAIRNDEELNK.L
	HsFLAG-UTX1_Ti_2	5.5814	0.272	2271.31	2272.78	5991.5	1	679	47.7	34	K.LLGGVTIAQGGVLPNIQAVLLPK.K
	HsFLAG-ARP6_Ti_1	5.3074	0.2108	2272.4	2272.78	7635.3	1	1565.9	40.9	3	K.LLGGVTIAQGGVLPNIQAVLLPK.K
gi|5453607|re	26	183	52.30%	543	59367	7.6	chaperonin containing TCP1, subunit 7 isoform a [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.0742	0.3168	2830.89	2831.075	4591.7	1	356.9	34.6	2	K.EGTDSSQGIPQLVSNISACQVIAEAVR.T
*	HsFLAG-ARP6_Ti_1	2.6331	0.211	1064.52	1063.285	4820.5	1	505.1	66.7	6	K.LLDVVHPAAK.T
*	HsFLAG-ARP6_Ti_1	3.6471	0.3747	1064.6	1063.285	4791.7	6	921.6	83.3	5	K.LLDVVHPAAK.T
*	HsFLAG-ARP6_Ti_1	5.9376	0.5559	2253.84	2253.468	6502.7	1	1758.6	66.7	33	K.SQDAEVGDGTTSVTLLAAEFLK.Q
*	HsFLAG-ARP6_Ti_1	5.1981	0.3087	2254.74	2253.468	9357	1	1774.6	38.1	5	K.SQDAEVGDGTTSVTLLAAEFLK.Q
*	HsFLAG-ARP5_Ti_1	2.8657	0.3561	2019.8	2020.382	6347.5	1	482.7	46.9	3	K.QVKPYVEEGLHPQIIIR.A
*	HsFLAG-ARP6_Ti_1	4.0077	0.392	1665.38	1664.945	3760.4	3	548.3	42.3	1	K.PYVEEGLHPQIIIR.A
*	HsFLAG-ARP6_Ti_1	4.3819	0.3859	1666	1664.945	5090.7	1	1253.4	80.8	2	K.PYVEEGLHPQIIIR.A
*	HsFLAG-ARP6_Ti_1	5.0177	0.3226	1835.7	1835.286	8891.3	1	2709	80	8	K.MVVDAVMMLDDLLQLK.M
*	HsFLAG-ARP6_Ti_1	5.7798	0.5256	1917.19	1918.2	9625.5	1	3406.6	77.8	7	K.KVQGGALEDSQLVAGVAFK.K
	HsFLAG-ARP6_Ti_1	3.3405	0.1006	1255.8	1255.541	5541.9	3	918.4	80	3	K.IALLNVELELK.A
	HsFLAG-ARP6_Ti_1	5.1866	0.4052	2521.81	2522.773	7909.5	1	1503.2	57.5	2	R.VHTVEDYQAIVDAEWNILYDK.L
	HsFLAG-ARP6_Ti_1	6.692	0.443	2892.54	2893.222	6406.4	1	1106.8	37	23	R.VHTVEDYQAIVDAEWNILYDKLEK.I
	HsFLAG-ARP6_Ti_1	4.4023	0.3619	1566.26	1566.754	7942.8	1	2390	88.5	6	K.LPIGDVATQYFADR.D
	HsFLAG-ARP6_Ti_1	4.2092	0.3393	3214.92	3215.571	6798.5	1	597.5	26.9	3	K.LPIGDVATQYFADRDMFCAGRVPEEDLK.R
	HsFLAG-ARP6_Ti_1	4.3253	0.3686	2496.32	2496.826	9511.1	1	1655.6	37	1	K.RTMMACGGSIQTSVNALSADVLGR.C
	HsFLAG-ARP6_Ti_1	5.8698	0.5489	2339.52	2340.638	9328.3	1	2613	65.9	2	R.TMMACGGSIQTSVNALSADVLGR.C
	HsFLAG-ARP6_Ti_1	2.2226	0.3025	1133.12	1134.243	6595.8	1	503.5	68.8	1	R.YNFFTGCPK.A
	HsFLAG-ARP6_Ti_1	3.0882	0.2804	1134.19	1134.243	5234.4	1	998.3	93.8	1	R.YNFFTGCPK.A
	HsFLAG-ARP6_Ti_1	2.6952	0.1912	1154.48	1155.401	4212.1	1	594.1	72.2	5	R.SLHDAIMIVR.R
	HsFLAG-ARP6_Ti_1	3.5328	0.315	1155.79	1155.401	4525.4	1	958.6	88.9	8	R.SLHDAIMIVR.R
	HsFLAG-ARP6_Ti_1	1.8789	0.2265	1104.28	1105.323	2808.5	3	178.2	72.2	1	K.QQLLIGAYAK.A
	HsFLAG-ARP6_Ti_1	5.2815	0.4657	3653	3653.964	7956.9	1	839	25	7	R.HAQGGTWYGVDINNEDIADNFEAFVWEPAMVR.I
	HsFLAG-ARP6_Ti_1	5.7038	0.4229	2289.42	2290.582	6673.7	1	1634.2	42.9	18	R.INALTAASEAACLIVSVDETIK.N
	HsFLAG-ARP6_Ti_1	5.2334	0.4947	2289.71	2290.582	7942	1	1302.4	54.8	24	R.INALTAASEAACLIVSVDETIK.N
	HsFLAG-ARP5_Ti_1	4.789	0.439	2658.13	2657.99	6276.2	1	1486.5	37.5	6	R.INALTAASEAACLIVSVDETIKNPR.S
gi|14591909|	14	86	52.20%	297	34363	9.7	ribosomal protein L5 [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	3.2125	0.2659	1695.48	1693.91	10456.5	1	1208.5	61.5	1	R.VTNRDIICQIAYAR.I
*	HsFLAG-ARP6_Ti_1	4.0305	0.3234	1918.24	1918.181	6057.5	1	1223	65.6	5	R.IEGDMIVCAAYAHELPK.Y
*	HsFLAG-ARP6_Ti_1	3.6956	0.104	1918.44	1918.181	2764.7	1	730.1	50	1	R.IEGDMIVCAAYAHELPK.Y

*	HsFlag-NUFIP_Ti_11	5.6926	0.5489	1927.94	1928.205	7692.9	1	1908.3	70.6	32	K.VGLTNYAAAYCTGLLLAR.R
*	HsFLAG-TCF3_Ti_1	4.097	0.2712	3839.36	3839.083	9235	1	644.8	22.8	4	K.IYEGQVEVTGDEYNVESIDGQPGAFTCYLDAGLAR.T
	HsFLAG-TCF3_Ti_1	3.0837	0.3144	1339.44	1339.491	5312.9	1	540.1	53.8	5	K.GAVDGGLSIPHSTK.R
	HsFLAG-TCF3_Ti_1	4.3443	0.334	1339.55	1339.491	5330.6	1	1242.6	73.1	15	K.GAVDGGLSIPHSTK.R
*	HsFlag-Ies6_293_Ti_	3.1039	0.2148	1186.39	1186.266	4563.3	3	724.5	77.8	5	K.RFPGYDSESK.E
	HsFlag-NUFIP_Ti_1	2.7438	0.2254	1002.12	1002.074	4232.6	5	454.5	85.7	2	K.EFNAEVHR.K
	HsFLAG-TCF3_Ti_1	2.5478	0.1733	1130.53	1130.249	7159.6	5	507.4	68.8	1	K.EFNAEVHRK.H
*	HsFlag-NUFIP_Ti_1	4.1787	0.3444	1435.43	1435.659	4128.4	1	1179.6	90.9	9	K.HIMGQNVADYMR.Y
*	HsFlag-NUFIP_Ti_1	2.8373	0.2685	1435.61	1435.659	5661.2	3	440.8	59.1	3	K.HIMGQNVADYMR.Y
*	HsFlag-Ies6_293_Ti_	3.4582	0.2226	1534.47	1534.678	6348	1	1310.6	81.8	2	R.YLMEEDEDAYKK.Q
*	HsFLAG-ARP6_Ti_1	3.5728	0.3501	1704.32	1703.981	4019.2	1	528.3	65.4	1	K.NSVTPDMMEEMYKK.A
gi|4507129|re	3	36	52.20%	92	10804	9.4	small nuclear ribonucleoprotein polypeptide E [Homo sapiens]				
	HsFlag-NUFIP_Ti_1	3.5115	0.2383	1330.56	1330.675	4657.9	1	765.5	80	21	K.VMVQPINLIFR.Y
	HsFlag-VPS71_Ti_1	6.5728	0.3545	2915.07	2912.204	5474.5	1	1148.3	36.5	13	R.IEGCIIGFDEYMNLVLDDAEEIHSK.T
	HsFLAG-TCF3_Ti_1	3.2466	0.1744	1262.67	1261.375	6961.7	1	855.9	68.2	2	K.GDNITLLQSVSN.-
gi|13699824|r	53	472	51.90%	1056	119159	5.6	kinesin family member 11 [Homo sapiens]				
*	HsFLAG-ARP8_Ti_2	2.512	0.2111	1162.96	1163.288	5844.1	1	699	81.2	1	R.CRPFNLAER.K
*	HsFLAG-ARP8_Ti_2	3.6228	0.4237	1569.68	1569.724	6705.3	1	1061.2	69.2	28	K.ASAHSIVECDPVRK.E
*	HsFLAG-TIP49a_Ti_	4.9394	0.4141	3168.5	3169.446	8174.1	1	998.7	27.9	3	K.TFTMEGERSPNEEYTWEEDPLAGIIPR.T
*	HsFLAG-Lin9_Ti_20	5.8273	0.5301	2216.74	2217.397	9378.5	1	2328	66.7	29	R.SPNEEYTWEEDPLAGIIPR.T
*	HsFlag-FLJ90652_2	1.9307	0.149	1015.44	1016.185	4588.3	6	338.8	64.3	1	R.TLHQIFEK.L
*	HsFLAG-RPB5MP_2	2.839	0.1141	1016.19	1016.185	5646.1	5	659.4	85.7	5	R.TLHQIFEK.L
*	HsFLAG-RPB5MP_2	2.9366	0.2082	1211.06	1211.314	5525.9	2	675.1	75	1	K.LTDNGTEFSVK.V
*	HsFLAG-Lin9_Ti_20	3.7905	0.3635	2782.9	2783.061	10191.6	1	1148.9	33.7	1	K.VSLLEIYNEELFDLLNPSSDVSER.L
*	HsFlag-NUFIP_Ti_1	5.1961	0.2798	2783.34	2783.061	8903.3	2	795.7	39.1	37	K.VSLLEIYNEELFDLLNPSSDVSER.L
*	HsFLAG-RPB5MP_2	4.3937	0.2807	2258.07	2258.533	9584.7	1	1117.5	52.8	3	K.GLEEITVHNKDEVYQILEK.G
*	HsFLAG-RPB5MP_2	4.5217	0.3151	2260.61	2258.533	8099.4	1	1023.2	37.5	3	K.GLEEITVHNKDEVYQILEK.G
*	HsFLAG-KIAA0515_	2.7163	0.1524	1136.42	1137.275	9287.1	7	1027.9	75	1	K.DEVYQILEK.G
*	HsFLAG-KIAA0515_	2.8092	0.1165	1137.96	1137.275	4147.2	5	816	81.2	2	K.DEVYQILEK.G
*	HsFLAG-ARP8_Ti_2	4.6717	0.4222	1544.58	1543.738	8293.4	1	1099.4	69.2	7	K.RTTAATLMNAYSSR.S
*	HsFLAG-KIAA0515_	2.8433	0.2948	1389.14	1387.551	5747.1	1	644.9	62.5	1	R.TTAATLMNAYSSR.S
*	Hs293Flag-Ies2_Ti_1	5.4227	0.2156	1470.66	1471.654	8066.9	1	2305.6	88.5	29	K.LNLVDLAGSENIGR.S
*	HsFLAG-ARP6_Ti_1	4.2412	0.3831	1486.21	1486.668	8615.7	1	1163.2	69.2	21	R.EAGNINQSLLTLGR.V
*	HsFLAG-RPB5MP_2	2.5072	0.2139	959.12	959.09	4637.6	1	1012.1	87.5	1	R.ILQDSLGGR.T
*	HsFLAG-Lin9_Ti_20	3.5127	0.1891	2831.57	2832.18	4635.2	1	566.5	29	1	R.TSIIATISPASLNLEETLSTLEYAHR.A
*	Hs293Flag-Ies2_Ti_1	3.348	0.357	2833.61	2832.18	9393	1	618.5	36	4	R.TSIIATISPASLNLEETLSTLEYAHR.A
*	HsFlag-FLJ20643_Ti	3.5177	0.0861	1298.64	1297.497	5740.8	3	931	80	12	K.NILNKPEVNQK.L
*	HsFLAG-KIAA0515_	1.9392	0.2153	1068.41	1069.113	1951	6	113.8	64.3	1	K.EYTEEIER.L
*	HsFLAG-RPB5MP_2	3.0582	0.1397	1328.31	1328.424	5155.6	1	1084.6	80	4	K.NGVYISEENFR.V
*	HsFLAG-KIAA0515_	5.1219	0.2516	1673.35	1671.929	6407.1	1	1391.9	76.9	34	K.LTVQEEQIVELIEK.I
*	HsFLAG-KIAA0515_	2.5378	0.1796	1129.42	1130.243	3469.4	1	375.8	72.2	1	K.IGAVEEELNR.V
*	HsFLAG-RPB5MP_2	3.7007	0.2857	1130.19	1130.243	5310.1	1	1354.4	94.4	4	K.IGAVEEELNR.V
*	HsFLAG-KIAA0515_	2.5167	0.1318	1096.5	1097.271	6053.6	4	543.2	75	2	R.VTELFMDNK.N

*	HsFLAG-ARP6_Ti_1	4.5941	0.4132	1986.43	1985.182	9633.9	1	1956.1	70	2	R.VTELFMDNKNELDQCK.S
*	Hs293Flag-Ies2_Ti_1	6.2264	0.5225	2211.27	2211.471	9667.6	1	3249.5	77.8	10	K.LQLVKEEYITSALESTEEK.L
*	HsFLAG-ARP6_Ti_1	5.0683	0.3783	2212.01	2211.471	8110.6	1	1162.9	37.5	1	K.LQLVKEEYITSALESTEEK.L
*	HsFLAG-RPB5MP_2	4.6467	0.4329	2933.22	2934.27	7798	1	1421.8	37	1	K.LQLVKEEYITSALESTEEKLHDAASK.L
*	HsFlag-Ies6_293_Ti_	3.7994	0.3777	1629.26	1629.715	7016.4	1	1249.7	73.1	6	K.EEYITSALESTEEK.L
*	HsTIP60_Ti_102.148	2.7778	0.1187	1147.45	1148.299	7319.6	6	566.8	72.2	6	K.LLNTVEETTK.D
*	HsTIP60_Ti_102.148	3.4118	0.2117	1147.83	1148.299	4225.6	1	950.3	88.9	2	K.LLNTVEETTK.D
*	HsFlag-Ies6_293_Ti_	4.9945	0.3763	1642.87	1643.753	8414.9	1	2009.8	75	33	K.AVDQHNAEAQDIFGK.N
*	HsFLAG-TCF3_Ti_1	4.551	0.3772	1679.81	1679.929	5528.1	1	912.4	69.2	16	K.NLNSLFNNMEELIK.D
*	HsFlag-FLJ90652_2	4.5436	0.1865	1270.57	1270.555	10122.4	1	1954.7	85	31	K.TVLQELINVLK.T
*	HsFLAG-FLJ20729_	3.6589	0.2703	2159.65	2160.615	5710.1	1	743	47.4	2	K.TDLLSSLEMILSPTVVSILK.I
*	HsFLAG-ARP8_Ti_1	2.0899	0.2354	835.35	834.945	5703	6	414.1	71.4	2	K.TSLTVADK.I
*	HsFLAG-RPB5MP_2	2.5145	0.1827	1576.07	1576.787	6560.3	5	702.2	57.7	1	K.TSLTVADKIEDQKK.E
*	HsFLAG-TCF3_Ti_1	6.4375	0.3959	3404.32	3405.716	11581.9	1	1824.9	32.1	35	K.ELDGFLSILCNNLHELQENTICSLVESQK.Q
*	HsFLAG-FLJ20436_	1.9212	0.0829	896.41	896.982	7882.1	1	954.8	83.3	1	R.FCALEEK.C
*	Hs293Flag-Ies2_Ti_1	5.2854	0.2735	2143.45	2144.356	5057.9	1	1187.1	70.6	4	K.CENIQKPLSSVQENIQQK.S
*	HsFLAG-RPB5MP_2	4.9439	0.4568	1533.44	1532.573	5820.1	1	1669.4	87.5	7	K.FCADSDGFSQELR.N
*	HsFLAG-ARP6_Ti_1	3.4689	0.2991	1844.89	1846.006	9476.9	1	845.4	57.1	10	R.TVYFSEQWVSSLNER.E
*	HsFLAG-ARP6_Ti_1	5.6847	0.3762	2907.15	2907.047	9442.5	1	1943.6	36.5	7	R.EQELHNLLEVVSQCCEASSSDITEK.S
*	Hs293Flag-Ies2_Ti_1	3.4903	0.253	1849.19	1848.037	4335.9	2	378.6	57.1	1	K.QHNIFLDQMTIDEDK.L
*	HsFLAG-RPB5MP_2	4.529	0.173	1499.05	1499.748	6818.4	1	1591.2	83.3	27	K.LIAQNLELNETIK.I
*	HsFLAG-ARP6_Ti_1	3.7306	0.1746	1279.91	1280.43	6511.4	2	1326	88.9	12	K.LNCFLEQDLK.L
*	HsFLAG-RPB5MP_2	2.8012	0.0962	1200.53	1199.349	4312.7	2	683	85	1	K.LDIPTGTTPQR.K
*	HsFLAG-Lin9_Ti_20	2.5771	0.1238	1199.39	1199.392	5132.9	3	651.9	72.2	1	K.SYLYPSTLVR.T
*	Hs293Flag-Ies2_Ti_1	2.1851	0.2436	1500.37	1501.677	4035.1	1	289.6	54.2	1	R.SKVEETTEHLVTK.S
*	HsFlag-Ies6_293_Ti_	4.6779	0.2924	1501.59	1501.677	7774.1	1	2145.1	87.5	15	R.SKVEETTEHLVTK.S
gi|4506669|re	2	29	51.80%	114	11514	4.3	ribosomal protein P1 isoform 1 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.9266	0.2884	1705.72	1703.981	4430.2	1	618.8	60	18	K.AAGVNVEPFWPGLFAK.A
	HsFlag-NUFIP_Ti_1	6.097	0.513	3809.88	3811.21	10667.4	1	1285.5	23.8	11	EEK.K
gi|39930355|r	12	67	51.70%	203	23240	9	DPCD protein [Homo sapiens]				
*	HsFlag-DPCD_Ti_20	3.0529	0.201	1203.32	1204.414	5906.3	2	719.1	72.2	2	R.KVHYLFPDGK.E
*	HsFlag-DPCD_Ti_20	3.5302	0.2407	1204.28	1204.414	7482.9	1	1257.6	83.3	2	R.KVHYLFPDGK.E
*	HsFlag-DPCD_Ti_20	2.8743	0.2585	1075.46	1076.24	4089.4	1	492.3	68.8	9	K.VHYLFPDGK.E
*	HsFlag-DPCD_Ti_20	2.8855	0.1751	1075.68	1076.24	3952.1	1	660.9	81.2	5	K.VHYLFPDGK.E
*	HsFlag-DPCD_Ti_20	4.9201	0.493	2990.01	2991.432	6591.4	1	886.4	39.7	8	K.SALGAMGQWQLEVGDPAPLGAGNLGPELIK.E
*	HsFlag-DPCD_Ti_20	6.3572	0.4453	2993.04	2991.432	10144.1	1	1732.9	31.9	23	K.SALGAMGQWQLEVGDPAPLGAGNLGPELIK.E
*	HsFlag-DPCD_Ti_20	2.9988	0.2372	1180.13	1179.336	5060.3	1	723.9	83.3	2	K.ESNANPIFMR.K
*	HsFLAG-TIP49b_Ti_	2.1353	0.3102	1139.79	1140.235	7888.4	9	459.8	61.1	1	K.DVYSVSVDQK.E
*	HsFlag-DPCD_Ti_20	2.5012	0.1524	1092.48	1091.252	4838.3	2	357.7	68.8	3	K.KFSIPDLDR.H
*	HsFlag-DPCD_Ti_20	4.8963	0.3676	2869.63	2870.244	6257.7	1	857.8	33.3	2	R.HQLPLDDALLSFAHANCTLIISYQK.P
*	HsFlag-DPCD_Ti_20	3.3754	0.2447	1230.48	1231.389	5849.4	1	665.7	75	5	K.EVVVAESELQK.E
*	HsFlag-DPCD_Ti_20	3.725	0.2527	1231.26	1231.389	6444.6	1	1310	85	5	K.EVVVAESELQK.E
gi|13569879|r	10	107	51.50%	268	30692	3.8	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E [Homo sapiens]				

*	HsH2AZ-FLAG_293_	3.8814	0.4179	3465.25	3466.713	8644.5	1	830.8	25.9	1	R.NRSPEEVTELVLDNCLCVNGEIEGLNDTFK.E
*	HsH2AZ-FLAG_293_	5.5787	0.4846	1910.6	1910.193	8821.3	1	2393.7	75	14	K.ELEFLSMANVELSSLAR.L
*	HsH2AZ-FLAG_293_	6.9513	0.3888	2027.87	2029.339	7369.1	1	3449.8	83.3	20	R.KLELSDNIISGGLEVLAEK.C
*	HsH2AZ-FLAG_293_	6.6681	0.2118	2030.27	2029.339	6107.4	1	3444.5	59.7	10	R.KLELSDNIISGGLEVLAEK.C
*	HsH2AZ-FLAG_293_	5.2324	0.4269	1902.06	1901.164	6630	1	1891.6	76.5	18	K.LELSDNIISGGLEVLAEK.C
*	HsH2AZ-FLAG_293_	4.4296	0.3181	1496.51	1494.654	5467.4	1	1081.5	83.3	2	K.CPNLTYLNLSGNK.I
*	HsH2AZ-FLAG_293_	3.4931	0.1954	1330.51	1331.509	5549.1	2	525.9	63.6	2	K.DLSTVEALQNLK.N
*	HsH2AZ-FLAG_293_	4.9223	0.1468	1331.31	1331.509	6288.2	1	1490.8	86.4	3	K.DLSTVEALQNLK.N
*	HsH2AZ-FLAG_293_	6.1031	0.4501	2002.25	2003.139	8011	1	2170.2	76.7	30	K.SLDLFNCEITNLEDYR.E
*	HsH2AZ-FLAG_293_	5.8504	0.3663	3661.28	3660.526	8235.5	1	1275.2	30.8	7	K.EEIQDEEDDDDYVEEGEEEEEEEEGGLRGEK.R
gi|24041018|r	9	105	51.50%	169	19597	7.1	ubiquitously-expressed transcript isoform 1 [Homo sapiens]				
gi|4759298|re	9	105	55.40%	157	18246	7.6	ubiquitously-expressed transcript isoform 2 [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.6016	0.4252	1740.3	1740.012	5732.5	1	1097.1	73.1	3	K.VLRYETFISDVLQR.D
	HsFlag-NUFIP_Ti_1(	4.3457	0.4019	1371.51	1371.533	6141.2	1	1310.4	85	40	R.YETFISDVLQR.D
	HsFLAG-p53-DNA-D	2.6068	0.1816	1094.49	1094.253	6544	9	476	62.5	1	R.DKVYEQLAK.Y
	HsFlag-NUFIP_Ti_11	2.8979	0.31	2931.18	2931.212	9848.1	1	818.4	39.6	1	K.HSELYMQVDLGCNFFVDTVVPDTSR.I
	HsFLAG-p53-DNA-D	4.1065	0.3488	1521.53	1521.751	6485.4	1	980.7	69.2	3	R.KSSLLTELSNSLTK.D
	HsFLAG-p53-DNA-D	2.4989	0.184	1392.69	1393.577	5331.7	1	403.2	58.3	1	K.SSLLTELSNSLTK.D
	HsFlag-NUFIP_Ti_1(	4.9752	0.3504	1393.46	1393.577	8384.9	1	1887.6	83.3	15	K.SSLLTELSNSLTK.D
	HsFlag-NUFIP_Ti_11	4.0094	0.3764	1290.53	1290.569	6238	1	1412.7	85	21	K.AHIHMLLEGLR.E
	HsFLAG-UTX1_Ti_2(	4.097	0.2691	1675.26	1674.856	6885.4	3	593	57.7	20	R.ELQGLQNFPEKPHH.-
gi|27734727|r	13	381	51.20%	244	26478	8.3	hypothetical protein LOC283899 [Homo sapiens]				
*	HsFlag-FLJ90652_2(	4.205	0.2899	1912.97	1914.091	4151.7	1	779.5	48.1	2	K.FLIYEHECFQEELR.K
*	HsFlag-FLJ90652_2(	5.1907	0.3809	1914.37	1914.091	8566.7	1	1996	80.8	114	K.FLIYEHECFQEELR.K
*	HsFlag-FLJ90652_2(	5.3393	0.3415	2041.44	2042.265	8263.3	1	1524.3	71.4	102	K.FLIYEHECFQEELRK.A
*	HsFlag-FLJ90652_2(	3.8939	0.2307	2041.58	2042.265	4141.7	1	738	46.4	6	K.FLIYEHECFQEELRK.A
*	HsFLAG-TCF3_Ti_1(	5.127	0.3969	3853.54	3853.321	4443.5	1	378.6	20.5	1	.Y
*	HsFlag-FLJ90652_2(	4.8437	0.3612	2526.67	2526.938	5810.8	1	671.1	50	28	R.YPPFPSDYLALQLPEPSPLRPK.R
*	HsFlag-FLJ90652_2(	5.5464	0.448	1925.84	1926.207	7738	1	1674.9	44.4	2	K.MAVGPPDCPVGGPLTFPGR.G
*	HsFLAG-ARP8_Ti_2	4.857	0.5262	1926.05	1926.207	7898.2	1	1346.4	63.9	19	K.MAVGPPDCPVGGPLTFPGR.G
*	HsFLAG-ARP8_Ti_2	3.1693	0.3504	1549.74	1550.795	8032.5	1	591.9	53.1	14	R.GSGAGVGTTLTPLPPPK.M
*	HsFlag-FLJ90652_2(	5.0166	0.4332	1550.62	1550.795	7569.3	1	1165.3	62.5	70	R.GSGAGVGTTLTPLPPPK.M
*	HsFLAG-ARP5_Ti_1	4.632	0.2678	2842.08	2841.382	5524.7	1	991	31.2	3	R.GSGAGVGTTLTPLPPPKMPPPTILSTVPR.Q
*	HsFlag-FLJ90652_2(	2.166	0.2555	1307.73	1309.61	3409.3	1	285.9	63.6	2	K.MPPPTILSTVPR.Q
*	HsFlag-FLJ90652_2(	3.9532	0.2593	1309.63	1309.61	3750.3	2	640.9	81.8	18	K.MPPPTILSTVPR.Q
gi|4506643|re	4	7	51.10%	92	10275	10.4	ribosomal protein L37a [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1(	2.4549	0.1779	1053.51	1054.235	5423	1	568.9	68.8	1	K.KIEISQHAK.Y
	HsFLAG-TCF3_Ti_1(	1.8646	0.2098	1022.42	1023.063	6506.6	1	517.9	71.4	1	K.YTCSFCGK.T
*	HsFLAG-ARP6_Ti_1	3.6797	0.288	1405.99	1406.575	5109.9	1	1129.4	81.8	2	R.AVGIWHCGSCMK.T
*	HsFLAG-ARP6_Ti_1	4.4349	0.4071	1828.44	1828.032	6758.7	1	991.2	58.8	3	K.TVAGGAWTYNTTSAVTVK.S
gi|4506003|re	15	137	50.90%	330	37512	6.3	protein phosphatase 1, catalytic subunit, alpha isoform 1 [Homo sapiens]				
*	HsFLAG-UTX1_Ti_2(	3.3467	0.154	1184.34	1184.381	6364.3	9	1446.9	85	10	R.LLEVQGSRPGK.N
	HsFlag-NUFIP_Ti_1(	5.6621	0.4071	2196.86	2197.623	6879.7	1	1530.1	63.9	15	K.SREIFLSQPILLELEAPLK.I

	HsFlag-NUFIP_Ti_1	5.5555	0.2355	2197.28	2197.623	5469.5	1	994	41.7	8	K.SREIFLSQPILLELEAPLK.I
	HsFLAG-UTX1_Ti_2	5.8482	0.3752	1954.5	1954.357	3528.8	1	1020.8	78.1	26	R.EIFLSQPILLELEAPLK.I
	HsFlag-NUFIP_Ti_1	5.236	0.4906	2597.77	2599.858	3690.3	1	845	59.5	11	R.LFEYGGFPPESNYLFLGDYVDR.G
	HsFLAG-UTX1_Ti_2	3.1849	0.2992	1553.73	1552.818	5504.8	1	712.9	70.8	6	K.QSLETICLLLAYK.I
	HsFLAG-p53-DNA-D	2.758	0.1574	1441.48	1440.728	4335.3	1	826.3	80	1	K.IKYPENFFLLR.G
	HsFLAG-UTX1_Ti_2	3.0584	0.3282	1199.35	1199.395	4678.9	1	820	93.8	2	K.YPENFFLLR.G
	HsFlag-NUFIP_Ti_1	5.4504	0.4606	2114.06	2115.32	6688.8	1	1505.3	70.6	19	K.TFTDCFNCLPIAAIVDEK.I
	HsFlag-NUFIP_Ti_1	5.5834	0.4263	2249.12	2249.479	7631.2	1	1500.9	61.1	13	K.IFCCHGGLSPDLQSMEQIR.R
	HsFlag-NUFIP_Ti_1	4.7195	0.3543	2249.42	2249.479	8083.2	1	1565.6	43.1	6	K.IFCCHGGLSPDLQSMEQIR.R
	HsFlag-NUFIP_Ti_1	3.2996	0.1719	2686.23	2686.018	8541.8	2	442.3	36.4	1	R.IMRPTDVPDQGLLCDLLWSDPDK.D
	HsFLAG-p53-DNA-D	4.5257	0.4111	1641.05	1640.792	7920.9	1	2058	80.8	15	R.AHQVVEDGYEFFAK.R
	HsFLAG-p53-DNA-D	3.9193	0.406	1914.81	1915.162	8182.1	1	516.1	47.1	2	K.YGQFSGLNPGGRPITPPR.N
	HsFLAG-p53-DNA-D	4.1049	0.2606	1915.58	1915.162	5537.8	1	782.9	36.8	2	K.YGQFSGLNPGGRPITPPR.N
gi|13129110|r	13	117	50.60%	342	36724	5.2	methylosome protein 50 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.9544	0.1777	1373.27	1373.638	8127.2	4	697.7	58.3	2	R.KETPPPLVPPAAR.E
*	HsFLAG-ARP6_Ti_1	4.9949	0.2947	1722.78	1723.927	5089.5	1	1496.9	75	13	R.YRSDGALLLGASSLSGR.C
*	HsFLAG-ARP6_Ti_1	3.6178	0.1857	1723.5	1723.927	7770.3	1	1382.5	42.2	2	R.YRSDGALLLGASSLSGR.C
*	HsFLAG-Lin9_Ti_20	4.3676	0.4338	1403.43	1404.563	8482.1	1	1491.1	67.9	7	R.SDGALLLGASSLSGR.C
*	HsFlag-FLJ90652_2	3.3379	0.2765	1268.83	1268.467	5829.1	1	1128.5	88.9	11	R.CWAGSLWLFK.D
*	HsFlag-NUFIP_Ti_11	3.0742	0.2816	2788.7	2789.109	8975.6	2	407.9	30	1	R.GILVASDSGAVELWELDENETLIVSK.F
*	HsFlag-FLJ90652_2	6.5755	0.5295	2466.79	2467.649	9912.9	1	2364.2	58.7	27	K.YEHDDIVSTVSVLSSGTQAVSGSK.D
*	HsFlag-FLJ90652_2	4.8468	0.0903	1664.68	1664.902	7203.1	1	2355.3	84.6	11	K.VWDLAQQVVLSSYR.A
*	HsFlag-VPS71_Ti_1	3.7869	0.4554	1547.67	1548.708	5626.6	1	661.6	57.1	10	R.AHAAQVTCVAASPHK.D
*	HsFLAG-ARP6_Ti_1	5.447	0.4686	1548.15	1548.708	9133.1	1	2771.1	82.1	28	R.AHAAQVTCVAASPHK.D
*	HsFlag-FLJ90652_2	3.5338	0.3614	1548.93	1548.708	6829.3	1	1291.4	50	1	R.AHAAQVTCVAASPHK.D
*	HsFlag-Ies6_293_Ti_	3.7432	0.4088	1429.4	1429.449	5136.3	1	914.5	77.3	1	K.DSVFLSCSEDNR.I
*	HsFlag-FLJ90652_2	4.638	0.2938	4492.51	4492.909	6230.5	1	423.7	20.1	3	DTK.S
gi|11321634|r	29	59	50.10%	639	71451	6.4	CD2-associated protein [Homo sapiens]				
*	HsFlag-FLJ90652_2	3.7039	0.252	1758.91	1758.929	9877	1	1756.5	71.4	2	K.KLQEEGWLEGELNGR.R
*	HsFlag-FLJ90652_2	3.5643	0.2448	1081.49	1081.22	7655.6	1	1931.8	94.4	2	R.HGNVASLVQR.I
*	HsFlag-FLJ90652_2	2.8391	0.3715	1865.42	1866.127	4272.1	1	428.4	52.9	2	R.ISTYGLPAGGIQPHPQTK.N
*	HsFlag-FLJ90652_2	4.1123	0.255	1979.01	1980.222	3606.4	1	580.3	63.3	1	K.VLFEYIPQNEDELELK.V
*	HsFlag-FLJ90652_2	4.7784	0.3996	2619.08	2618.816	9247.3	1	924.5	45.5	5	K.VGDIIDINEEVEEGWWSGTLNNK.L
*	HsFlag-FLJ90652_2	2.0618	0.1549	1121.47	1122.353	6081.1	4	479.3	66.7	1	K.LGLFPSNFVK.E
*	HsFlag-FLJ90652_2	2.0037	0.2865	953.34	954.114	5796.7	4	481.7	68.8	1	R.GIGFGDIFK.E
*	HsFlag-FLJ90652_2	4.0956	0.389	1537.43	1537.664	9576.7	1	1974.3	76.9	2	K.TQSVEITKTDTEGK.I
*	HsFlag-FLJ90652_2	3.107	0.1414	1877.99	1879.03	8876.2	1	796.9	56.7	1	R.TLFAYEGTNEDELTFK.E
*	HsFlag-FLJ90652_2	2.1473	0.2138	1138.5	1139.337	2485.9	2	264.1	66.7	1	K.EGEIIHLISK.E
*	HsFlag-FLJ90652_2	3.2108	0.2032	1139.13	1139.337	4922	1	772.5	83.3	2	K.EGEIIHLISK.E
*	HsFlag-FLJ90652_2	4.1858	0.3198	1935.83	1936.128	6754.4	1	891.4	62.5	1	K.EGVFPDNFAVQINELDK.D
*	HsFlag-FLJ90652_2	2.6563	0.1831	1334.51	1335.586	4192.2	1	298.6	45.8	2	K.APAPKPELIAAEK.K
*	HsFlag-FLJ90652_2	3.0491	0.3717	1335.22	1335.586	6283.7	1	1102.8	79.2	2	K.APAPKPELIAAEK.K
*	HsFlag-FLJ90652_2	3.3928	0.331	1512.47	1513.687	3449	1	414.9	77.3	2	K.YFSLKPEEKDEK.S

*	HsFlag-FLJ90652_2	3.6498	0.3199	1903.54	1904.217	5498.5	1	650.2	52.9	2	K.STLEQKPSKPAAPQVPPK.K
*	HsFlag-FLJ90652_2	3.097	0.289	904.98	905.085	4923.7	1	1260.5	87.5	4	K.PAAPQVPPK.K
*	HsFlag-FLJ90652_2	2.8534	0.1406	1121.17	1121.233	5158.7	2	786.2	80	2	K.INGEVSSISSK.F
*	HsFlag-FLJ90652_2	2.0888	0.1283	936.3	937.037	5132	5	560.7	78.6	1	K.FETEPVSK.L
*	HsFlag-FLJ90652_2	4.0384	0.2397	1537.55	1537.843	7575.5	2	1130.9	70.8	2	K.LKLDSEQLPLRPK.S
*	HsFlag-FLJ90652_2	3.3293	0.2776	1139.11	1139.251	4591.2	2	920.4	88.9	2	K.SVDFDSLTVR.T
*	HsFlag-FLJ90652_2	4.1067	0.327	2799.35	2800.054	6568.6	1	483.6	39.6	3	K.ETDVVNFDDIASSENLLHLTANRPK.M
*	HsFlag-FLJ90652_2	3.8403	0.2087	2800.24	2800.054	6149.8	9	512.2	28.1	2	K.ETDVVNFDDIASSENLLHLTANRPK.M
*	HsFlag-FLJ90652_2	2.3463	0.311	1394.63	1395.474	2900.4	1	425.1	66.7	2	R.FNGGHSPTHSPEK.I
*	HsFlag-FLJ90652_2	3.2109	0.3151	1394.83	1395.474	5184.6	1	1038.8	83.3	2	R.FNGGHSPTHSPEK.I
*	HsFlag-FLJ90652_2	2.6393	0.1818	1244.13	1244.387	6493.7	6	460.7	65	1	K.LPKEEDSANLK.P
*	HsFlag-FLJ90652_2	3.5642	0.2456	1418.56	1419.661	4479.2	1	812.2	70.8	2	K.ANTTAFLTPLEIK.A
*	HsFlag-FLJ90652_2	3.0061	0.2024	1419.56	1419.661	5373.1	8	372.8	54.2	3	K.ANTTAFLTPLEIK.A
*	HsFlag-FLJ90652_2	5.2325	0.3677	1741.54	1742.119	8305	1	2221.6	78.6	4	R.AQIIELLCIVEALKK.D
gi|5031753|re		17	276	50.10%	449	49229	6.3	heterogeneous nuclear ribonucleoprotein H1 [Homo sapiens]			
*	HsFLAG-ARP6_Ti_1	3.7624	0.4423	1505.34	1505.593	2869.7	1	513.9	79.2	4	R.GLPWSCSADEVQR.F
*	HsFLAG-Lin9_Ti_20	4.9901	0.365	2106.93	2108.223	9811.8	1	1423.9	58.3	6	R.EGRPSGEAFVELESEDEVK.L
	HsFLAG-Lin9_Ti_20	4.61	0.2933	1685.59	1685.75	7123.9	1	2387.3	56.7	4	K.HTGPNSPDTANDGFVR.L
	HsFlag-NUFIP_Ti_1	4.405	0.4586	1685.6	1685.75	7380.1	1	1743.8	76.7	40	K.HTGPNSPDTANDGFVR.L
*	HsFLAG-p53-DNA-D	5.0196	0.3656	3751.9	3753.256	6508.1	1	798.3	27.3	12	R.GLPFGCSKEEIVQFFSGLEIVPNGITLPVDFQGR.S
*	HsFLAG-Lin9_Ti_20	4.069	0.3865	2904.99	2906.308	6477.3	1	707.6	42	7	K.EEIVQFFSGLEIVPNGITLPVDFQGR.S
	HsFLAG-FLJ20309_	5.6045	0.4433	1844.33	1843	8624.1	1	2117.4	71.9	80	R.STGEAFVQFASQEIAEK.A
*	HsMRGBP-FLAG_Ti	4.3303	0.4165	2718.67	2718.681	9763.2	1	1215.5	42	3	R.GAYGGGYGGYDDYNGYNDGYGFGSDR.F
	HsFLAG-ARP6_Ti_1	3.8358	0.4546	1603.44	1602.684	8040.3	1	1209.8	75	3	R.DLNYCFSGMSDHR.Y
*	HsFLAG-TIP49b_Ti_	4.8986	0.4988	2098.23	2099.208	10937	1	1226	50	9	R.YGDGGSTFQSTTGHCVHMR.G
*	HsFLAG-TIP49b_Ti_	4.12	0.2675	2100.88	2099.208	6114.4	1	952	40.3	2	R.YGDGGSTFQSTTGHCVHMR.G
	HsH2AZ-FLAG_293_	5.0454	0.3774	1997.32	1998.202	8397.3	1	1161	59.4	53	R.ATENDIYNFFSPLNPVR.V
	HsYL1_Ti_102.2959.	5.4927	0.2675	1998.86	1998.202	7998.6	1	1939.6	48.4	8	R.ATENDIYNFFSPLNPVR.V
	HsFLAG-TCF3_Ti_1	2.9392	0.214	1092.51	1093.228	6901.6	1	869.9	72.2	12	R.VHIEIGPDGR.V
	HsFLAG-ARP6_Ti_1	3.664	0.2731	1093.44	1093.228	6216	1	1638.1	88.9	29	R.VHIEIGPDGR.V
*	HsFLAG-ARP6_Ti_1	3.4299	0.2344	2179.67	2179.363	7635.4	1	570.7	40	1	R.VTGEADVEFATHEDAVAAMSK.D
*	HsFLAG-Lin9_Ti_20	3.8129	0.4321	2145.76	2143.32	10008.2	1	1225.5	52.6	3	R.YVELFLNSTAGASGGAYEHR.Y
gi|24307939|r		19	153	49.90%	541	59671	5.6	chaperonin containing TCP1, subunit 5 (epsilon) [Homo sapiens]			
*	HsFLAG-ARP5_Ti_1	4.3097	0.3774	3114.49	3115.375	8537.2	1	800.3	37.9	2	K.SQDDEIGDGTTGVVVLAGALLEEAEQLLDR.G
*	HsFLAG-ARP6_Ti_1	3.536	0.3352	1095.38	1094.169	5306.7	1	1224.5	94.4	2	R.IADGYEQAAR.V
*	HsFLAG-ARP5_Ti_1	7.9511	0.5084	3091.42	3092.557	8904.4	1	2236.1	37	7	R.VAIEHLDKISDSVLVDIKDTEPLIQTAK.T
*	HsFLAG-ARP6_Ti_1	4.9144	0.3608	2185.42	2186.508	7734.1	1	1098.2	52.6	11	K.ISDSVLVDIKDTEPLIQTAK.T
*	HsFLAG-ARP6_Ti_1	4.8386	0.3304	2185.75	2186.508	5785.9	1	1436.3	44.7	4	K.ISDSVLVDIKDTEPLIQTAK.T
*	HsFLAG-ARP6_Ti_1	3.7823	0.4109	1961.32	1962.287	10546.1	1	1391.5	58.8	2	R.QMAEIAVNAVLTVADMER.R
*	HsFLAG-ARP6_Ti_1	4.5199	0.2887	1392.06	1392.592	9176.8	1	2235.6	86.4	9	R.DVDFELIKVEGK.V
*	HsFLAG-ARP5_Ti_1	4.5222	0.3882	1698.53	1698.978	6774.1	1	1223	67.9	4	K.GVIVDKDFSHPQMPK.K
*	HsFLAG-ARP6_Ti_1	3.4756	0.3223	1610.57	1611.931	5815.9	1	931.3	69.2	12	K.IAILTCPFEPPKPK.T
*	HsFLAG-ARP6_Ti_1	3.9102	0.408	1434.24	1434.589	5229.1	1	1418.6	90.9	6	K.HKLDVTSVEDYK.A

*	HsFLAG-ARP5_Ti_1	3.8361	0.1932	1845.4	1844.133	9809.6	1	1349.3	65.4	2	K.YEKEKFEEMIQQIK.E
*	HsFLAG-ARP6_Ti_1	5.3402	0.452	3381.82	3381.695	6286.6	1	782.7	29.3	7	K.ETGANLAICQWGFDDEANHLLLQNNLPAVR.W
*	HsFLAG-ARP6_Ti_1	4.8768	0.3935	1739.89	1740.012	7856.7	1	1780.2	68.8	32	R.WVGGPEIELIAIATGGR.I
*	HsFLAG-ARP6_Ti_1	5.9317	0.3513	1668.4	1668.93	6659.7	1	1848.3	76.7	35	K.LGFAGLVQEISFGTTK.D
*	HsFLAG-ARP6_Ti_1	2.4022	0.0844	1020.37	1021.226	8736.8	3	813.6	78.6	2	K.MLVIEQCK.N
*	HsFLAG-ARP6_Ti_1	5.44	0.4302	2196	2196.385	7286	1	1576.6	57.1	9	R.VVYGGGAAEISCALAVSQEADK.C
*	HsFLAG-ARP6_Ti_1	3.4942	0.1261	1405.83	1403.683	7009.5	5	775.4	68.2	3	K.KQQISLATQMVR.M
*	HsFLAG-ARP6_Ti_1	2.8812	0.2091	1277.13	1275.509	4923.5	1	620.8	80	1	K.QQISLATQMVR.M
*	HsFLAG-ARP6_Ti_1	3.3263	0.1936	1388.39	1388.474	6014.9	1	801.5	77.3	3	K.IDDIRKPGESEE.-
gi|14043072|r	16	184	49.90%	353	37430	8.9	heterogeneous nuclear ribonucleoprotein A2/B1 isoform B1 [Homo sapiens]				
gi|4504447|re	16	184	51.60%	341	36006	8.6	heterogeneous nuclear ribonucleoprotein A2/B1 isoform A2 [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.236	0.1789	1928.37	1928.192	9741.4	1	2229.2	71.9	1	R.KLFIGGLSFETTEESLR.N
	HsFLAG-p53-DNA-D	4.9264	0.3623	1799.62	1800.018	6865.5	1	2312.6	83.3	71	K.LFIGGLSFETTEESLR.N
	HsFLAG-p53-DNA-D	2.5801	0.1913	1087.5	1088.164	4499.2	2	316.7	71.4	4	R.NYYEQWGK.L
	HsFLAG-TIP49b_Ti_	3.3037	0.2301	1492.41	1492.697	3937.7	4	527.4	70.8	5	K.LTDCVVMRDPASK.R
	HsFlag-NUFIP_Ti_1	3.3412	0.165	1338.85	1339.491	4277.7	1	568.5	70.8	9	R.EESGKPGAHVTVK.K
	HsFLAG-p53-DNA-D	4.7769	0.3184	2220.9	2221.425	8609.6	1	1331.9	58.8	2	R.DYFEEYGKIDTIEIITDR.Q
	HsFLAG-Lin9_Ti_20	4.1113	0.1557	1189.29	1189.351	7603.1	1	1651.4	94.4	3	K.IDTIEIITDR.Q
	HsFLAG-p53-DNA-D	3.7564	0.3059	1852.69	1853.001	5432.1	1	545.7	56.7	11	K.RGFGFVTFDDHDPVDK.I
	HsFLAG-Lin9_Ti_20	3.6608	0.3204	1853.33	1853.001	5722.5	1	799.2	41.7	2	K.RGFGFVTFDDHDPVDK.I
	HsFlag-NUFIP_Ti_1	4.5037	0.4279	1697.53	1696.813	7705.8	1	1860.9	78.6	24	R.GFGFVTFDDHDPVDK.I
	HsFLAG-p53-DNA-D	4.0483	0.2555	1411.43	1411.52	8531.2	1	2107.3	86.4	14	K.YHTINGHNAEVR.K
	HsFLAG-Lin9_Ti_20	2.9009	0.0866	1541.14	1539.694	9347.2	1	1622.9	75	1	K.YHTINGHNAEVRK.A
	HsFLAG-p53-DNA-D	2.7455	0.1418	1014.08	1014.042	5903	1	1365.9	83.3	1	R.GGNFGFGDSR.G
	HsFLAG-FLJ20309_	3.0826	0.2506	1377.87	1378.447	6297.5	1	744	64.3	15	R.GGGGNFGPGPGSNFR.G
	HsFlag-VPS71_Ti_1	5.1533	0.4558	2496.25	2496.53	8726.7	1	752.6	35.2	7	R.GFGDGYNGYGGGPGGGNFGGSPGYGGGR.G
	HsFLAG-ARP6_Ti_1	5.6933	0.5452	2190.52	2191.255	6832.1	1	1831.9	62.5	14	R.NMGGPYGGGNYGPGGSGGSGGYGGR.S
gi|4757718|re	28	513	49.40%	429	47461	5.6	actin-like 6A isoform 1 [Homo sapiens]				
	HsH2AZ-FLAG_293_	2.1579	0.2779	1067.29	1068.094	7909.3	3	634.3	61.1	1	R.AGYAGEDCPK.V
	HsFlag-VPS71_Ti_1	2.5094	0.1996	1070.75	1068.094	5449.1	3	825	77.8	1	R.AGYAGEDCPK.V
*	HsFlag-VPS71_Ti_1	5.03	0.4726	2485	2483.765	5616.4	1	769.2	47.7	4	R.AGYAGEDCPKVDFPTAIGMVVER.D
*	HsMRGBP-FLAG_Ti_	4.7807	0.3838	3861.37	3861.207	6909.4	1	779.1	23.6	1	R.AGYAGEDCPKVDFPTAIGMVVERDDGSTLMEIDGDK.G
*	HsMRGBP-FLAG_Ti_	4.2408	0.2847	1434.41	1434.693	6290.9	1	1601.9	83.3	11	K.VDFPTAIGMVVER.D
*	HsFLAG-TIP49a_Ti_	2.5735	0.25	2810.79	2812.136	4717.1	2	213.9	32	1	K.VDFPTAIGMVVERDDGSTLMEIDGDK.G
	HsFlag-Ies6_293_Ti_	4.3588	0.4624	1397.58	1396.466	5423.6	1	1184.3	83.3	8	R.DDGSTLMEIDGDK.G
	HsSrcap_Ti_202.218	3.7517	0.3845	1569.31	1569.714	6391.4	1	799.2	69.2	25	K.QGGPTYYIDTNALR.V
	HsH2AZ-FLAG_293_	2.8551	0.2342	1131.4	1132.317	3196.2	2	348.8	72.2	3	R.ENMEAISPLK.N
	HsTIP60_Ti_102.17	3.1045	0.1289	1132.93	1132.317	5415.7	8	881	83.3	1	R.ENMEAISPLK.N
	HsMRGBP-FLAG_Ti_	5.3471	0.4482	2270.18	2270.478	9066.5	1	2474.2	69.4	74	K.NGMVEDWDSFQAILDHTYK.M
	HsFlag-VPS71_Ti_1	3.6371	0.2876	2270.92	2270.478	3558.4	2	499.2	38.9	1	K.NGMVEDWDSFQAILDHTYK.M
	HsFLAG-TIP49a_Ti_	4.8402	0.4595	2026.73	2026.274	4015	1	688.3	58.8	41	K.SEASLHPVLMSEAPWNTR.A
	HsMRGBP-FLAG_Ti_	4.9182	0.2749	2026.88	2026.274	5447.7	1	1114.8	44.1	14	K.SEASLHPVLMSEAPWNTR.A
	HsYL1_Ti_106.2799.	3.0549	0.3073	2531.72	2531.938	6243.4	1	650.8	44.7	1	R.EKLTELMFEHYNIPAFFLCK.T

	HsFLAG-ARP5_Ti_1	3.6736	0.1071	2532.39	2531.938	5732.9	7	485.8	30.3	1	R.EKLTELMFEHYNIPAFFLCK.T
	HsFLAG-ARP8_Ti_2	4.5023	0.2315	2274.41	2274.648	4837.7	1	981.6	45.6	6	K.LTELMFEHYNIPAFFLCK.T
	HsFLAG-TIP49a_Ti_	5.5797	0.3831	2274.58	2274.648	5501.9	1	1243.3	64.7	51	K.LTELMFEHYNIPAFFLCK.T
	HsFLAG-TIP49b_Ti_	2.8957	0.2638	1120.59	1121.282	3394.4	1	218.4	65	7	K.TAVLTAFANGR.S
	HsTIP60_Ti_104.185	3.8654	0.3093	1121.27	1121.282	7947.3	1	1548.4	85	31	K.TAVLTAFANGR.S
	HsFlag-VPS71_Ti_10	4.3694	0.3819	3093.2	3093.507	7439.5	1	615	34.5	29	R.STGLILDSGATHTTAIPVHDGYVLQQGIVK.S
	HsH2AZ-FLAG_293_	7.5475	0.3819	3094.53	3093.507	8476.8	1	3060.2	40.5	97	R.STGLILDSGATHTTAIPVHDGYVLQQGIVK.S
	HsMRGBP-FLAG_Ti_	2.52	0.3586	1496.59	1496.687	3562.4	1	236.9	54.2	5	K.SPLAGDFITMQCR.E
	HsFlag-VPS71_Ti_10	4.8455	0.3964	1496.81	1496.687	6966.3	1	1826	83.3	44	K.SPLAGDFITMQCR.E
	HsFlag-VPS71_Ti_10	3.4625	0.1868	2253.98	2253.677	3704.1	1	506.4	52.8	2	R.ELFQEMNIELVPPYMIASK.E
	HsScrap_Ti_102.226	3.1132	0.3386	1315.37	1316.497	5047	1	924.6	72.7	11	K.IPEGLFDPSNVK.G
	HsTIP60_Ti_105.208	3.5991	0.3139	1317.25	1316.497	4309	1	760.1	77.3	29	K.IPEGLFDPSNVK.G
	HsFlag-VPS71_Ti_10	3.2874	0.247	1131.59	1131.274	3714	1	681.8	88.9	13	K.LIANNTTVER.R
gi|4506007|re	14	126	48.90%	323	36984	6.5	protein phosphatase 1, catalytic subunit, gamma isoform [Homo sapiens]				
*	HsFLAG-Lin9_Ti_202	3.5746	0.1427	1071.47	1072.25	7639.3	2	1467.9	93.8	1	K.LNIDSIIQR.L
*	HsFLAG-Lin9_Ti_201	3.5073	0.2193	1243.27	1243.362	8858.7	1	1467.3	83.3	2	K.NVQLQENEIR.G
	HsFlag-NUFIP_Ti_10	5.6621	0.4071	2196.86	2197.623	6879.7	1	1530.1	63.9	15	K.SREIFLSQPILLELEAPLK.I
	HsFlag-NUFIP_Ti_10	5.5555	0.2355	2197.28	2197.623	5469.5	1	994	41.7	8	K.SREIFLSQPILLELEAPLK.I
	HsFLAG-UTX1_Ti_20	5.8482	0.3752	1954.5	1954.357	3528.8	1	1020.8	78.1	26	R.EIFLSQPILLELEAPLK.I
	HsFlag-NUFIP_Ti_10	5.236	0.4906	2597.77	2599.858	3690.3	1	845	59.5	11	R.LFEYGGFPPESNYLFLGDYVDR.G
	HsFLAG-UTX1_Ti_20	3.1849	0.2992	1553.73	1552.818	5504.8	1	712.9	70.8	6	K.QSLETICLLLAYK.I
	HsFLAG-p53-DNA-D	2.758	0.1574	1441.48	1440.728	4335.3	1	826.3	80	1	K.IKYPENFFLLR.G
	HsFLAG-UTX1_Ti_20	3.0584	0.3282	1199.35	1199.395	4678.9	1	820	93.8	2	K.YPENFFLLR.G
	HsFlag-NUFIP_Ti_10	5.4504	0.4606	2114.06	2115.32	6688.8	1	1505.3	70.6	19	K.TFTDCFNCLPIAAIVDEK.I
	HsFlag-NUFIP_Ti_10	5.5834	0.4263	2249.12	2249.479	7631.2	1	1500.9	61.1	13	K.IFCCHGGLSPDLQSMEQIR.R
	HsFlag-NUFIP_Ti_10	4.7195	0.3543	2249.42	2249.479	8083.2	1	1565.6	43.1	6	K.IFCCHGGLSPDLQSMEQIR.R
	HsFlag-NUFIP_Ti_10	3.2996	0.1719	2686.23	2686.018	8541.8	2	442.3	36.4	1	R.IMRPTDVPDQGLLCDLLWSDPDK.D
	HsFLAG-p53-DNA-D	4.5257	0.4111	1641.05	1640.792	7920.9	1	2058	80.8	15	R.AHQVVEDGYEFFAK.R
gi|34452705|r	50	326	48.80%	951	102839	4.7	bromodomain containing 8 isoform 1 [Homo sapiens]				
	HsMRGBP-FLAG_Ti_	2.0226	0.2157	1456.74	1457.67	4867.7	1	261.2	50	2	K.LLSTGPTEPWSIR.E
	HsTIP60_Ti_105.439	3.8274	0.3482	1457.17	1457.67	6458.9	1	1009.9	75	42	K.LLSTGPTEPWSIR.E
	HsMRGBP-FLAG_Ti_	2.9386	0.1988	1715.66	1714.959	4586.4	1	534.2	57.1	2	K.LLSTGPTEPWSIREK.L
	HsH2AZ-FLAG_293_	3.756	0.2525	1235.22	1235.299	6670.3	1	1344.5	85	5	R.SGDQNWVSVSR.A
	HsFLAG-TIP49b_Ti_	3.4912	0.3232	2071.37	2072.374	7251	1	594.6	47.1	3	R.AIKPFAEPGRPPDWFSQK.H
	HsFLAG-TIP49a_Ti_	4.0402	0.3557	1758.92	1759.962	5287.4	1	865.2	67.9	7	K.PFAEPGRPPDWFSQK.H
	HsMRGBP-FLAG_Ti_	6.1679	0.4254	1995.94	1995.116	8602.2	1	2262	75	24	K.HCASQYSELLETTETPK.R
	HsMRGBP-FLAG_Ti_	4.492	0.5213	2149.93	2151.304	9414.1	1	1543.9	61.8	4	K.HCASQYSELLETTETPKR.K
	HsTIP60_Ti_106.261	2.7748	0.2621	1443.62	1444.625	6228.3	1	445.7	54.2	6	K.GEVVETVEDVIVR.K
	HsTIP60_Ti_105.260	5.0826	0.4028	1445.43	1444.625	7442.6	1	1965.9	83.3	36	K.GEVVETVEDVIVR.K
	HsMRGBP-FLAG_Ti_	4.6171	0.3099	1572.95	1572.799	7041.6	1	2393	84.6	5	K.GEVVETVEDVIVRK.L
	HsTIP60_Ti_106.200	3.6807	0.1134	1317.48	1316.541	8314.9	1	1186	80	1	R.KLTAERVEELK.K
	HsTIP60_Ti_103.147	2.989	0.1546	1188.23	1188.367	4520.4	4	864	88.9	1	K.LTAERVEELK.K
	HsMRGBP-FLAG_Ti_	4.539	0.3681	1599.81	1599.762	3593.4	1	801.4	80.8	6	K.RDAELIQAGHMDSR.L

	HsMRGBP-FLAG_Ti	2.4023	0.2981	1442.65	1443.574	4320.4	7	345.8	54.2	1	R.DAELIQAGHMDSR.L
	HsMRGBP-FLAG_Ti	4.1991	0.2181	1444.14	1443.574	6400.3	1	1426.6	79.2	12	R.DAELIQAGHMDSR.L
	HsYL1_Ti_101.1824.	3.1613	0.3282	1291.45	1292.395	5376.6	1	562.8	70	6	R.LDELCNDIATK.K
	HsTIP60_Ti_102.163	4.4047	0.3234	1293.26	1292.395	5324.5	1	1195.7	90	7	R.LDELCNDIATK.K
	HsTIP60_Ti_103.150	3.2386	0.1314	1421.66	1420.569	7637	7	669.4	63.6	2	R.LDELCNDIATKK.K
	HsMRGBP-FLAG_Ti	3.5468	0.2542	1332.47	1332.494	5455.5	1	1348.4	90	2	K.KKLEEEEAEVK.R
	HsTIP60_Ti_106.090	2.7091	0.273	1251.44	1251.388	8121.4	7	519.1	55	1	K.RKATDAAYQAR.Q
	HsFLAG-TIP49b_Ti_	2.9182	0.1791	972.24	972.237	7353.6	1	1163.6	92.9	6	R.RLPTVMVR.S
	HsTIP60_Ti_106.285	1.871	0.1735	1463.58	1463.758	3296.7	7	226.9	50	1	K.ATPPPSPLLSELLK.K
	HsTIP60_Ti_106.211	2.5765	0.0985	1055.61	1056.25	4980.7	2	383.6	66.7	1	K.KGSLLPTSPR.L
	HsTIP60_Ti_106.211	3.4319	0.1454	1056.07	1056.25	4338.3	3	829.1	83.3	4	K.KGSLLPTSPR.L
	HsMRGBP-FLAG_Ti	4.8381	0.4094	2704.04	2704.092	4390.5	1	790.2	50	7	R.LLEAGPTQFTTPLASFTTVASEPPVK.L
	HsTIP60_Ti_106.295	4.4432	0.3658	2704.83	2704.092	7174.9	1	883.1	31	1	R.LLEAGPTQFTTPLASFTTVASEPPVK.L
	HsH2AZ-FLAG_293_	1.8819	0.2781	1001.3	1002.112	4307.7	1	307.7	55	1	R.SGVAEAPVGSK.A
	HsMRGBP-FLAG_Ti	5.1237	0.2917	1615.77	1615.778	7779.6	1	1677.5	75	10	K.APSIDGKEELDLAEK.M
	HsMRGBP-FLAG_Ti	5.8536	0.3949	4642.58	4641.928	5301.3	1	974.5	26.9	3	ER.D
	HsMRGBP-FLAG_Ti	2.8359	0.2805	1521.66	1522.843	4392.1	1	480.7	57.7	4	R.DKPVPLPAPEMTVK.Q
	HsFLAG-TIP49b_Ti_	3.2891	0.1402	1522.26	1522.843	3898.8	1	524.6	65.4	14	R.DKPVPLPAPEMTVK.Q
	HsTIP60_Ti_104.151	3.7905	0.2657	1538.55	1538.611	6980.4	1	688.6	68.2	5	K.QERLDFEETENK.G
	HsTIP60_Ti_102.153	3.1339	0.1272	1124.35	1125.177	5245	7	831.6	87.5	4	R.LDFEETENK.G
	HsYL1_Ti_101.1662.	2.0585	0.0952	1124.52	1125.177	4394.4	9	399	68.8	1	R.LDFEETENK.G
	HsMRGBP-FLAG_Ti	2.7704	0.2218	1051.63	1052.219	6208.9	8	527	62.5	2	K.GIHELVDIR.E
	HsMRGBP-FLAG_Ti	2.9567	0.1587	1052.57	1052.219	3939	3	841	87.5	3	K.GIHELVDIR.E
	HsMRGBP-FLAG_Ti	4.869	0.3196	1806.89	1807.057	6883.9	1	1382	66.7	5	K.GIHELVDIREPSAEIK.V
	HsMRGBP-FLAG_Ti	4.5076	0.2349	3927.7	3927.456	5677.3	1	385.9	19.6	4	R.EPSAEIKVEPAEPEPVISGAEIVAGVVPATSMEPPELR.S
	HsMRGBP-FLAG_Ti	2.9361	0.3705	3171.22	3172.618	6022.3	1	619	36.7	1	K.VEPAEPEPVISGAEIVAGVVPATSMEPPELR.S
	HsTIP60_Ti_105.311	6.035	0.4134	2516.9	2518.691	8543.1	1	1632.8	52.1	8	R.SQDLDEELGSTAAGEIVEADVAIGK.G
	HsMRGBP-FLAG_Ti	6.1888	0.2731	3574.38	3573.844	5268.8	1	1397.2	33.1	21	R.SQDLDEELGSTAAGEIVEADVAIGKGDETPLTNVK.T
	HsMRGBP-FLAG_Ti	5.1769	0.4353	2234.28	2234.483	7486.9	1	1412.2	60.5	5	K.FEMSDSLKEESGTIFGSQIK.D
	HsMRGBP-FLAG_Ti	2.345	0.1391	1295.65	1296.42	3191.8	6	185	54.5	1	K.EESGTIFGSQIK.D
	HsTIP60_Ti_102.185	3.4538	0.4027	1296.16	1296.42	4631.6	1	646.3	72.7	4	K.EESGTIFGSQIK.D
	HsFLAG-TIP49b_Ti_	4.8152	0.1605	3492.22	3490.999	4563	1	498.5	26.7	3	R.YANVFLQPVTDDIAPGYHSIVQRPMDLSTIK.K
	HsYL1_Ti_106.2480.	3.7038	0.1736	3620.32	3619.173	4232.3	1	286.6	23.4	1	R.YANVFLQPVTDDIAPGYHSIVQRPMDLSTIKK.N
	HsMRGBP-FLAG_Ti	6.1234	0.3873	2880.09	2880.283	9862.8	1	1257.2	44	4	R.DVLEQIQQFLATQLIMQTSESGISAK.S
	HsMRGBP-FLAG_Ti	5.0433	0.3437	2882.69	2880.283	6152.4	1	852.6	32	2	R.DVLEQIQQFLATQLIMQTSESGISAK.S
*	HsTIP60_Ti_106.397	4.7682	0.5182	2066.67	2068.352	4692.1	1	610.5	57.9	25	K.DSVPMGSPAFLLSLFDGGTR.G
gi|4503471|re	24	319	48.70%	462	50141	9	eukaryotic translation elongation factor 1 alpha 1 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	4.6953	0.3853	1589.5	1589.835	9070.4	1	1844.8	71.4	16	K.THINIVVIGHVDSGK.S
	HsSrcap_Ti_206.252	2.9506	0.4242	1589.65	1589.835	7888.4	1	828.8	60.7	1	K.THINIVVIGHVDSGK.S
	HsTIP60_Ti_105.137	1.9632	0.1372	1120.39	1121.279	6519.3	3	584.4	66.7	1	K.STTTGHLIYK.C
	HsFLAG-p53-DNA-D	3.1463	0.3628	1121.3	1121.279	8751.6	1	1234	77.8	21	K.STTTGHLIYK.C
	HsFLAG-ARP5_Ti_1	2.541	0.1763	1611.43	1611.851	9393	1	594.7	53.8	1	R.TIEKFEKEAAEMGK.G
	HsFLAG-FLJ20729_	3.9563	0.2962	1405.38	1405.596	3703.6	1	888.6	54.5	2	K.YYVTIIDAPGHR.D

	HsFLAG-Lin9_Ti_205	2.135	0.1226	1405.66	1405.596	5203.2	2	284.2	54.5	1	K.YYVTIIDAPGHR.D
	HsFlag-VPS71_Ti_10	3.6822	0.3307	1406.68	1405.596	5821.5	1	1234.3	81.8	68	K.YYVTIIDAPGHR.D
	HsSrcap_Ti_204.512	3.2119	0.2572	2910.96	2911.263	8701.9	2	388.9	28.6	2	K.NMITGTSQADCAVLIVAAGVGEFEAGISK.N
	HsFlag-VPS71_Ti_10	4.5563	0.1844	2913.87	2911.263	6269.6	1	1050.3	33	12	K.NMITGTSQADCAVLIVAAGVGEFEAGISK.N
	HsFlag-VPS71_Ti_10	3.8784	0.3946	1314.66	1315.555	4878	1	770	72.7	24	R.EHALLAYTLGVK.Q
	HsFLAG-p53-DNA-D	3.6805	0.3101	1315.6	1315.555	7027.5	1	1495	86.4	27	R.EHALLAYTLGVK.Q
*	HsFLAG-p53-DNA-D	5.3726	0.3935	3697.05	3698.205	7214.2	1	1106.8	28.9	16	K.KIGYNPDTVAFVPISGWNGDNMLEPSANMPWFK.G
	HsFLAG-TCF3_Ti_10	6.2873	0.4401	2784.44	2785.09	7148.2	1	1431.7	38	4	R.KDGNASGTTLLEALDCILPPTRPTDK.P
*	HsFLAG-p53-DNA-D	4.8334	0.3656	3151.75	3151.554	7453.4	1	948.2	29.5	1	R.KDGNASGTTLLEALDCILPPTRPTDKPLR.L
	HsFLAG-FLJ20309_	4.4387	0.3105	2655.12	2656.916	7839.9	1	578.3	37.5	33	K.DGNASGTTLLEALDCILPPTRPTDK.P
	HsFLAG-FLJ20729_	5.3432	0.2989	2656.04	2656.916	4798.2	1	626.4	32.3	25	K.DGNASGTTLLEALDCILPPTRPTDK.P
*	HsFLAG-TCF3_Ti_10	4.3666	0.2614	3978.45	3980.517	10389.3	1	616.9	20	1	K.DGNASGTTLLEALDCILPPTRPTDKPLRLPLQDVYK.I
	HsFlag-DPCD_Ti_20	1.8412	0.2195	1025.34	1026.224	4853.1	6	236.2	60	1	K.IGGIGTVPVGR.V
	HsFLAG-ARP6_Ti_1	3.7953	0.3438	1026.89	1026.224	5194.3	2	970.8	85	12	K.IGGIGTVPVGR.V
	HsFLAG-p53-DNA-D	5.3017	0.4413	2516.01	2516.999	4507.5	1	741	52.2	42	R.VETGVLKPGMVVTFAPVNVTTEVK.S
	HsFlag-NUFIP_Ti_20	4.1135	0.2792	2517.87	2516.999	4807.9	1	681.4	33.7	2	R.VETGVLKPGMVVTFAPVNVTTEVK.S
	HsFlag-VPS71_Ti_10	4.1033	0.2634	1791.5	1790.128	5866.5	1	689.1	53.1	2	K.PGMVVTFAPVNVTTEVK.S
*	HsFLAG-FLJ20729_	4.8388	0.4594	2997.39	2997.374	7268.9	1	1376.2	33.3	4	K.SGDAAIVDMVPGKPMCVESFSDYPPLGR.F
gi|18375623|r	26	126	48.60%	428	48991	5.7	HLA-B associated transcript 1 [Homo sapiens]				
gi|4758112|re	26	126	48.60%	428	48991	5.7	HLA-B associated transcript 1 [Homo sapiens]				
	HsFLAG-Lin9_Ti_204	3.0073	0.2799	1296.63	1297.413	4711.8	2	221.9	54.5	3	K.GSYVSIHSSGFR.D
	HsFLAG-FLJ20729_	3.6241	0.3653	1296.99	1297.413	6359.8	1	982	72.7	7	K.GSYVSIHSSGFR.D
	HsFLAG-Lin9_Ti_203	2.6521	0.1748	1243.61	1244.52	3979.5	1	468.9	77.8	1	R.DFLLKPELLR.A
	HsFlag-NUFIP_Ti_10	3.2269	0.1338	1244.76	1244.52	4710.6	2	906.8	83.3	2	R.DFLLKPELLR.A
	HsFLAG-FLJ20729_	6.4447	0.4235	3653	3654.027	6880.9	1	1503.5	33.1	11	R.AIVDCGFEHPSEVQHECIPQAILGMDVLCQAK.S
	HsFLAG-Lin9_Ti_202	2.3675	0.1628	1137.9	1138.395	8766.4	8	689.9	65	1	K.VAVFFGGLSIK.K
	HsFLAG-Lin9_Ti_203	3.4367	0.3219	1139.07	1138.395	6751.1	1	1213.8	80	3	K.VAVFFGGLSIK.K
	HsFLAG-p53-DNA-D	3.9484	0.3314	1435.47	1435.635	8193.9	1	1242.8	75	6	K.KNCPHIVVGTPGR.I
	HsFLAG-Lin9_Ti_206	2.4181	0.2932	1306.53	1307.461	4507.3	4	188.8	54.5	1	K.NCPHIVVGTPGR.I
	HsH2AZ-FLAG_293_	4.035	0.3869	1308.34	1307.461	6873.4	1	1320.4	81.8	9	K.NCPHIVVGTPGR.I
	HsFLAG-Lin9_Ti_203	3.1797	0.1953	1176.4	1177.265	5215.2	1	688.8	75	3	K.HFILDECDK.M
	HsFLAG-Lin9_Ti_203	3.0843	0.1069	1177.17	1177.265	4666.4	5	864.8	81.2	2	K.HFILDECDK.M
	HsFlag-VPS71_Ti_10	4.2756	0.4438	1846.56	1846.077	5547.9	1	2021.5	89.3	9	K.FMQDPMEIFVDDETK.L
	HsFLAG-Lin9_Ti_205	3.2061	0.3726	1462.54	1463.72	5019	2	426	59.1	2	K.LTLHGLQQYYVK.L
	HsFLAG-Lin9_Ti_205	3.5535	0.2277	1462.54	1463.72	6395.9	1	1144.6	54.5	1	K.LTLHGLQQYYVK.L
	HsFLAG-p53-DNA-D	3.4387	0.3284	1464.78	1463.72	6416.1	1	1051.3	77.3	8	K.LTLHGLQQYYVK.L
	HsFlag-NUFIP_Ti_11	5.8021	0.4298	2277.86	2278.669	8055.1	1	2325.2	68.4	6	R.CIALAQLLVEQNFPAIAIHR.G
	HsFlag-DPCD_Ti_20	5.8238	0.335	2278.16	2278.669	4665.2	1	1120.4	47.4	14	R.CIALAQLLVEQNFPAIAIHR.G
	HsFLAG-FLJ20729_	3.868	0.3173	1260.58	1260.525	6371.3	1	891.1	75	4	R.RILVATNLFGR.G
	HsFLAG-Lin9_Ti_202	2.2326	0.1198	1104.68	1104.338	5498.1	2	339.8	66.7	2	R.ILVATNLFGR.G
	HsFLAG-Lin9_Ti_202	3.4027	0.2346	1105.14	1104.338	6349.5	1	1134.3	83.3	7	R.ILVATNLFGR.G
	HsFLAG-FLJ20729_	4.54	0.3819	2299.96	2301.492	4743.3	1	619.6	52.8	3	R.VNIAFNYDMPEDSDTYLHR.V
	HsFLAG-Lin9_Ti_202	4.8327	0.4231	1480.33	1480.615	7594.8	1	2068.7	84.6	6	K.GLAITFVSDENDAK.I

	HsFLAG-Lin9_Ti_202	3.7762	0.3725	1480.73	1480.615	8409.7	1	923.6	61.5	4	K.GLAITFVSDENDAK.I
	HsFLAG-Lin9_Ti_205	5.8394	0.3282	3553.48	3552.874	8811	1	862.4	27.6	7	K.ILNDVQDRFEVNISELPDEIDISSYIEQTR.-
	HsFLAG-Lin9_Ti_202	4.2176	0.323	2597.11	2598.823	5530.4	1	914.8	54.8	4	R.FEVNISELPDEIDISSYIEQTR.-
gi|4506701|re	6	16	48.30%	143	15808	10.5	ribosomal protein S23 [Homo sapiens]				
*	HsFLAG-TIP49b_Ti_	1.944	0.1428	810.47	810.972	4667.6	7	421.3	71.4	3	K.AHLGTALK.A
*	HsFlag-FLJ20643_Ti	2.5799	0.1346	1056.79	1057.154	5253.5	1	620.8	70	3	K.ANPFGGASHAK.G
*	HsFlag-NUFIP_Ti_10	2.5984	0.2152	1057.14	1057.154	4227.4	1	571.7	75	1	K.ANPFGGASHAK.G
	HsFLAG-ARP6_Ti_1	4.7312	0.2999	3125.64	3126.459	8243.1	1	1108.3	30.6	4	K.KITAFVPNDGCLNFIEENDEVLVAGFGR.K
	HsFLAG-TCF3_Ti_10	2.8741	0.1999	1078.39	1078.216	5284.1	5	572.3	70	1	K.GHAVGDIPGVR.F
	HsFLAG-ARP6_Ti_1	4.3825	0.3125	1191.16	1191.456	5250.6	1	1304.4	90	4	K.VANVSLLALYK.G
gi|56549696|r	135	853	47.70%	3122	339693	9.2	E1A binding protein p400 [Homo sapiens]				
*	HsMRGBP-FLAG_Ti_	4.1266	0.3873	4178.47	4178.564	7006.6	1	621.3	21.7	1	.A
*	HsMRGBP-FLAG_Ti_	4.3758	0.3392	2530.51	2530.806	8129.1	1	1416.5	33.7	1	R.AGAPGPGLGLCSSSPTGGFVDASVLVR.Q
*	HsYL1-FLAG_Ti_206	4.7571	0.4611	2531.19	2530.806	3901.1	1	496.3	46.2	18	R.AGAPGPGLGLCSSSPTGGFVDASVLVR.Q
	HsYL1-FLAG_Ti_206	4.4456	0.4387	2578.03	2578.946	5095.8	1	557.9	40.7	3	R.TPGVLLPGAGGAAGFGMTSPPPPTSPSR.T
	HsTIP60_Ti_106.011	3.8731	0.4046	2029.09	2028.372	3245.1	4	214.6	42.5	2	R.TAVPPGLSSLPLTSVGNTGMK.K
	HsMRGBP-FLAG_Ti_	4.6866	0.4365	2030.87	2028.372	6675.5	1	1003.2	37.5	1	R.TAVPPGLSSLPLTSVGNTGMK.K
	HsTIP60_Ti_106.223	4.1117	0.3041	1828.51	1828.152	2939.6	1	504.9	70	7	K.KLEEIPPASPEMAQMR.K
	HsMRGBP-FLAG_Ti_	3.9763	0.1089	1831.09	1828.152	7435.3	1	1379.4	46.7	1	K.KLEEIPPASPEMAQMR.K
*	HsFLAG-TIP49b_Ti_	2.4326	0.2398	1231.36	1232.428	5699.6	1	496	72.2	2	K.HYAPLQAYLR.Q
*	HsMRGBP-FLAG_Ti_	2.9787	0.168	1232.69	1232.428	3574.8	1	673.2	83.3	5	K.HYAPLQAYLR.Q
*	HsTIP60_Ti_102.177	4.8464	0.1556	2394.53	2395.314	8601.8	1	1297.5	58.3	2	R.QNDLDIEEEEEEEEEEEK.S
*	HsMRGBP-FLAG_Ti_	4.0208	0.4051	2822.14	2823.083	6148.3	1	861.6	38.9	1	K.SEVINDEQALAGSLVAGAGSTVETDLFK.R
*	HsTIP60_Ti_105.131	5.0881	0.4079	1650.61	1650.865	6675.7	1	1608.6	78.6	12	K.RQQAMPSTGMAEQSK.R
*	HsYL1_Ti_105.3322.	3.9131	0.2771	3629.22	3628.207	5071.6	1	340.3	21.3	1	R.LPPAGVPTAALSSALQFAQQPQVVEAQTQLQIPVK.T
*	HsTIP60_Ti_106.253	5.2651	0.436	2030.52	2031.335	5756	1	1234.7	66.7	6	K.VQVQASQLSSLPQMVASTR.L
*	HsYL1-FLAG_Ti_205	4.6974	0.4565	2208.42	2208.433	5637.1	1	1393.5	41.3	3	R.PLPTSSTSSLAPVSGSGPGPSPAR.S
*	HsMRGBP-FLAG_Ti_	5.0974	0.4174	2208.63	2208.433	4225.5	1	1031.7	58.7	13	R.PLPTSSTSSLAPVSGSGPGPSPAR.S
*	HsYL1_Ti_104.0922.	3.315	0.3305	1345	1345.455	6226	2	555.2	62.5	1	R.SSPVNRPSSATNK.A
*	HsYL1_Ti_105.1736.	4.9515	0.419	4548.94	4549.866	6897	1	630.5	19	6	VHQR.I
*	HsH2AZ-FLAG_293_	2.6386	0.1126	818.23	817.923	3662.3	5	594.1	91.7	1	K.AGLWSQR.R
*	HsMRGBP-FLAG_Ti_	5.2444	0.3329	2024.64	2024.244	5870.4	1	1399.9	73.3	23	R.EIECFWSNIEQVVEIK.L
*	HsYL1-FLAG_Ti_203	5.2804	0.4155	1758.45	1757.869	9838.3	1	2449.5	75	10	K.GFDALQESSLDSGMSGR.K
*	HsMRGBP-FLAG_Ti_	4.6601	0.4053	4203.88	4205.308	6890.3	1	827.2	23.6	2	K.ASISLTDDEVDDEEETIEEEEANEGVVDHQTELSNLAK.E
*	HsTIP60_Ti_105.330	2.7437	0.148	1271.6	1272.543	2600.5	2	427.2	80	3	K.EAELPLLDLMK.L
*	HsYL1_Ti_102.2911.	2.714	0.2718	1271.61	1272.543	2922.7	1	307.3	70	1	K.EAELPLLDLMK.L
*	HsYL1_Ti_106.2960.	4.1365	0.3673	1927.18	1926.322	6405.7	1	1339.3	70	1	R.KDLVLIDSLFIMDQFK.A
*	HsH2AZ-FLAG_293_	2.6696	0.132	1799.61	1798.147	9511.3	1	1057.2	60.7	2	K.DLVLIDSLFIMDQFK.A
*	HsTIP60_Ti_106.315	5.4718	0.4067	1526.48	1526.77	5905.5	1	2136.2	89.3	26	K.DIADVTAVAEAILPK.G
*	HsTIP60_Ti_105.364	4.4984	0.2096	1526.85	1526.77	8259.3	2	2230.9	57.1	1	K.DIADVTAVAEAILPK.G
*	HsYL1_Ti_103.2372.	2.9831	0.2252	1321.56	1322.55	3351.5	1	220.3	59.1	2	K.FNAPSLLYGALR.D
*	HsH2AZ-FLAG_293_	4.023	0.3164	1321.79	1322.55	4913.2	1	1113.7	86.4	18	K.FNAPSLLYGALR.D
*	HsMRGBP-FLAG_Ti_	2.7648	0.1191	916.34	916.108	2713.9	4	686.9	92.9	2	K.IGLDWLAK.L

*	HsTIP60_Ti_105.222	4.6973	0.3369	1385.05	1385.56	5270.6	1	1349	84.6	4	K.NLNGILADEAGLGK.T
*	HsTIP60_Ti_105.222	3.0731	0.336	1385.49	1385.56	4995.7	2	303.3	53.8	1	K.NLNGILADEAGLGK.T
*	HsH2AZ-FLAG_293_	3.3698	0.218	1047.43	1046.214	4481.4	1	1010.3	93.8	6	K.ILSYIGSHR.E
*	HsFLAG-TIP49b_Ti_	4.6425	0.5091	1631.69	1630.803	7003.3	1	1601.7	79.2	2	R.HWEAVFTLQSQQR.L
*	HsTIP60_Ti_106.191	1.9514	0.089	916.46	917.096	4656.5	2	471.3	75	1	K.KYEHVLK.C
*	HsFLAG-TIP49b_Ti_	3.0354	0.0841	916.9	917.096	5091.8	2	855.3	100	3	K.KYEHVLK.C
*	HsYL1_Ti_102.2078.	4.0027	0.1935	1889.03	1889.156	4169.4	1	934.5	68.8	17	K.ALYEDVILQPGTQEALK.S
*	HsFLAG-TIP49b_Ti_	2.4201	0.1066	1291.56	1292.447	4464.4	3	433.4	65	4	R.ICNHPGLVEPR.H
*	HsMRGBP-FLAG_Ti_	3.4377	0.2836	1294.23	1292.447	5142.9	1	1039.3	80	10	R.ICNHPGLVEPR.H
*	HsFLAG-TIP49b_Ti_	5.149	0.4411	2187.38	2187.5	8614.1	1	1164.8	52.5	22	R.HPGSSYVAGPLEYPSASLILK.A
*	HsYL1-FLAG_Ti_205	4.1734	0.4019	1696.51	1695.925	6199.7	1	1377.7	71.4	7	K.EADLSMFDLIGLENK.I
*	HsMRGBP-FLAG_Ti_	3.123	0.2071	1297.71	1297.497	5716.4	1	999.9	80	2	K.ITRHEAELLSK.K
*	HsH2AZ-FLAG_293_	2.0304	0.1025	926.31	927.045	4135.9	1	530.6	78.6	2	R.HEAELLSK.K
*	HsH2AZ-FLAG_293_	2.8583	0.1635	929.38	927.045	5566.5	1	932.9	92.9	2	R.HEAELLSK.K
*	HsMRGBP-FLAG_Ti_	4.6458	0.1972	1575.81	1575.821	6787.2	1	2104.2	78.6	4	R.KLMEEISTSAAPAAR.P
*	HsFLAG-TIP49b_Ti_	5.5117	0.4504	2013.64	2014.348	8300.8	1	1894.1	65.8	5	R.KLMEEISTSAAPAARPAAAK.L
*	HsFLAG-TIP49b_Ti_	5.0002	0.3616	2013.85	2014.348	7105.7	1	1263	40.8	4	R.KLMEEISTSAAPAARPAAAK.L
*	HsYL1-FLAG_Ti_202	2.7011	0.2179	1447.82	1447.646	8254.2	1	1336.4	69.2	1	K.LMEEISTSAAPAAR.P
*	HsMRGBP-FLAG_Ti_	3.7661	0.2625	1886.95	1886.174	4030.7	2	752.3	40.3	2	K.LMEEISTSAAPAARPAAAK.L
*	HsMRGBP-FLAG_Ti_	4.0028	0.4133	1886.95	1886.174	5681.6	1	712.9	50	13	K.LMEEISTSAAPAARPAAAK.L
*	HsFLAG-TIP49b_Ti_	4.1768	0.3793	1646.76	1647.874	7076.7	1	1263	73.1	11	R.LFQPVQYGQKPEGR.T
*	HsYL1-FLAG_Ti_206	2.2208	0.2389	1209.64	1210.378	3556.7	3	217.8	65	3	R.TVAFPSTHPPR.T
*	HsFLAG-TIP49b_Ti_	3.0316	0.2347	1210.15	1210.378	4715.3	1	959.7	80	11	R.TVAFPSTHPPR.T
*	HsFLAG-TIP49b_Ti_	2.9212	0.2483	1509.46	1510.69	3375.4	1	176.1	50	9	R.TAAPTTASAAPQGPLR.G
*	HsTIP60_Ti_104.145	3.9967	0.3473	1510.44	1510.69	5695.9	1	1128	73.3	12	R.TAAPTTASAAPQGPLR.G
*	HsH2AZ-FLAG_293_	3.9714	0.3148	1556.04	1556.762	6556.5	2	1546.6	51.8	1	R.GRPPIATFSANPEAK.A
*	HsH2AZ-FLAG_293_	4.2397	0.2281	1556.57	1556.762	5462.1	1	857.1	64.3	16	R.GRPPIATFSANPEAK.A
*	HsYL1-FLAG_Ti_202	4.8415	0.2856	1633.73	1632.773	6087.4	1	1521.2	75	8	K.AAAAPFQTSQASASAPR.H
*	HsH2AZ-FLAG_293_	5.0985	0.4854	1715.96	1716.851	3728.5	1	1074.8	76.5	11	R.HQPASASSTAASPAHPAK.L
*	HsTIP60_Ti_106.163	4.3225	0.4303	1716.37	1716.851	7341.1	1	1451.1	47.1	4	R.HQPASASSTAASPAHPAK.L
*	HsFLAG-TIP49b_Ti_	3.5113	0.3675	3177.19	3178.448	7944.9	1	297.1	27.4	3	R.AQTTAQASTPGQPPPQPQAPSHAAGQSALPQR.L
*	HsFLAG-TIP49b_Ti_	5.8956	0.3791	3179.03	3178.448	4483.6	1	966.7	33.1	11	R.AQTTAQASTPGQPPPQPQAPSHAAGQSALPQR.L
*	HsH2AZ-FLAG_293_	3.1913	0.3097	1341.31	1342.538	3794.6	1	280.5	66.7	10	K.IAQLASITGPQSR.V
*	HsTIP60_Ti_104.171	3.9199	0.3468	1342.36	1342.538	6760.7	1	1353.3	79.2	10	K.IAQLASITGPQSR.V
*	HsH2AZ-FLAG_293_	3.8541	0.3418	1730.54	1730.959	4876.9	1	834.8	70	11	R.VAQPETPVTLQFQGSK.F
*	HsFLAG-TIP49b_Ti_	2.8212	0.2945	1088.81	1089.239	6829.7	1	935	87.5	6	K.FTLSHSQLR.Q
*	HsYL1_Ti_104.2979.	3.1994	0.4667	2863.13	2864.318	6061	1	521.1	38.5	1	R.QLTAGQPLQLQGSVLQIVSAPGQPYLR.A
*	HsTIP60_Ti_103.167	2.6886	0.4292	1483.58	1484.693	7505.1	1	822.2	56.7	1	R.VAVNALAVGEPGTASK.P
*	HsMRGBP-FLAG_Ti_	4.3495	0.3811	1485.69	1484.693	6464.5	1	1029.3	66.7	5	R.VAVNALAVGEPGTASK.P
*	HsH2AZ-FLAG_293_	4.5387	0.3222	2775.35	2777.104	6056.2	1	1003.3	31.2	9	R.VAVNALAVGEPGTASKPASPIGGPTQEEK.T
*	HsYL1_Ti_103.1626.	4.5684	0.4105	2777.38	2777.104	4095.8	1	334	37.5	13	R.VAVNALAVGEPGTASKPASPIGGPTQEEK.T
*	HsYL1_Ti_103.1704.	4.2557	0.2815	1550.79	1548.739	5959.6	1	1314.8	81.8	14	K.ERLDQIYLVNER.R
*	HsTIP60_Ti_103.188	3.8703	0.3191	1262.56	1263.436	4825.8	2	729.9	77.8	1	R.LDQIYLVNER.R

*	HsH2AZ-FLAG_293_	2.8976	0.291	1196.12	1194.302	5851.8	1	510.6	66.7	1	R.RCSQAPVYGR.D
*	HsFLAG-TIP49b_Ti_	2.7941	0.1279	1011.31	1011.135	3379.1	2	939.4	93.8	2	R.ICALPSHGR.V
*	HsFLAG-TIP49b_Ti_	5.1146	0.4571	2611.75	2611.806	9701.9	1	922.7	43.5	8	K.EAGPAHSYTSSSESPSELMLTLCR.C
*	HsMRGBP-FLAG_Ti_	4.3942	0.2526	2613.25	2611.806	9055.3	1	1568.1	34.8	2	K.EAGPAHSYTSSSESPSELMLTLCR.C
*	HsMRGBP-FLAG_Ti_	4.3446	0.3707	1292.74	1292.354	7760.1	1	1667.4	90	4	R.CGESLQDVIDR.V
*	HsFLAG-TIP49b_Ti_	4.6896	0.2978	1633.88	1634.018	5489.9	7	1199.3	48.3	5	R.VAFVIPPVVAAPPSLR.V
*	HsYL1_Ti_106.2534.	4.0717	0.2894	1635.2	1634.018	3301.1	2	479.2	63.3	7	R.VAFVIPPVVAAPPSLR.V
*	HsTIP60_Ti_106.222	2.1745	0.2131	1359.59	1360.515	3489.3	1	244.6	60	2	R.EHAAPYFQQLR.Q
*	HsTIP60_Ti_106.222	3.0585	0.2852	1360.67	1360.515	4369.9	1	763.1	80	6	R.EHAAPYFQQLR.Q
*	HsMRGBP-FLAG_Ti_	3.0033	0.1217	1017.54	1016.228	4380.6	4	830.6	92.9	5	R.LLQFPELR.L
*	HsH2AZ-FLAG_293_	4.2831	0.1568	1987.32	1987.39	5790.4	1	972.9	39.7	2	R.LVQFDSGKLEALAILLQK.L
*	HsFLAG-TIP49b_Ti_	4.5468	0.3058	1987.84	1987.39	11719.8	1	1809.1	61.8	8	R.LVQFDSGKLEALAILLQK.L
*	HsH2AZ-FLAG_293_	3.6665	0.3035	1305.49	1305.486	6428.9	1	1418	85	11	R.IFCAILSTHSR.T
*	HsMRGBP-FLAG_Ti_	4.4277	0.5186	2855.09	2856.174	5228.5	1	739.8	44	5	R.TTGINLVEADTVVFYDNDLNPVMDAK.A
*	HsMRGBP-FLAG_Ti_	3.6402	0.3716	2856.55	2856.174	10214.3	1	690.1	26	1	R.TTGINLVEADTVVFYDNDLNPVMDAK.A
*	HsMRGBP-FLAG_Ti_	5.0944	0.4626	1902.67	1902.089	7287.2	1	1185.5	62.5	11	R.EVAAQGNDYSMAFLTQR.T
*	HsMRGBP-FLAG_Ti_	4.4697	0.3571	1903.5	1902.089	7317	1	1258.1	42.2	1	R.EVAAQGNDYSMAFLTQR.T
*	HsMRGBP-FLAG_Ti_	4.7111	0.43	2288.34	2287.589	5291.2	1	973.8	57.9	6	R.TIQELFEVYSPMDDAGFPVK.A
*	HsMRGBP-FLAG_Ti_	4.8148	0.3049	4444.81	4444.007	6684.2	1	880.6	23.7	2	R.TIQELFEVYSPMDDAGFPVKAEEFVVLSQEPSVTETIAPK.I
*	HsMRGBP-FLAG_Ti_	5.878	0.2954	2176.42	2175.441	6278.2	1	1259.7	60.5	16	K.AEEFVVLSQEPSVTETIAPK.I
*	HsMRGBP-FLAG_Ti_	4.3534	0.2291	2176.55	2175.441	7000.4	1	1285.7	42.1	1	K.AEEFVVLSQEPSVTETIAPK.I
*	HsTIP60_Ti_102.169	4.3428	0.2697	1324.28	1325.415	6946	1	1478.4	85	5	K.SIEYLEEDAQK.S
*	HsYL1_Ti_101.1862.	3.4053	0.168	1325.59	1325.415	8514.5	4	968.1	70	2	K.SIEYLEEDAQK.S
*	HsH2AZ-FLAG_293_	5.7121	0.426	2098.29	2099.348	7769.6	1	1743.1	71.9	24	K.YALNYLELFHTSIEQEK.E
*	HsH2AZ-FLAG_293_	4.0072	0.2487	2098.75	2099.348	4568.7	1	702.8	39.1	5	K.YALNYLELFHTSIEQEK.E
*	HsFLAG-TIP49b_Ti_	4.664	0.3493	1478.45	1478.62	4930.2	1	1210.1	83.3	6	K.ERNSEDAVMTAVR.A
*	HsMRGBP-FLAG_Ti_	2.6599	0.1372	1094.5	1094.258	3246.3	2	777.8	85.7	1	R.AWEFWNLK.T
*	HsMRGBP-FLAG_Ti_	6.4578	0.3924	1867.05	1865.094	7749.1	1	2455.7	82.1	10	R.LRLEQEEAELLTYTR.E
*	HsMRGBP-FLAG_Ti_	3.615	0.3785	1595.59	1595.747	6223.5	1	1283.7	75	1	R.LEQEEAELLTYTR.E
*	HsTIP60_Ti_106.188	2.5902	0.2318	1246.51	1246.415	4818.2	1	518.3	70	2	K.QRHGEAVVPPR.S
*	HsFLAG-TIP49b_Ti_	3.38	0.284	963.49	962.096	4983.4	1	692	81.2	11	R.HGEAVVPPR.S
*	HsMRGBP-FLAG_Ti_	3.6541	0.3638	963.51	962.096	7059.7	1	1909.2	100	21	R.HGEAVVPPR.S
*	HsMRGBP-FLAG_Ti_	5.5942	0.3562	3565.14	3564.032	9132.2	1	1088.4	25.8	3	K.PLPTFAKPTAEPGQDNPEWLISEDWALLQAVK.Q
*	HsMRGBP-FLAG_Ti_	4.6207	0.5104	2808.14	2809.105	6897.6	1	861.6	41.7	6	K.PTAEPGQDNPEWLISEDWALLQAVK.Q
*	HsMRGBP-FLAG_Ti_	3.6529	0.2815	2809.12	2809.105	7238.8	1	1147.7	35.4	1	K.PTAEPGQDNPEWLISEDWALLQAVK.Q
*	HsFLAG-TIP49a_Ti_	4.8568	0.3242	3592.93	3590.037	5309.7	1	677	28.2	7	K.QLLELPLNLTIVSPAHTPNWDLVSDVVNSCSR.I
*	HsMRGBP-FLAG_Ti_	2.0768	0.0867	1273.75	1274.465	3262.3	9	184.8	61.1	1	R.NRYENVIIPR.E
*	HsYL1_Ti_104.1528.	3.6521	0.152	1274.35	1274.465	5065.2	1	987.1	83.3	15	R.NRYENVIIPR.E
*	HsFLAG-TIP49b_Ti_	3.2941	0.4119	2942.64	2944.202	11583.4	1	822.6	35.4	3	R.TSQIYAQDENATHTQLYTSHFDLMK.M
*	HsMRGBP-FLAG_Ti_	4.3	0.2649	2944.41	2944.202	5759.4	1	674.4	30.2	3	R.TSQIYAQDENATHTQLYTSHFDLMK.M
*	HsFLAG-TIP49b_Ti_	5.5029	0.4392	2675.24	2677.076	7208.7	1	1100.6	47.9	6	K.HASVLAESGINYDKPLPPIQVASLR.A
*	HsTIP60_Ti_106.236	5.4258	0.5654	1728.55	1727.999	5387.3	1	1528.2	75	14	K.AQPAITTGGSAAVLAGTIK.T
*	HsTIP60_Ti_105.364	4.1352	0.1418	3393.91	3392.849	4616.4	5	301.3	20.6	1	K.TSVTGTSMPTGAVSGNVIVNTIAGVPAATFQSINK.R

*	HsTIP60_Ti_105.225	4.4418	0.4949	2130.35	2131.409	5168.9	1	725.5	52.4	11	R.AVGSPATATPDLVSMATTQGVR.A
*	HsMRGBP-FLAG_Ti_	4.7083	0.377	1711.43	1709.984	5106.8	1	1128.5	68.8	15	R.SLVPQVSQATGVQLPGK.T
*	HsFLAG-TIP49b_Ti_	2.642	0.1611	1296.48	1297.543	4453.1	2	254.2	60	1	K.TITPAHFQLLR.Q
*	HsFLAG-TIP49b_Ti_	3.0554	0.197	1297.32	1297.543	5691.2	1	584.9	70	3	K.TITPAHFQLLR.Q
*	HsMRGBP-FLAG_Ti_	3.514	0.4064	1683.57	1682.961	6894.2	1	752.9	53.1	3	R.PGALLTGTTVANLQVAR.L
*	HsFLAG-TIP49a_Ti_	4.3718	0.3266	1920.52	1920.28	4757	1	770.2	58.8	14	K.AAGQTVVAQPVHMQQLLK.L
*	HsTIP60_Ti_104.135	4.3044	0.3016	1606.27	1606.822	6872.3	1	1376.1	48.3	2	K.AIQPQAAQGPAAVQQK.I
*	HsTIP60_Ti_104.135	4.5205	0.4676	1606.44	1606.822	6042.1	1	1084.4	66.7	10	K.AIQPQAAQGPAAVQQK.I
*	HsTIP60_Ti_103.142	2.0138	0.2567	1484.55	1485.681	5438.9	5	286.8	46.2	2	K.ITAQQITTPGAQQK.V
*	HsYL1_Ti_102.1422.	4.4747	0.1296	1487.1	1485.681	5872.4	3	798.7	65.4	5	K.ITAQQITTPGAQQK.V
*	HsYL1_Ti_102.1386.	2.6223	0.2436	1031.65	1032.228	5128.7	4	629.3	66.7	4	K.VAYAAQPALK.T
*	HsTIP60_Ti_103.14	3.4472	0.322	1031.78	1032.228	6233.2	1	1609.7	88.9	4	K.VAYAAQPALK.T
*	HsTIP60_Ti_103.386	4.1067	0.3163	1462.54	1463.674	6408.6	1	1510.3	83.3	23	K.TQFLTTPISQAQK.L
*	HsMRGBP-FLAG_Ti_	2.6063	0.2805	1463.66	1463.674	6485.4	3	358.6	50	4	K.TQFLTTPISQAQK.L
*	HsYL1-FLAG_Ti_20	4.0467	0.3487	1582.81	1583.828	7310.2	1	746.8	57.1	6	K.LAGAQQVQTQIQVAK.L
*	HsMRGBP-FLAG_Ti_	5.2339	0.1908	1584.24	1583.828	8102.8	1	1296.6	67.9	11	K.LAGAQQVQTQIQVAK.L
*	HsYL1-FLAG_Ti_20	4.5191	0.3383	3742.12	3741.15	5959.5	1	589.9	22.2	10	K.LIQQQVVTTASAPLQTPGAPNPAQVPASSDSPSQQPK.L
gi|14165464|r		22	259	47.60%	550	59037	9.2	polypyrimidine tract-binding protein 1 isoform b [Homo sapiens]			
gi|4506243|re		22	259	47.00%	557	59633	9.2	polypyrimidine tract-binding protein 1 isoform a [Homo sapiens]			
gi|14165466|r		22	259	49.30%	531	57221	9.2	polypyrimidine tract-binding protein 1 isoform c [Homo sapiens]			
	HsFLAG-p53-DNA-D	6.0625	0.5056	2112	2113.502	8692.8	1	2927.3	73.7	33	R.KLPIDVTEGEVISLGLPFGK.V
	HsFLAG-FLJ20729_	3.8365	0.2806	2112.99	2113.502	6658.7	1	922.4	35.5	3	R.KLPIDVTEGEVISLGLPFGK.V
	HsFLAG-FLJ20309_	5.8117	0.513	1984.9	1985.328	9573.4	1	2685.9	69.4	22	K.LPIDVTEGEVISLGLPFGK.V
	HsFLAG-p53-DNA-D	3.1954	0.267	1432.45	1432.622	4557.9	1	728.2	72.7	17	R.GQPIYIQFSNHK.E
	HsFlag-VPS71_Ti_1	5.7021	0.4921	3684.59	3683.193	8671.6	1	937.6	23	6	R.I
	HsFLAG-p53-DNA-D	4.5342	0.3786	2488.4	2489.96	4882.1	1	774.5	37.5	13	R.IIVENLFYPVTLDVLHQIFSK.F
	HsFLAG-p53-DNA-D	4.434	0.3972	2489.01	2489.96	4687.7	1	493.7	47.5	13	R.IIVENLFYPVTLDVLHQIFSK.F
	HsFLAG-p53-DNA-D	5.2614	0.4844	2243.61	2244.472	7116.9	1	1126.6	57.9	18	K.NNQFQALLQYADPVSAQHAK.L
	HsFLAG-UTX1_Ti_2	5.8021	0.3697	2245.95	2244.472	6195.1	1	1313.6	43.4	17	K.NNQFQALLQYADPVSAQHAK.L
	HsFLAG-FLJ20729_	4.497	0.3186	1898.54	1899.043	5559	1	801.2	63.3	8	K.LSLDGQNIYNACCTLR.I
	HsARP6-FLAG_Ti_1	5.8915	0.4869	2275.53	2276.641	6017.9	1	1836.7	70.5	35	R.IAIPGLAGAGNSVLLVSNLNPER.V
	HsFLAG-p53-DNA-D	5.3335	0.4058	2277.01	2276.641	6915.2	1	1280.8	39.8	10	R.IAIPGLAGAGNSVLLVSNLNPER.V
	HsARP6-FLAG_Ti_1	5.3045	0.3742	2039.5	2040.37	7983.6	1	1966.9	48.5	7	R.VTPQSLFILFGVYGDVQR.V
	HsFLAG-Lin9_Ti_20	5.7329	0.5427	2039.95	2040.37	8433.1	1	2625	76.5	36	R.VTPQSLFILFGVYGDVQR.V
	HsFLAG-p53-DNA-D	2.1483	0.1959	820.58	821.013	4338.6	1	357.7	83.3	4	K.LHGKPIR.I
	HsFLAG-Lin9_Ti_20	1.9757	0.1111	991.49	992.126	6845.7	6	502.8	71.4	1	K.HQNVQLPR.E
	HsFlag-DPCD_Ti_20	3.1713	0.18	992.06	992.126	5582.1	1	1000.7	92.9	3	K.HQNVQLPR.E
	HsFLAG-p53-DNA-D	2.1395	0.2256	1058.45	1059.126	2975.3	3	297.3	75	1	K.DYGNSPLHR.F
	HsFLAG-p53-DNA-D	4.5902	0.3295	2995.05	2996.346	5340.4	1	720.1	44.2	3	K.NFQNIFPPSATLHLSNIPPSVSEEDLK.V
	HsFLAG-p53-DNA-D	4.6889	0.3206	2996.75	2996.346	4887.7	1	813.7	34.6	4	K.NFQNIFPPSATLHLSNIPPSVSEEDLK.V
	HsFlag-VPS71_Ti_1	1.9205	0.1218	1106.58	1107.295	5729.9	8	295.4	55	1	K.VLFSSNGGVVK.G
	HsFLAG-p53-DNA-D	5.8092	0.2644	3492.22	3492.953	6143.8	1	1021.8	31.7	4	K.MALIQMGSVEEAVQALIDLHNHDLGENHHLR.V
gi|4758560|re		11	37	47.60%	357	39299	8.1	WD repeat domain 57 (U5 snRNP specific) [Homo sapiens]			

*	HsFLAG-p53-DNA-D	3.2244	0.2236	1333.74	1333.66	4445.5	1	599.8	72.7	4	R.KGPELPLVPVKR.Q
*	HsFlag-ZnF-HIT2_Ti_	6.0179	0.3756	2850.7	2851.195	7902.3	1	2901.9	41.4	5	R.HELLLGAGSGPGAGQQQATPGALLQAGPPR.C
*	HsFlag-ZnF-HIT2_Ti_	3.8929	0.3285	1576.91	1577.696	3277.9	1	560.7	67.9	2	K.FHPNGSTLASAGFDR.L
*	HsFlag-ZnF-HIT2_Ti_	2.7819	0.2782	2172.86	2172.452	7204.3	1	560.9	47.1	1	R.LILLWNVYGDCDNYATLK.G
*	HsFlag-ZnF-HIT2_Ti_	3.8451	0.3096	1495.78	1496.588	7009.6	1	1463.7	79.2	2	K.GHTSFVNSCYPAR.K
*	HsFlag-ZnF-HIT2_Ti_	6.8371	0.4744	3702.01	3703.054	7897.6	1	1447.9	30.3	6	K.AAIQTFQNTYQVLAVTFNDTSDQIISGGIDNDIK.V
*	HsScrap_Ti_105.212	2.8894	0.1746	1215.68	1215.44	4251.5	7	707.9	83.3	2	R.VWDVRPFAPK.E
*	HsFlag-ZnF-HIT2_Ti_	2.9397	0.247	1332.46	1333.489	5121.6	1	412.8	60	1	K.IFQGNVHNFEK.N
*	HsFlag-ZnF-HIT2_Ti_	4.1945	0.3563	1333.45	1333.489	6782.1	1	1570.4	90	7	K.IFQGNVHNFEK.N
*	HsFlag-ZnF-HIT2_Ti_	5.99	0.4579	2802.99	2803.101	6847	1	1130.2	32.7	5	K.LPGHAGSINEVAFHPDEPIIISASSDK.R
*	HsSrcap_Ti_205.249	4.1242	0.3423	2803.16	2803.101	6470.6	1	563.4	36.5	2	K.LPGHAGSINEVAFHPDEPIIISASSDK.R
gi|4503745|re	81	357	47.40%	2647	280759	6.1	filamin 1 (actin-binding protein-280) [Homo sapiens]				
*	HsFLAG-ARP6_Ti_2	3.5989	0.3342	1443.36	1443.516	6015.6	1	1002.6	65.6	3	R.AGQSAAGAAPGGGVDTR.D
*	HsFLAG-Lin9_Ti_20	3.1046	0.2153	1572.55	1572.762	5977	1	938.9	69.2	2	K.RIANLQTDLSDGLR.L
*	HsFLAG-p53-DNA-D	3.9845	0.2649	1416.59	1416.574	7686.4	1	1347.7	79.2	3	R.IANLQTDLSDGLR.L
	HsFLAG-p53-DNA-D	4.3406	0.3465	1227.4	1227.53	5275.5	1	1365.1	90	13	R.LIALLEVLSQK.K
	HsFLAG-p53-DNA-D	3.4629	0.0813	972.27	972.175	2910.7	4	584.7	92.9	2	R.LLGWIQNK.L
*	HsFLAG-UTX1_Ti_2	2.7766	0.1423	1286.54	1286.517	3193.9	1	715.4	90	2	K.LPQLPITNFSR.D
*	HsFlag-VPS71_Ti_1	4.4143	0.464	2593.03	2592.754	4248.2	1	710.2	50	1	R.ALGALVDSCAPGLCPDWDSWDASK.P
*	HsFLAG-p53-DNA-D	4.3538	0.3957	3230.61	3231.478	5752	1	858.1	30.2	2	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E
*	HsFLAG-p53-DNA-D	5.4656	0.3911	4571.61	4573.102	4532	1	710.4	26.3	1	.A
*	HsFLAG-p53-DNA-D	3.2676	0.344	2313.4	2314.47	4620.5	1	288.3	35.7	1	R.SAGQGEVLVYYVEDPAGHQEEAK.V
*	HsFLAG-p53-DNA-D	3.5937	0.3765	1750.6	1751.979	5965.8	1	554.5	57.1	7	R.TFSVWYVPEVTGTHK.V
*	HsFLAG-p53-DNA-D	4.1195	0.2523	1284.43	1284.544	6055.7	1	1409	86.4	12	K.VTVLFAGQHIAK.S
*	HsFLAG-Lin9_Ti_20	4.1521	0.4129	1653.21	1653.833	5463.3	1	1157.3	71.9	7	K.VTAQGPGLEPSGNIANK.T
*	HsFLAG-Lin9_Ti_20	3.5821	0.3106	2683.2	2685.039	5188.9	1	597.2	30.4	1	R.CSYQPTMEGVHTVHVTFAGVPIPR.S
*	HsFLAG-p53-DNA-D	2.8893	0.2077	1227.27	1227.406	7756.9	1	1068.8	75	1	R.AWGPGLEGGVVGK.S
*	HsFLAG-p53-DNA-D	4.0814	0.3937	2536.93	2537.714	6498.1	1	745.7	50	5	R.YWPQEAGEYAVHVLCNSEDIR.L
*	HsFLAG-p53-DNA-D	4.088	0.3471	1647.48	1647.869	5146.6	1	1103.5	70	2	K.TGVAVNKPAEFTVDAK.H
*	HsFLAG-p53-DNA-D	4.8023	0.3784	1786.18	1785.958	7899.8	1	1530.4	70	2	R.VQVQDNEGCPVEALVK.D
*	HsFLAG-p53-DNA-D	5.4977	0.558	1943.83	1944.218	6908.4	1	1574.9	70.6	2	K.HTAMVSWGGVSIPNSPFR.V
*	HsFLAG-ARP5_Ti_1	4.0132	0.1583	1307.26	1307.495	9962.4	1	1898.4	79.2	2	R.VNVGAGSHPNKVK.V
*	HsFlag-FLJ20643_Ti	2.0978	0.2021	790.61	790.938	5262.4	7	388.5	64.3	2	K.VYGPGVAK.T
*	HsFLAG-p53-DNA-D	4.9325	0.329	2297.61	2297.631	8142.9	1	892.3	47.6	6	R.GAGSYTIMVLFADQATPTSPIR.V
*	HsFLAG-UTX1_Ti_2	2.8913	0.1904	1197.31	1197.334	4546.1	1	889.1	85	1	R.VKVEPSHDASK.V
*	HsFLAG-UTX1_Ti_2	5.002	0.3499	1699.5	1699.947	4378.9	1	759.6	66.7	10	R.TGVELGKPTHFTVNAK.A
*	HsFLAG-Lin9_Ti_20	3.5632	0.3085	1785.38	1785.908	10500.8	1	1010.1	57.1	1	R.DVDIIDHHDNTYTVK.Y
*	HsFLAG-p53-DNA-D	4.6663	0.4711	2286.84	2287.577	6354.5	1	959.6	57.1	9	K.YTPVQQGPVGVNVTYGGDPIPK.S
*	HsFLAG-p53-DNA-D	3.8946	0.2934	1534.54	1534.75	6323.8	1	1073.1	67.9	4	K.SPFSVAVSPSLDLSK.I
*	HsFlag-FLJ90652_2	2.8536	0.1847	1535.54	1534.75	4550.1	3	255.2	50	1	K.SPFSVAVSPSLDLSK.I
*	HsFLAG-p53-DNA-D	3.5874	0.3643	1366.16	1365.526	5557.9	1	1141.6	86.4	3	K.VDVGKDQEFTVK.S
*	HsFLAG-p53-DNA-D	4.0499	0.2504	2449.62	2450.764	7169.1	1	1191.3	34.4	4	K.IVGPSGAAVPCKVEPGLGADNSVVR.F
*	HsFLAG-p53-DNA-D	4.4921	0.4121	2450.92	2450.764	4701.1	1	510.8	45.8	3	K.IVGPSGAAVPCKVEPGLGADNSVVR.F

*	HsFlag-VPS71_Ti_1	4.8129	0.2669	4001.74	4001.525	5755.9	1	666.5	23.6	2	R.FLPREEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V
*	HsFLAG-Lin9_Ti_20	6.2647	0.4322	3485.54	3487.885	8633.5	1	1693.6	32	17	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V
*	HsFLAG-FLJ20309_	4.0262	0.2027	1430.59	1430.563	6545.4	1	1400.6	76.7	17	K.AFGPGLQGGSAGSPAR.F
*	HsFLAG-UTX1_Ti_2	5.2065	0.4856	2764.36	2765.018	9848.8	1	1297.9	46	5	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E
*	HsFlag-DPCD_Ti_20	4.2709	0.3239	2766.01	2765.018	8807.4	1	911.7	31	1	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E
*	HsFLAG-p53-DNA-D	3.1623	0.3246	1109.16	1109.271	6854.3	1	673.5	65	4	R.ALTQTGGPHVK.A
*	HsFLAG-p53-DNA-D	5.1774	0.5057	1764.4	1764.889	6226	1	1490.6	80	4	R.VANPSGNLTETYVQDR.G
*	HsFLAG-Lin9_Ti_20	3.9304	0.3798	4297.59	4299.57	8057.5	1	519	19.7	2	V
*	HsFLAG-Lin9_Ti_20	4.7343	0.4085	1636.35	1635.82	6416.7	1	1015.7	63.3	11	R.VHGPGIQSGTTNKPNK.F
*	HsFLAG-p53-DNA-D	4.0166	0.4269	1572.41	1571.728	8724	1	1002.1	55.9	2	R.GAGTGGLGLAVEGPSEAK.M
*	HsFLAG-UTX1_Ti_2	3.7275	0.2805	3581.5	3581.84	3758.3	1	423.1	25	2	K.DGSCSVEYIPYEAGTYSLNVTYGGHQVPGSPFK.V
*	HsFLAG-p53-DNA-D	3.0267	0.3095	1167.53	1168.292	7348.6	1	812.8	65	1	K.VPVHDVTDASK.V
*	HsFlag-FLJ90652_2	2.9708	0.3382	1168.4	1168.292	8606	1	1275.4	80	5	K.VPVHDVTDASK.V
*	HsFLAG-p53-DNA-D	2.5357	0.2678	1395.4	1395.599	9030	1	1208	66.7	1	K.VPVHDVTDASKVK.C
*	HsFLAG-Lin9_Ti_20	3.6481	0.3538	1435.49	1435.577	5775.5	1	711.6	66.7	3	R.ANLPQSFQVDTSK.A
*	HsFLAG-p53-DNA-D	2.1455	0.1337	882.55	883.079	4897.2	1	497.6	68.8	1	K.AGVAPLQVK.V
*	HsFlag-DPCD_Ti_20	6.2329	0.4022	2544.64	2545.765	9298.9	1	2256.9	58.7	9	K.GLVEPVDVVDNADGTQTVNYVPSR.E
*	HsFLAG-p53-DNA-D	4.4012	0.3528	1910.18	1911.075	7810	1	1097.7	62.5	3	R.EGPYSISVLYGDEEVPR.S
*	HsFLAG-Lin9_Ti_20	4.5215	0.4423	2342.77	2343.639	4680.3	1	576.8	47.8	14	K.ASGPGLNTTGVPASLPVEFTIDAK.D
*	HsFLAG-p53-DNA-D	4.9386	0.3447	1938.3	1939.173	6546.9	1	1548.9	63.9	7	K.DAGEGLLAVQITDPEGKPK.K
*	HsFLAG-p53-DNA-D	3.1622	0.087	1401.5	1401.518	3801.8	7	498.2	68.2	1	K.YGGDEIPFSPYR.V
*	HsFLAG-p53-DNA-D	4.8022	0.2466	2947.04	2947.28	5312.1	1	803.6	32.4	4	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S
*	HsFlag-VPS71_Ti_1	1.8622	0.1976	1086.55	1087.218	5590	2	430.9	66.7	1	K.VAQPTITDNK.D
*	HsFlag-VPS71_Ti_1	3.2191	0.1686	1088.32	1087.218	2987.8	1	476.3	83.3	3	K.VAQPTITDNK.D
*	HsFlag-DPCD_Ti_20	3.698	0.3212	1501.31	1501.634	8172.2	1	1655.5	73.3	1	K.DAGEGGLSLAIEGPSK.A
*	HsFLAG-UTX1_Ti_2	4.0206	0.3504	1604.78	1603.734	3393.3	1	665.2	76.9	13	K.YNEQHVPGSPFTAR.V
*	HsFLAG-Lin9_Ti_20	2.9505	0.3333	2894.25	2895.28	8032.7	1	458.2	30.4	1	K.VGSAADIPINISETDLSLLTATVVPPSGR.E
*	HsFLAG-Lin9_Ti_20	4.699	0.3213	3766.98	3765.259	4014.5	2	320.7	22.1	6	K.VGSAADIPINISETDLSLLTATVVPPSGREEPCLLK.R
*	HsFLAG-Lin9_Ti_20	2.5744	0.3508	1154.45	1155.342	3514	1	481.7	75	2	R.NGHVGISFVPK.E
*	HsFLAG-Lin9_Ti_20	2.3848	0.2541	1148.34	1149.292	4288.5	6	284.3	55.6	2	K.ETGEHLVHVK.K
*	HsFLAG-Lin9_Ti_20	4.9679	0.3772	2448.95	2449.683	6843.8	1	1053.7	50	2	K.NGQHVASSPIPVVISQSEIGDASR.V
*	HsFlag-NUFIP_Ti_2	3.5451	0.2248	2449.63	2449.683	9088.4	1	863.5	29.3	1	K.NGQHVASSPIPVVISQSEIGDASR.V
*	HsFLAG-p53-DNA-D	4.988	0.4442	2441.02	2441.662	7311.8	1	741.2	42.9	6	R.VSGQGLHEGHTFEPAEFIIDTR.D
*	HsFLAG-p53-DNA-D	4.9699	0.3445	2441.46	2441.662	7824.9	1	1755.2	41.7	3	R.VSGQGLHEGHTFEPAEFIIDTR.D
*	HsFLAG-Lin9_Ti_20	3.62	0.1945	1517.58	1516.696	4094.9	1	940.4	80.8	11	K.FADQHVPGSPFSVK.V
*	HsFLAG-p53-DNA-D	4.2831	0.3367	1656.71	1655.814	6074.2	1	785.4	60	2	R.APSVANVGSHCDLSLK.I
*	HsFlag-DPCD_Ti_20	5.7658	0.462	2004.19	2003.275	8033.8	1	2055.2	69.4	5	K.IPEISIQDMTAQVTSPSGK.T
*	HsFLAG-Lin9_Ti_20	5.3786	0.4359	2059.36	2059.166	7437.7	1	1824.9	71.9	1	K.THEAEIVEGENHTYCIR.F
*	HsFLAG-UTX1_Ti_2	4.0357	0.3473	1506.53	1503.756	3519.6	1	595.3	76.9	18	R.FVPAEMGTHTVSVK.Y
	HsFLAG-Lin9_Ti_20	3.8552	0.2523	2304.71	2305.558	4151	1	606.8	35.2	1	K.GQHVPGSPFQFTVGPLGEGGAHK.V
*	HsARP6-FLAG_Ti_1	3.084	0.1445	1534.1	1534.712	3697.9	1	467.3	65.4	1	R.AEAGVPAEFSIWTR.E
*	HsMRGBP-FLAG_Ti	4.7088	0.4383	2258.47	2259.397	5588.7	1	722.6	50	6	K.DGSCGVAYVVQEPGDYEVSVK.F
*	HsFLAG-Lin9_Ti_20	4.7615	0.3307	2469.12	2468.685	5104.5	1	632.9	47.7	7	K.FNEEHIPDSPFVVPVASPSGDAR.R

*	HsFLAG-p53-DNA-D	4.1592	0.308	1418.66	1418.633	8541.7	1	2014.3	83.3	3	R.RLTVSSLQESGLK.V
*	HsFLAG-p53-DNA-D	3.8937	0.3914	1503.28	1503.698	4371.1	1	771.3	71.4	3	K.VNQPASFAVSLNGAK.G
*	HsFLAG-p53-DNA-D	4.6871	0.4896	2277.82	2278.4	7459.7	1	1530.5	60.5	1	K.VHSPSGALEECYVTEIDQDK.Y
*	HsFLAG-p53-DNA-D	2.7738	0.2914	1741.61	1742.083	5092.7	1	713.7	60	2	R.VTYTPMAPGSYLISIK.Y
*	HsFLAG-p53-DNA-D	5.2037	0.4783	2200.21	2201.441	10857.9	1	1489.2	55.3	5	R.LVSNHSLHETSSVFVDSLTK.A
*	HsFLAG-p53-DNA-D	4.6486	0.4827	1790.63	1790.896	7629.8	1	1471.5	66.7	18	K.ATCAPQHGAPGPGPADASK.V
*	HsFLAG-p53-DNA-D	3.6488	0.2843	1435.24	1435.687	7073.7	1	814.1	61.5	1	K.AGNNMLLVGVHGPR.T
gi|4504041|re	12	37	47.30%	355	40451	5.5	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.7857	0.445	1737.84	1738.095	8464.8	1	1855.2	73.3	7	R.AVVYSNTIQSIMAIVK.A
*	HsFLAG-ARP6_Ti_1	4.5852	0.4027	2619.58	2619.898	5891	1	897.3	50	2	R.QLFALSCTAEEQGVLPDDLSGVIR.R
*	HsFLAG-ARP6_Ti_1	4.0565	0.4289	1517.22	1517.653	7134.8	1	1425.4	79.2	2	R.LWADHGVQACFGR.S
*	HsFLAG-ARP6_Ti_1	3.3598	0.2993	2077.59	2078.199	7062.7	1	1203.3	56.2	1	R.EYQLNDSAAYYLNDLER.I
*	HsFLAG-ARP6_Ti_1	3.9927	0.2312	1748.39	1747.946	3500.5	1	622.9	71.4	1	R.IAQSDYIPTQQDVLR.T
	HsFLAG-ARP6_Ti_1	3.3505	0.2431	1381.35	1381.571	5505.5	1	661.5	68.2	5	K.TTGIVETHFTFK.D
	HsFLAG-ARP6_Ti_1	3.8486	0.2132	1599.42	1598.882	7907.5	1	1179.4	70.8	2	K.WFTDTSIILFLNK.K
	HsFLAG-ARP6_Ti_1	3.3093	0.3202	1727.16	1727.056	5833.3	1	574.2	53.8	3	K.WFTDTSIILFLNKK.D
*	HsFLAG-ARP6_Ti_1	4.5912	0.4609	2051.04	2050.285	6052.6	1	720.7	58.8	3	K.ITHSPLTICFPEYTGANK.Y
*	HsFLAG-ARP6_Ti_1	4.6692	0.4351	3304.93	3306.619	4291.7	1	634.9	30.4	3	K.ITHSPLTICFPEYTGANKYDEAASYIQSK.F
	HsFLAG-ARP6_Ti_1	3.3771	0.3264	1587.44	1587.692	7621.9	1	909.3	66.7	2	K.EIYTHFTCATDTK.N
	HsFLAG-ARP6_Ti_1	3.2254	0.2473	1708.53	1708.995	6149.4	1	791.4	57.1	6	K.NVQFVFDAVTDVIIK.N
gi|13514822|r	12	115	47.20%	235	24336	10.1	DEAH (Asp-Glu-Ala-His) box polypeptide 9 isoform 2 [Homo sapiens]				
	HsFLAG-ARP6_Ti_2	3.4378	0.3035	1317.61	1318.514	5631.8	1	986.1	80	20	K.YPSPFFVFGEK.I
*	HsFlag-NUFIP_Ti_10	4.8391	0.4198	1733.2	1733.163	3727	1	774.7	70	22	K.GMTLVTPLQLLLFASK.K
	HsFLAG-p53-DNA-D	5.4654	0.3775	1845.43	1844.118	7887.5	1	1665.6	70	7	K.KVQSDGQIVLVDDWIK.L
	HsFLAG-FLJ20309_	4.8924	0.3788	1717.24	1715.944	7152.9	1	1200.2	67.9	6	K.VQSDGQIVLVDDWIK.L
	HsFlag-NUFIP_Ti_10	5.258	0.4263	1640.29	1640.846	7628.4	1	1890	75	12	K.LQISHEAAACITGLR.A
	HsFLAG-FLJ20309_	4.5725	0.2924	1261.29	1261.519	6164.2	1	1670.6	81.8	14	R.AAMEALVVEVTK.Q
	HsFLAG-p53-DNA-D	3.5996	0.3327	2823.05	2823.277	7397.5	2	495.7	26	1	R.AAMEALVVEVTKQPAIISQLDPVNER.M
	HsFlag-NUFIP_Ti_10	3.4529	0.3515	1579.91	1580.781	6517.9	1	939.5	73.1	12	K.QPAIISQLDPVNER.M
*	HsFlag-NUFIP_Ti_11	4.642	0.398	1872.96	1873.181	4456.7	1	434.1	52.9	7	R.QISRPSAAGINLMIGSTR.Y
*	HsFlag-NUFIP_Ti_11	4.1451	0.3157	1873.42	1873.181	8214.4	2	1007.5	38.2	1	R.QISRPSAAGINLMIGSTR.Y
	HsFlag-NUFIP_Ti_10	3.0058	0.3262	1388.64	1388.625	9432	1	808.2	61.5	1	R.PSAAGINLMIGSTR.Y
	HsFLAG-FLJ20309_	3.1395	0.1749	987.26	987.103	6653.1	4	755.5	75	12	R.YGDGPRPPK.M
gi|4503297|re	55	637	47.10%	1279	142069	6.6	DEAH (Asp-Glu-Ala-His) box polypeptide 9 isoform 1 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	2.9228	0.2069	1159.12	1159.296	5750.8	7	978.8	81.2	2	K.NFLYAWCGK.R
*	HsFLAG-FLJ20309_	2.8073	0.1427	1159.52	1159.296	7258.2	2	559	68.8	8	K.NFLYAWCGK.R
*	HsFLAG-FLJ20309_	3.4469	0.2345	1026.29	1026.18	5994.6	2	1124	92.9	7	R.DFVNYLVR.I
*	HsFLAG-ARP6_Ti_1	4.8173	0.506	2162.61	2164.252	4998	1	889.2	60	21	K.AENNSEVGASGYGVPGPTWDR.G
*	HsFlag-NUFIP_Ti_11	6.8985	0.4099	3483.23	3483.727	12140.9	1	2333.3	32.5	82	R.KEEQEVQATLESEEVDLNAGLHGNWTLENAK.A
*	HsFLAG-p53-DNA-D	3.4209	0.3334	1187.43	1187.257	4954.5	1	778.9	83.3	11	K.YTQVGPDHNR.S
*	HsFlag-NUFIP_Ti_11	3.2333	0.2408	1318.5	1316.598	6916	1	910.8	70	2	R.SFIAEMTIYIK.Q
*	HsFLAG-ARP6_Ti_1	4.4161	0.3866	1417.12	1417.658	6823.2	1	1667.4	83.3	8	K.KLAAQSCALSLVR.Q
*	HsFlag-NUFIP_Ti_11	3.9204	0.1646	1418.21	1417.658	9369.5	1	1714.8	54.2	2	K.KLAAQSCALSLVR.Q

*	HsFlag-NUFIP_Ti_10	4.5423	0.3326	1289.41	1289.484	7852.7	1	1875.9	86.4	9	K.LAAQSCALSLVR.Q
*	HsFlag-NUFIP_Ti_10	2.9562	0.2383	1308.17	1308.474	6966.5	1	950.5	75	1	K.KKEGETVEPYK.V
*	HsFlag-DPCD_Ti_20	5.0287	0.2813	4330.93	4329.938	4980.1	1	703.4	25	9	K.VNLSQDLEHQLQNIIQELNLEILPPPEDPSVPVALNIGK.L
*	HsFLAG-p53-DNA-D	5.3988	0.4737	2487.53	2487.747	9719.9	1	1684.5	57.9	8	K.NELMYQLEQDHDLQAILQER.E
*	HsFLAG-Lin9_Ti_20	4.3725	0.3303	2488.22	2487.747	6862.6	1	1337.8	40.8	2	K.NELMYQLEQDHDLQAILQER.E
*	HsFlag-NUFIP_Ti_11	5.554	0.2953	2176.06	2176.518	10987.8	1	3058.3	48.6	11	K.KFESEILEAISQNSVVIIR.G
*	HsFlag-NUFIP_Ti_11	6.4105	0.4915	2176.26	2176.518	7642.7	1	2289.1	72.2	24	K.KFESEILEAISQNSVVIIR.G
*	HsFLAG-ARP6_Ti_1	5.3362	0.4051	2050.77	2051.263	4727.2	1	1254.9	75	45	K.TTQVPQFILDDFIQNDR.A
*	HsFLAG-p53-DNA-D	3.7786	0.1512	1359.37	1358.503	9071.1	1	1788.3	77.3	15	R.AAECNIVVTQPR.R
*	HsFlag-NUFIP_Ti_10	3.7771	0.1832	1088.78	1088.252	7114.9	1	1397.9	94.4	36	R.RISAVSVAER.V
*	HsFLAG-FLJ20309_	2.978	0.2283	931.64	932.065	6107.1	1	1431.6	93.8	1	R.ISAVSVAER.V
*	HsFlag-NUFIP_Ti_10	3.1527	0.1946	1219.05	1219.34	4351.7	7	801	80	3	R.VAFERGEEPGK.S
*	HsFlag-NUFIP_Ti_11	5.484	0.4806	1701.82	1702.034	8117.5	1	2329.8	85.7	12	R.PHASIMFCTVGVLLR.K
*	HsFLAG-FLJ20729_	4.2758	0.3335	1504.4	1504.686	5922.5	1	1176.5	75	18	R.GISHVIVDEIHER.D
*	HsFlag-NUFIP_Ti_10	4.3683	0.2984	1504.73	1504.686	7294.2	2	1826.4	58.3	7	R.GISHVIVDEIHER.D
*	HsFlag-NUFIP_Ti_10	3.3671	0.2226	1176.53	1176.315	7361.4	1	1253.7	83.3	2	R.DVVQAYPEVR.I
*	HsFlag-NUFIP_Ti_10	3.5822	0.4601	2839.94	2841.217	8472.9	1	578	36.4	4	R.TYPVQEYFLEDCIQMTHFVPPPK.D
*	HsFLAG-Lin9_Ti_20	4.3627	0.4976	3045.4	3046.928	8786.3	1	952.2	40.4	3	K.DKDDDGGEDDDANCNLICGDEYGPETR.L
*	HsFLAG-Lin9_Ti_20	5.5212	0.4125	3046.4	3046.928	6006.5	1	1091.6	35.6	3	K.DKDDDGGEDDDANCNLICGDEYGPETR.L
*	HsFLAG-ARP6_Ti_1	3.9253	0.4245	2802.47	2803.666	5627.2	1	714.1	45.8	1	K.DDDGGEDDDANCNLICGDEYGPETR.L
*	HsFLAG-FLJ20309_	2.3179	0.1421	1049.51	1050.215	5401.5	9	392.1	68.8	1	R.LSMSQLNEK.E
*	HsFLAG-FLJ20309_	3.8167	0.3221	1403.3	1403.659	5047.9	4	763.2	77.3	35	K.ETPFELIEALLK.Y
*	HsFLAG-p53-DNA-D	4.9162	0.1853	2980.77	2981.566	5592.1	1	743.9	44	6	K.YIETLNVPGAVLVFLPGWNLIYTMQK.H
*	HsFLAG-FLJ20729_	5.6691	0.3001	2981.66	2981.566	6820.5	1	1630.6	37	2	K.YIETLNVPGAVLVFLPGWNLIYTMQK.H
*	HsFlag-NUFIP_Ti_11	4.3609	0.342	1462.41	1462.629	7030.6	1	1604.9	86.4	7	K.HLEMNPHFGSHR.Y
*	HsFlag-NUFIP_Ti_10	2.4899	0.2564	1465.1	1465.739	6319.8	1	610.9	63.6	4	R.YQILPLHSQIPR.E
*	HsFlag-NUFIP_Ti_10	3.7965	0.1826	1465.6	1465.739	4090.5	1	799.6	77.3	29	R.YQILPLHSQIPR.E
*	HsFlag-NUFIP_Ti_10	3.96	0.369	1286.6	1286.557	4072.8	3	751.5	77.3	9	R.KVFDPVPVGVTK.V
*	HsFlag-NUFIP_Ti_11	2.909	0.2054	2769.77	2769.128	7132.7	1	398.6	33.3	2	K.VILSTNIAETSITINDVVYVIDSCK.Q
*	HsFLAG-Lin9_Ti_20	3.4934	0.1036	2085.57	2086.329	7699.9	1	504.5	44.1	2	K.LFTAHNNMTNYSTVWASK.T
*	HsFLAG-p53-DNA-D	2.7303	0.1485	1221.61	1222.47	5607.6	3	535.1	65	6	R.TPLHEIALSIK.L
*	HsFLAG-p53-DNA-D	3.4781	0.1698	1222.73	1222.47	7698.8	1	1498.9	85	26	R.TPLHEIALSIK.L
*	HsFlag-NUFIP_Ti_10	3.974	0.1596	1223.41	1222.47	5612.7	1	1312.9	62.5	1	R.TPLHEIALSIK.L
*	HsFlag-NUFIP_Ti_10	3.9303	0.2347	1004.18	1004.217	3560.7	1	933.9	94.4	11	R.LGGIGQFLAK.A
*	HsFlag-NUFIP_Ti_10	4.1136	0.4737	1971.78	1972.249	3150.6	1	890.6	76.5	19	K.AIEPPPLDAVIEAEHTLR.E
*	HsFlag-NUFIP_Ti_10	4.733	0.2738	1741.89	1742.88	8081.9	1	1942.7	70	15	R.ELDALDANDELTPLGR.I
*	HsFlag-NUFIP_Ti_10	4.6096	0.3089	2077.68	2078.291	7693.1	1	1524.4	44.1	8	R.FSDHVALLSVFQAWDDAR.M
*	HsFlag-NUFIP_Ti_10	5.9344	0.4643	2078.29	2078.291	9354.7	1	2131.7	67.6	29	R.FSDHVALLSVFQAWDDAR.M
*	HsFlag-NUFIP_Ti_11	3.0118	0.1301	976.6	975.197	8094.1	1	1277.9	100	4	K.RLNMATLR.M
	HsFLAG-p53-DNA-D	5.4654	0.3775	1845.43	1844.118	7887.5	1	1665.6	70	7	K.KVQSDGQIVLVDDWIK.L
	HsFLAG-FLJ20309_	4.8924	0.3788	1717.24	1715.944	7152.9	1	1200.2	67.9	6	K.VQSDGQIVLVDDWIK.L
	HsFlag-NUFIP_Ti_10	5.258	0.4263	1640.29	1640.846	7628.4	1	1890	75	12	K.LQISHEAAACITGLR.A
	HsFLAG-FLJ20309_	4.5725	0.2924	1261.29	1261.519	6164.2	1	1670.6	81.8	14	R.AAMEALVVEVTK.Q

	HsFLAG-p53-DNA-D	3.5996	0.3327	2823.05	2823.277	7397.5	2	495.7	26	1	R.AAMEALVVEVTKQPAIISQLDPVNER.M
	HsFlag-NUFIP_Ti_1	3.4529	0.3515	1579.91	1580.781	6517.9	1	939.5	73.1	12	K.QPAIISQLDPVNER.M
	HsFLAG-FLJ20309_	3.1395	0.1749	987.26	987.103	6653.1	4	755.5	75	12	R.YGDGPRPPK.M
gi|4503529|re	12	32	47.00%	406	46154	5.5	eukaryotic translation initiation factor 4A, isoform 1 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.56	0.2768	4168.65	4169.451	7061.3	1	792.5	22.9	1	R.SRDNGPDGMEPEGVIESNWNEIVDSFDDMNLSESLLR.G
	HsFLAG-Lin9_Ti_20	2.3621	0.254	1047.39	1048.183	9240.5	1	837.8	75	2	R.GIYAYGFEK.P
	HsFLAG-ARP6_Ti_1	4.6012	0.3935	1829.59	1829.065	4460.2	1	954.3	73.3	7	R.GIYAYGFEKPSAIQQR.A
	HsFlag-VPS71_Ti_1	2.4711	0.1893	1140.69	1141.356	5645.4	8	331.1	60	1	K.ATQALVLAPTR.E
*	HsFLAG-Lin9_Ti_20	4.3153	0.3344	1619.38	1619.922	6005.9	1	1160.8	71.4	6	K.LQMEAPHIIVGTPGR.V
	HsFlag-VPS71_Ti_1	4.883	0.3827	1556.72	1556.789	7213.7	1	2553.4	91.7	2	K.MFVLDEADEMLSR.G
	HsFLAG-p53-DNA-D	4.3902	0.3541	1502.13	1502.71	8870.8	1	1923	81.8	2	R.GFKDQIYDIFQK.L
*	HsFlag-VPS71_Ti_1	3.9952	0.3051	2460.72	2460.846	6664.5	1	605	40.9	4	K.LNSNTQVVLLSATMPSDVLEVTK.K
	HsFLAG-FLJ20729_	3.4722	0.294	1582.36	1582.743	7203.5	1	1047.7	69.2	1	R.DFTVSAMHGDMDQK.E
	HsFLAG-Lin9_Ti_20	3.6979	0.2526	1115.19	1115.359	6528.4	1	1517.9	94.4	2	R.VLITTDLLAR.G
	HsFLAG-Lin9_Ti_20	5.0028	0.364	2144.5	2145.42	8462.8	1	1564.8	58.3	3	R.GIDVQQVSLVINYDLPTNR.E
*	HsFLAG-p53-DNA-D	2.917	0.1347	2430.63	2428.713	6541.5	2	518.8	42.5	1	R.DIETFYNTSIEEMPLNVADLI.-
gi|4507691|re	174	848	46.90%	3830	434416	8.2	transformation/transcription domain-associated protein [Homo sapiens]				
*	HsYL1_Ti_103.2312.	3.5668	0.3316	2153.73	2154.425	8321.6	1	1042.7	52.8	1	K.KYLQFVAALTDVNTPDETK.L
*	HsYL1_Ti_104.2308.	3.5455	0.3415	2393.75	2395.758	9349.2	1	1062.5	45	2	K.KYLQFVAALTDVNTPDETKLK.M
*	HsMRGBP-FLAG_Ti_	5.2741	0.3947	2027.45	2026.251	7932.2	1	1618.8	64.7	9	K.YLQFVAALTDVNTPDETK.L
*	HsMRGBP-FLAG_Ti_	4.5144	0.2868	2268.31	2267.584	7984.2	1	822.6	44.7	9	K.YLQFVAALTDVNTPDETKLK.M
*	HsMRGBP-FLAG_Ti_	5.7757	0.4184	3315.49	3315.697	4958.8	1	781.1	32.4	4	K.MMQEVSENFENVTSSPQYSTFLEHIIPR.F
*	HsMRGBP-FLAG_Ti_	6.0558	0.4182	1943.73	1943.207	8445.4	1	2498	80	11	R.FLTFLQDGEVQFLQEK.P
*	HsYL1_Ti_103.2775.	4.4155	0.4102	2637.05	2637.01	5117.7	1	691.2	47.6	2	R.FLTFLQDGEVQFLQEKPAQQLR.K
*	HsMRGBP-FLAG_Ti_	3.0437	0.0847	994.63	993.238	4641.3	7	983.3	92.9	1	K.LVLEIIHR.I
*	HsFLAG-TIP49b_Ti_	2.4131	0.1222	824.5	823.971	4496.4	1	385.4	83.3	2	R.THSIIPR.G
*	HsMRGBP-FLAG_Ti_	3.6184	0.3583	1382.75	1382.599	3942.6	1	513.5	72.7	3	K.ELYADFIAAQIK.T
*	HsMRGBP-FLAG_Ti_	4.4022	0.3539	1384.38	1382.599	7284.7	1	1527.2	81.8	12	K.ELYADFIAAQIK.T
*	HsFLAG-TIP49b_Ti_	4.7984	0.4272	1911.44	1912.18	6322.1	1	1006.7	62.5	5	K.GMLQLLSNCPAETAHLR.K
*	HsTIP60_Ti_106.214	3.081	0.2766	983.13	983.156	3072.3	1	633.4	92.9	2	K.HILTTELR.N
*	HsMRGBP-FLAG_Ti_	4.0489	0.3996	1642.77	1642.849	5256.6	1	1161.4	75	8	K.LFDESILIGSGYTAR.E
*	HsYL1_Ti_106.2539.	5.0655	0.3627	2193.13	2192.526	7346.4	1	1436.8	45.8	2	R.ETLRPLAYSTLADLVHHVR.Q
*	HsYL1_Ti_105.3244.	2.6373	0.1391	1881.69	1881.225	3301.7	1	254.7	50	1	R.QHLPLSDLSLAVQLFAK.N
*	HsTIP60_Ti_103.197	5.2013	0.4339	1925.11	1926.069	3470.1	1	819.6	71.9	5	K.NIDDESLPSSIQTMSCK.L
*	HsMRGBP-FLAG_Ti_	2.322	0.2515	1228.68	1229.472	4185	2	393.1	72.2	3	K.LLLNLVDCIR.S
*	HsMRGBP-FLAG_Ti_	3.6553	0.1501	1230.63	1229.472	7314.1	3	1815.3	94.4	8	K.LLLNLVDCIR.S
*	HsMRGBP-FLAG_Ti_	2.481	0.1187	969.47	970.156	6935.4	2	903.2	78.6	1	R.YQLSAIFK.K
*	HsTIP60_Ti_101.156	2.7211	0.2915	1156.27	1155.219	6770.7	2	690.4	75	2	K.QTFQVTDCR.S
*	HsMRGBP-FLAG_Ti_	2.0682	0.1513	1166.47	1167.314	6357.9	1	561.5	66.7	1	K.TITWGITSCK.A
*	HsTIP60_Ti_104.190	2.9682	0.1736	1167.77	1167.314	4362.9	1	637.4	77.8	1	K.TITWGITSCK.A
*	HsMRGBP-FLAG_Ti_	2.4169	0.164	1171.57	1172.326	4616.2	5	459.5	65	3	K.APGEAQFIPNK.Q
*	HsMRGBP-FLAG_Ti_	3.7033	0.2405	1172.56	1172.326	5342.8	1	1340.3	90	4	K.APGEAQFIPNK.Q
*	HsMRGBP-FLAG_Ti_	4.277	0.3382	2518.25	2517.862	7627.1	1	1292.3	50	2	K.YAMQALDIYQVQIAGNGQTYIR.V

*	HsYL1_Ti_104.3362.	2.7062	0.1972	2212.41	2212.63	7913.7	1	790.7	47.2	1	K.EVLEHFAGVFTMMNPLTFK.E
*	HsMRGBP-FLAG_Ti	2.8153	0.2358	1391.6	1392.61	5175.7	2	386.5	58.3	3	K.IVNSSMELAQTAK.E
*	HsMRGBP-FLAG_Ti	4.8102	0.129	1393.87	1392.61	7667.4	1	1985.1	83.3	2	K.IVNSSMELAQTAK.E
*	HsMRGBP-FLAG_Ti	4.4403	0.2547	2686.78	2686.99	6975.2	3	937.8	34.5	5	R.TLELCVDNLQPDFLYDHIQPVR.A
*	HsMRGBP-FLAG_Ti	4.2766	0.2729	2686.95	2686.99	4561.7	1	454.4	45.2	15	R.TLELCVDNLQPDFLYDHIQPVR.A
*	HsFLAG-TIP49b_Ti_	2.4449	0.0832	1117.49	1118.339	4424.1	4	358.9	75	2	R.AELMQALWR.T
*	HsH2AZ-FLAG_293_	2.959	0.2698	1700.69	1700.895	3806.3	1	632.4	67.9	1	R.TLRNPADSISHVAYR.V
*	HsFLAG-TIP49b_Ti_	4.3102	0.261	1701.31	1700.895	7529.1	1	1552.9	50	2	R.TLRNPADSISHVAYR.V
*	HsH2AZ-FLAG_293_	4.3352	0.3124	1331.38	1330.443	7606	1	1747.6	86.4	7	R.NPADSISHVAYR.V
*	HsFLAG-TIP49b_Ti_	5.2769	0.3889	2410.32	2409.664	7123.7	1	1489.2	62.5	4	K.LHYVVTEVQGPSITVEFSDCK.A
*	HsMRGBP-FLAG_Ti	2.8753	0.1876	1133.61	1134.281	8534.7	1	669.5	61.1	6	K.AIETALDCLK.S
*	HsTIP60_Ti_103.190	3.3927	0.2475	1134.03	1134.281	6493.3	1	1207.9	83.3	2	K.AIETALDCLK.S
*	HsFLAG-TIP49b_Ti_	4.6919	0.2512	1782.73	1783.04	7661.1	1	1984.5	55.4	1	K.HALYQLLAHPNFTEK.T
*	HsMRGBP-FLAG_Ti	5.235	0.4197	1784.87	1783.04	6748.5	1	1693.5	78.6	7	K.HALYQLLAHPNFTEK.T
*	HsYL1_Ti_104.3068.	3.6419	0.3463	1841.86	1843.191	6230.7	1	1143.3	65.6	3	R.KTFEQALTGAFMSAVIK.D
*	HsYL1_Ti_104.3075.	3.6442	0.3057	1843.75	1843.191	6635	2	966.5	39.1	1	R.KTFEQALTGAFMSAVIK.D
*	HsMRGBP-FLAG_Ti	6.1166	0.4341	1714.88	1715.017	6253.6	1	1967.4	80	10	K.TFEQALTGAFMSAVIK.D
*	HsMRGBP-FLAG_Ti	5.0588	0.351	1716.05	1715.017	7544.2	1	2203.4	53.3	5	K.TFEQALTGAFMSAVIK.D
*	HsYL1_Ti_105.2963.	3.9995	0.2085	1655.7	1655.981	5837.6	8	916.3	42.9	1	K.DLRPSALPFVASLIR.H
*	HsH2AZ-FLAG_293_	3.7736	0.252	1596.37	1596.833	3512.6	1	792.1	79.2	2	R.ACQLPLFSYIVER.L
*	HsMRGBP-FLAG_Ti	4.3156	0.3825	1724.76	1723.821	7138	1	1501.8	75	1	R.LCACCYEQAWYAK.L
*	HsFLAG-TIP49a_Ti_	3.6765	0.3541	1830.95	1830.18	5027.2	1	587.1	57.1	5	R.LPLTWVLQNQQTFLK.A
*	HsMRGBP-FLAG_Ti	3.5102	0.0933	1105.53	1105.338	6864.6	1	1400.4	93.8	6	K.TTLEQLLMR.C
*	HsMRGBP-FLAG_Ti	4.291	0.341	2288.57	2288.483	5069.4	1	495.1	32.9	2	R.CATPLKDEERAEEIVAAQEK.S
*	HsYL1_Ti_101.1266.	2.4972	0.0943	1087.65	1088.203	6963.9	2	753.2	61.1	1	R.AEEIVAAQEK.S
*	HsFLAG-TIP49b_Ti_	3.6146	0.4167	1348.38	1348.507	7210.5	1	1371.3	80	3	K.SFHHVTHDLVR.E
*	HsH2AZ-FLAG_293_	4.4963	0.2952	1610.49	1611.9	7041.2	1	1397.7	71.4	8	K.QAMHSLQVLAQVTGK.S
*	HsTIP60_Ti_105.149	2.647	0.2747	1140.42	1141.371	6952.1	7	467.3	61.1	2	K.SVTVIMEPHK.E
*	HsTIP60_Ti_105.149	2.932	0.2304	1141.19	1141.371	5514.5	1	748.4	77.8	4	K.SVTVIMEPHK.E
*	HsMRGBP-FLAG_Ti	4.4969	0.3925	2585.85	2585.863	7000.4	1	767.1	47.7	2	R.HQPANAQIGLMEGNTFCTTLQPR.L
*	HsFLAG-TIP49b_Ti_	3.5165	0.2567	1446.42	1446.704	8290.5	4	812	63.6	4	R.LFTMDLNVVEHK.V
*	HsH2AZ-FLAG_293_	6.0473	0.4576	2217.34	2217.444	6151.7	1	1431.3	66.7	26	K.VFYTELLNLCEAEDSALTK.L
*	HsMRGBP-FLAG_Ti	5.1405	0.4151	2219.9	2217.444	10868.8	1	2339.1	45.8	1	K.VFYTELLNLCEAEDSALTK.L
*	HsH2AZ-FLAG_293_	3.9758	0.1583	1846.48	1847.091	5227.9	1	889.6	59.4	4	R.IAALNALAACNYLPQSR.E
*	HsMRGBP-FLAG_Ti	5.789	0.4909	1981.69	1982.096	9366	1	2324	70.6	7	K.ALNSTNSELQEAGEACMR.K
*	HsTIP60_Ti_104.174	3.2128	0.2035	1016.2	1016.186	6470.3	8	1055.7	87.5	4	R.SLTLNVVNR.L
*	HsFLAG-TIP49b_Ti_	3.2558	0.2374	1367.46	1366.562	8738.3	1	1360.3	77.8	4	K.FCDQMMQHLR.K
*	HsFLAG-TIP49b_Ti_	4.9531	0.2888	1773.93	1773.144	9846.7	1	1446.8	63.3	8	R.AMLIEAGSPFREPLIK.F
*	HsH2AZ-FLAG_293_	3.1457	0.1132	970.25	970.073	5969.5	6	1083.9	81.2	1	R.DVLAANPNR.F
*	HsYL1-FLAG_Ti_206	2.7844	0.096	1558.16	1557.877	3759.4	5	622.7	60.7	1	R.FITLLLPGGAQTAVR.P
*	HsMRGBP-FLAG_Ti	4.3567	0.2916	1956.72	1957.11	6707.6	1	1191.1	62.5	2	K.NDDSWLASQHSLVSQLR.R
*	HsMRGBP-FLAG_Ti	4.0474	0.2769	1957.33	1957.11	6127.5	1	923.4	39.1	2	K.NDDSWLASQHSLVSQLR.R
*	HsFLAG-TIP49b_Ti_	4.2824	0.3745	1450.33	1450.597	8317.2	1	1742.6	90	5	R.RVWVSENFQER.H

*	HsTIP60_Ti_105.177	3.399	0.1172	1294.36	1294.409	5102.8	3	787.8	77.8	3	R.VWVSENFQER.H
*	HsTIP60_Ti_106.265	2.9078	0.2091	1431.49	1431.647	8111.1	5	644.5	60	3	K.LLAYCLLNYCK.R
*	HsMRGBP-FLAG_Ti	3.8095	0.3046	1432.34	1431.647	6202.3	1	1378.7	85	4	K.LLAYCLLNYCK.R
*	HsYL1_Ti_105.2055.	3.008	0.2151	1588.08	1587.835	6836	1	1353.4	77.3	2	K.LLAYCLLNYCKR.N
*	HsFLAG-TIP49b_Ti_	3.3308	0.3112	1750.61	1751.038	6359.5	2	566.3	57.7	1	K.RNYGDIELLFQLLR.A
*	HsMRGBP-FLAG_Ti	5.3487	0.3382	1597.14	1594.851	6983	1	2054.9	87.5	17	R.NYGDIELLFQLLR.A
*	HsMRGBP-FLAG_Ti	3.5552	0.2113	1175.46	1174.41	3513.8	1	810.2	87.5	2	R.FLCNMTFLK.E
*	HsH2AZ-FLAG_293_	4.5405	0.3715	1657.33	1657.777	5109	1	1466.1	84.6	19	R.FVDFNDPNFGDELK.A
*	HsH2AZ-FLAG_293_	5.2143	0.3193	1919.64	1920.262	5120.4	1	1367.9	76.7	8	K.VLQHILNPAFLYSFEK.G
*	HsYL1_Ti_106.2867.	4.2424	0.5152	4726.58	4728.312	6975.3	1	579.4	21.4	1	TK.V
*	HsFLAG-TIP49a_Ti_	4.625	0.3611	2826.91	2827.074	6022.9	1	740	44.2	14	K.GEGEQLLGPPNPEGDNPESITSVFITK.V
*	HsTIP60_Ti_105.305	4.6466	0.3445	2827.68	2827.074	5584.7	1	940.8	33.7	3	K.GEGEQLLGPPNPEGDNPESITSVFITK.V
*	HsYL1_Ti_103.2920.	3.6116	0.2941	1467.57	1467.776	4674	1	1059.1	81.8	10	R.LMTFAWPCLLSK.A
*	HsYL1-FLAG_Ti_206	1.8726	0.106	1468.81	1467.776	4246.4	1	296.2	54.5	1	R.LMTFAWPCLLSK.A
*	HsFLAG-TIP49b_Ti_	3.6979	0.2506	1297.32	1297.627	7197.9	1	1453.3	85	5	K.IVLQVFHSLLK.A
*	HsTIP60_Ti_105.195	4.2234	0.3372	1339.56	1339.639	6584	1	1496.1	79.2	3	R.QAMAILTPAVPAR.M
*	HsMRGBP-FLAG_Ti	4.216	0.3553	1642.69	1642.847	5428	1	1270.8	75	2	R.MEDGHQMLTHWTR.K
*	HsMRGBP-FLAG_Ti	2.1667	0.116	1347.73	1348.542	3755.8	3	168.8	54.5	1	R.LGFTPSVTIEQR.R
*	HsMRGBP-FLAG_Ti	3.8217	0.3372	1348.51	1348.542	4066.6	1	699.6	81.8	8	R.LGFTPSVTIEQR.R
*	HsMRGBP-FLAG_Ti	2.3107	0.2594	1185.73	1186.434	8065.1	7	521.1	55	1	R.LAVDLSEVVIK.W
*	HsMRGBP-FLAG_Ti	3.5917	0.1499	1186.96	1186.434	5271.3	1	1354.9	90	4	R.LAVDLSEVVIK.W
*	HsTIP60_Ti_104.161	5.146	0.3589	2821.81	2822.972	6409.1	1	1263	35.6	2	R.IKDQQPDSDMDPNSSGEGVNSVSSSIK.R
*	HsTIP60_Ti_104.161	4.0813	0.5323	2822.59	2822.972	3884.1	1	589.9	46.2	1	R.IKDQQPDSDMDPNSSGEGVNSVSSSIK.R
*	HsMRGBP-FLAG_Ti	5.1423	0.4857	2580.67	2581.638	5187.7	1	984.7	54.2	3	K.DQQPDSDMDPNSSGEGVNSVSSSIK.R
*	HsFLAG-TIP49b_Ti_	3.3484	0.1711	1289	1289.431	5427.7	5	729	68.2	5	K.RGLSVDSAQEVK.R
*	HsTIP60_Ti_105.204	4.3694	0.3937	1150.69	1151.308	6809.8	1	1716.1	90.9	14	R.TATGAISAVFGR.S
*	HsMRGBP-FLAG_Ti	2.4241	0.3366	1150.74	1151.308	3684.2	1	236	63.6	7	R.TATGAISAVFGR.S
*	HsMRGBP-FLAG_Ti	2.4942	0.1412	1286.51	1287.456	5829.9	1	443.1	54.2	1	R.SQSLPGADSLLAK.P
*	HsMRGBP-FLAG_Ti	4.2831	0.3096	1742.07	1740.995	3428.5	1	663.8	71.9	11	R.SQSLPGADSLLAKPIDK.Q
*	HsH2AZ-FLAG_293_	5.8156	0.4615	2190.04	2190.298	6949.2	1	1369.8	60	14	R.VACQVNDNTNTAGSPGEVLSR.R
*	HsYL1_Ti_102.1351.	2.8193	0.384	1283.35	1284.402	4091.2	1	316.1	59.1	3	R.GIAACMTCGNTK.V
*	HsTIP60_Ti_104.239	2.8435	0.2584	1783.12	1783.047	3513.1	1	305.2	46.9	1	R.LMSIFPTEPSTSSVASK.Y
*	HsH2AZ-FLAG_293_	4.5537	0.4367	1545.21	1545.695	7513.7	1	1716.7	79.2	4	K.YEELECLYAAVGK.V
*	HsMRGBP-FLAG_Ti	2.7367	0.2534	1328.53	1329.492	5238.6	1	479.9	65	3	K.VIYEGLTNYEK.A
*	HsMRGBP-FLAG_Ti	3.5988	0.3612	1331.37	1329.492	4489.1	1	1127.9	90	4	K.VIYEGLTNYEK.A
*	HsTIP60_Ti_106.307	5.0677	0.307	1819.5	1820.157	4176.4	1	1071.4	75	10	K.ATNANPSQLFGTLMILK.S
*	HsH2AZ-FLAG_293_	3.1042	0.3507	1385.13	1384.411	5706.1	1	1068.9	81.8	1	K.SACSNNPSYIDR.L
*	HsMRGBP-FLAG_Ti	4.0796	0.1736	3101.33	3101.453	9099.3	1	1080.7	27.6	3	R.EHLNPQAASGSTEATSGTSELVMLSLELVK.T
*	HsYL1_Ti_106.3140.	5.2571	0.2841	1618.94	1618.957	7305.8	1	2571	88.5	2	R.KNFIQAILTSLIEK.S
*	HsMRGBP-FLAG_Ti	2.952	0.1243	1489.84	1490.783	7159.8	1	607.7	62.5	5	K.NFIQAILTSLIEK.S
*	HsMRGBP-FLAG_Ti	5.399	0.2304	1491.23	1490.783	9071.3	1	2742.5	87.5	41	K.NFIQAILTSLIEK.S
*	HsFLAG-TIP49b_Ti_	3.6663	0.3029	1515.37	1515.684	9803.5	1	1206.7	69.2	5	K.NNSPMAANQTPTLR.E
*	HsMRGBP-FLAG_Ti	3.7573	0.1907	3849.02	3848.258	8419.7	1	880.5	25.8	3	K.RFPEDLELNAQFLDLVNYVYRDETLSGSELTAK.L

*	HsMRGBP-FLAG_Ti	5.318	0.2229	3693.63	3692.07	7329.5	1	633.5	23.4	6	R.FPEDLELNAQFLDLVNYVYRDETLSGSELTAK.L
*	HsMRGBP-FLAG_Ti	2.6565	0.1435	1103.45	1103.307	2810	4	586.9	83.3	1	K.LEPAFLSGLR.C
*	HsTIP60_Ti_105.245	3.0004	0.1592	1264.6	1264.438	6771.1	1	693.6	72.2	5	K.FFEVFDNSMK.R
*	HsMRGBP-FLAG_Ti	3.3018	0.182	1265.51	1264.438	4702.7	2	1116.5	88.9	3	K.FFEVFDNSMK.R
*	HsFLAG-TIP49a_Ti_	4.0573	0.2895	2959.09	2957.251	5000.5	1	511.8	27.8	2	K.STPIGTSCQGAMLPSITNVINLADSHDR.A
*	HsFLAG-TIP49a_Ti_	2.4935	0.3571	1074.36	1075.314	3623.2	1	480.9	66.7	1	R.AAFAMVTHVK.Q
*	HsFLAG-TIP49b_Ti_	3.7082	0.3573	1075.32	1075.314	6028.2	1	1168.4	83.3	10	R.AAFAMVTHVK.Q
*	HsYL1_Ti_106.2015.	4.3602	0.3204	1586.66	1585.864	6857.5	1	1346.9	73.1	1	R.AAFAMVTHVKQEPR.E
*	HsMRGBP-FLAG_Ti	4.1413	0.3656	1411.47	1412.607	7131	1	1586.3	86.4	10	K.DIGNQLHMLTNR.H
*	HsFLAG-TIP49b_Ti_	3.6793	0.3064	1792.47	1793.01	7328.3	1	844.8	60.7	3	K.DIGNQLHMLTNRHDK.F
*	HsH2AZ-FLAG_293_	5.7303	0.4505	2260.42	2261.59	8279.5	1	2106.1	62.5	15	K.TGALLSAFVQLCHISTTLAEK.T
*	HsTIP60_Ti_106.269	3.3253	0.1384	1047.28	1047.245	4395	6	970.3	92.9	1	K.TWVQLFPR.L
*	HsMRGBP-FLAG_Ti	3.2661	0.3656	1433.74	1434.65	5056.1	1	653.5	63.6	2	R.STLMLEHQAFEK.G
*	HsFLAG-TIP49b_Ti_	4.0864	0.3705	1434.32	1434.65	7107	1	1548.2	81.8	4	R.STLMLEHQAFEK.G
*	HsFLAG-TIP49b_Ti_	3.1519	0.1081	984.15	984.227	5708.6	1	1108.4	87.5	2	K.GLSLQIKPK.Q
*	HsMRGBP-FLAG_Ti	5.1958	0.3385	2928.64	2929.082	6222.6	1	1248.5	35.4	6	K.YSETATAIAYEQHGFFEQAQESYEK.A
*	HsMRGBP-FLAG_Ti	4.2831	0.384	2928.81	2929.082	8044.3	1	389.4	29.2	6	K.YSETATAIAYEQHGFFEQAQESYEK.A
*	HsMRGBP-FLAG_Ti	3.5891	0.3534	2461.85	2460.711	4227.5	1	366.3	44.7	8	R.SNASPAIFPEYQLWEDHWIR.C
*	HsH2AZ-FLAG_293_	4.8802	0.3196	1795.79	1796.931	7435.9	1	1589.1	75	8	K.ELNQWEALTEYGQSK.G
*	HsYL1_Ti_105.2544.	3.7886	0.4501	1729.67	1728.957	4007.7	1	736.6	65.4	1	K.GHINPYLVLECAWR.V
*	HsYL1_Ti_102.1623.	3.447	0.2501	1359.5	1359.529	3335.5	1	331.4	63.6	5	K.EALVQVEVSCPK.E
*	HsMRGBP-FLAG_Ti	3.7712	0.3442	1359.87	1359.529	6552.7	1	1248.7	77.3	4	K.EALVQVEVSCPK.E
*	HsMRGBP-FLAG_Ti	5.3828	0.3826	2190.9	2191.414	4205.4	1	1233	76.5	15	R.GYLAICHPEEQQLSFIER.L
*	HsMRGBP-FLAG_Ti	4.0973	0.3424	2193.22	2191.414	5397.1	1	1034.4	42.6	2	R.GYLAICHPEEQQLSFIER.L
*	HsMRGBP-FLAG_Ti	3.7898	0.2326	1190.92	1190.444	6620.6	1	2172.8	95	4	R.LVEMASSLAIR.E
*	HsFLAG-TIP49b_Ti_	4.2227	0.4022	1526.81	1526.82	7383.8	1	1507.8	73.1	4	R.KQGLVNVALDILSR.I
*	HsMRGBP-FLAG_Ti	3.9291	0.3538	1399.19	1398.646	7209.6	1	1194.2	79.2	6	K.QGLVNVALDILSR.I
*	HsFLAG-TIP49b_Ti_	3.9065	0.3231	1768.49	1769.06	3912.5	1	464.2	60.7	8	R.IHTIPTVPIVDCFQK.I
*	HsTIP60_Ti_105.236	4.9108	0.4066	1866.24	1866.06	8763.3	1	1931.9	73.3	7	K.NECMQGLEVIESTNLK.Y
*	HsFLAG-TIP49b_Ti_	4.8922	0.3584	1516.62	1516.799	8398.9	1	1912.7	80.8	12	K.AFSAAVQMHDVLVK.A
*	HsMRGBP-FLAG_Ti	5.0671	0.4483	1843.55	1844.138	5541.4	1	1575.9	78.6	3	K.AWAMWGDYLENIFVK.E
*	HsH2AZ-FLAG_293_	3.7454	0.2117	1352.67	1351.542	5740	1	1325.4	90	3	K.VLWLLSFDDDK.N
*	HsMRGBP-FLAG_Ti	4.7436	0.0938	1227.48	1226.505	7209.9	1	1998.2	95	4	K.LLLNLISQVGR.V
*	HsMRGBP-FLAG_Ti	2.4301	0.2211	1352.65	1353.607	6559	3	515.9	65	2	R.VYPQAVYFPIR.T
*	HsFLAG-TIP49b_Ti_	3.7044	0.4324	2471.29	2471.877	9453.9	1	897.9	47.5	1	R.ELHPTLLSSLEGIVDQMVWFR.E
*	HsTIP60_Ti_102.164	2.5265	0.3024	1004.16	1004.094	4345.1	2	706	92.9	1	K.CYSVAFEK.S
*	HsFLAG-TIP49b_Ti_	2.5471	0.1389	1169.55	1170.397	6493.2	7	551.2	66.7	2	K.ITPHTLNFVK.K
*	HsMRGBP-FLAG_Ti	4.0786	0.4092	2960.9	2962.301	5519.1	1	476.5	33.9	3	K.LVSTFGVGLENVSNVSTMFSSAASESLAR.R
*	HsH2AZ-FLAG_293_	3.4393	0.1458	1459.9	1460.633	3221.9	1	646.8	75	8	R.RAQATAQDPVFQK.L
*	HsYL1_Ti_102.1383.	3.0979	0.337	1303.53	1304.445	3794.7	1	311	59.1	1	R.AQATAQDPVFQK.L
*	HsTIP60_Ti_102.146	4.1856	0.3557	1304.96	1304.445	8668.4	1	1492.5	77.3	2	R.AQATAQDPVFQK.L
*	HsMRGBP-FLAG_Ti	4.3585	0.3629	1765.93	1764.947	5640.1	1	873.9	60	6	K.GQFTTDFDFSVPGSMK.L
*	HsMRGBP-FLAG_Ti	4.2806	0.3165	2457.81	2456.816	5710.6	1	660.7	45.2	3	R.FLSNFSAQTAEVEIPGEFLMPK.P

*	HsFLAG-TIP49b_Ti_	3.9321	0.185	3359.52	3359.864	7428.4	1	1011.2	28.6	1	R.FLSNFSAQTAEVEIPGEFLMPKPTHYYIK.I
*	HsTIP60_Ti_105.261	5.186	0.4902	1945.36	1946.192	5823.3	1	1392.9	73.3	2	K.IYPYLVMNDACLTESR.R
*	HsFLAG-TIP49b_Ti_	2.733	0.2052	1017.14	1017.219	4636.1	1	841.2	92.9	1	R.HLFFTVPR.V
*	HsYL1_Ti_102.2196.	5.6996	0.3537	1808.03	1807.051	4485.1	1	1264	80	27	R.LVEDNPSSLSLVEIYK.Q
*	HsFLAG-TIP49b_Ti_	3.9029	0.3858	1266.48	1266.399	7198.9	1	1631.3	90	7	K.KGIEHDNPISR.Y
*	HsMRGBP-FLAG_Ti_	2.8703	0.3343	1266.76	1266.399	5211.1	1	523	70	4	K.KGIEHDNPISR.Y
*	HsH2AZ-FLAG_293_	3.2103	0.3297	1138.35	1138.225	6959	1	1029.9	77.8	8	K.GIEHDNPISR.Y
*	HsTIP60_Ti_105.100	3.0457	0.224	1097.5	1097.219	6660.7	1	1206.1	83.3	4	R.GTQASHQVLR.D
*	HsMRGBP-FLAG_Ti_	3.4848	0.3371	2156.07	2156.364	5064	1	591.6	50	3	K.EWALHTFPNATDYWTFR.K
*	HsMRGBP-FLAG_Ti_	2.9047	0.2426	2759.9	2761.249	5260.9	1	382.7	34.6	1	R.LTPNISEFLTTIGVSGPLTASMIAVAR.C
*	HsYL1_Ti_104.1959.	3.137	0.2545	1637.84	1637.885	3421.3	4	376.1	61.5	2	R.CFAQPNFKVDGILK.T
*	HsFLAG-TIP49b_Ti_	3.0792	0.1161	1481.67	1481.738	5850.7	1	876.2	68.2	6	K.TVLRDEIIAWHK.K
*	HsYL1_Ti_102.2083.	5.1967	0.3385	3218.68	3218.517	6841.8	1	1329.5	35.3	4	K.KTQEDTSSPLSAAGQPENMDSQQLVSLVQK.A
*	HsYL1_Ti_102.2272.	3.859	0.2281	3089.49	3090.343	3436.8	1	386.8	37.5	1	K.TQEDTSSPLSAAGQPENMDSQQLVSLVQK.A
*	HsTIP60_Ti_103.253	4.5251	0.2698	3092.11	3090.343	6209.6	1	1227.7	33	2	K.TQEDTSSPLSAAGQPENMDSQQLVSLVQK.A
*	HsTIP60_Ti_102.150	1.802	0.1837	862.43	863.063	5590.6	5	305.2	71.4	1	K.AVTAIMTR.L
*	HsTIP60_Ti_105.156	4.1919	0.3504	1430.67	1430.56	7701.7	1	1286.9	70.8	5	R.LHNLAQFEGGESK.V
*	HsYL1_Ti_104.1483.	4.3241	0.2793	1432.63	1430.56	6042.4	1	1688.6	83.3	15	R.LHNLAQFEGGESK.V
*	HsH2AZ-FLAG_293_	5.9826	0.4316	1732.05	1731.913	9603.3	1	2893.2	83.3	11	K.VNTLVAAANSLDNLCR.M
gi|6678271|re	14	93	46.90%	414	44740	6.2	TAR DNA binding protein [Homo sapiens]				
*	HsFLAG-FLJ20729_T	4.2285	0.304	3874.51	3877.127	8121.4	1	476.7	19.3	5	R.VTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLR.Y
*	HsFLAG-ARP6_Ti_1	3.2284	0.3022	1311.91	1311.468	5935.8	1	807.8	77.8	2	R.YRNPVSQCMR.G
*	HsFLAG-p53-DNA-D	5.1939	0.3819	2625.1	2626.03	6592.3	1	1097.6	52.2	11	R.LVEGILHAPDAGWGNLVYVVNYPK.D
*	HsFLAG-p53-DNA-D	4.7349	0.2944	2625.61	2626.03	6788.2	1	889.4	31.5	18	R.LVEGILHAPDAGWGNLVYVVNYPK.D
*	HsFlag-VPS71_Ti_10	3.9434	0.3012	1439.37	1438.596	7221.3	1	1303.7	75	3	K.RKMDETDASSAVK.V
*	HsFLAG-Lin9_Ti_202	2.532	0.2638	1341.46	1342.621	8797.2	4	678.5	59.1	1	K.TSDLIVLGLPWK.T
*	HsFLAG-FLJ20729_T	4.3016	0.3586	1342.45	1342.621	6825.2	1	1853.6	86.4	14	K.TSDLIVLGLPWK.T
*	HsFLAG-ARP6_Ti_1	2.6927	0.2956	1776.45	1778.073	11051.3	1	1007	57.1	1	K.EYFSTFGEVLMVQVK.K
*	HsFLAG-p53-DNA-D	4.3542	0.3277	3704.22	3704.083	10441.3	1	978.2	25	3	R.CTEDMTEDELREFFSQYGDVMDVFIPKPFR.A
*	HsFLAG-p53-DNA-D	4.2128	0.4238	2324.34	2323.671	9117.7	1	797.9	47.2	2	R.EFFSQYGDVMDVFIPKPFR.A
*	HsFLAG-Lin9_Ti_204	5.4766	0.503	2672.79	2673.989	8336.3	1	1692.6	54.3	5	R.AFAFVTFADDQIAQSLCGEDLIIK.G
*	HsFLAG-Lin9_Ti_204	5.7469	0.396	2674.47	2673.989	7562.5	1	1984.4	39.1	2	R.AFAFVTFADDQIAQSLCGEDLIIK.G
*	HsFLAG-Lin9_Ti_204	2.9968	0.1539	1252.39	1252.413	6833.6	1	986.1	72.7	2	K.GISVHISNAEPK.H
*	HsFLAG-FLJ20729_T	5.0488	0.4729	1727.21	1727.793	7964.7	1	2419.7	76.5	24	R.FGGNPGGFGNQGGFGNSR.G
gi|5174525|re	84	448	46.80%	2468	270618	4.8	microtubule-associated protein 1B isoform 1 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	5.3685	0.4643	2016.99	2017.376	7045.9	1	2712.1	84.4	10	K.FYLLVVVGEIVTEEHLR.R
*	HsFLAG-Lin9_Ti_205	3.3219	0.1895	1212.32	1212.438	6787.2	1	1281	85	2	R.RAIGNIELGIR.S
*	HsFLAG-ARP6_Ti_2	5.011	0.3406	1979.79	1979.117	5486.9	1	1144.4	70	15	R.SWDTNLIECNLDQELK.L
*	HsFLAG-FLJ20309_T	4.3453	0.2432	2372.79	2373.62	5129.9	1	577.2	47.6	6	R.SDVLETVVLINPSDEAVSTEVR.L
	HsFLAG-Lin9_Ti_201	4.0338	0.2668	1653.57	1653.795	5333.2	1	1232.6	73.1	10	K.ASLTLFCPEEGDWK.N
	HsFLAG-Lin9_Ti_204	3.5334	0.2856	1241.51	1242.42	5574.1	1	720.7	77.8	1	R.HNLQDFINIK.L
	HsFLAG-p53-DNA-D	4.4458	0.2406	1242.39	1242.42	8223.1	1	1650.1	88.9	12	R.HNLQDFINIK.L
	HsFLAG-ARP6_Ti_1	3.3183	0.3072	1227.07	1227.337	8146.1	1	1775.3	94.4	2	K.PCCYIFPGGR.G

HsFLAG-p53-DNA-D	2.7614	0.2455	2171.83	2170.405	5510.6	5	201.6	35	2 R.GDSALFAVNGFNMLINGGSER.K
HsFLAG-FLJ20729_	6.8378	0.4055	3043.08	3044.456	10139.5	1	3087.2	42.3	1 R.HLDRVDSILLTHIGDDNLPGINSMLQR.K
HsARP6-FLAG_Ti_1	4.639	0.2798	2082.79	2082.448	6516.8	1	1239	41.7	5 K.NLISPDLGVVFLNVPENLK.N
HsFLAG-p53-DNA-D	5.523	0.3817	2082.83	2082.448	9023.1	1	2099.8	63.9	42 K.NLISPDLGVVFLNVPENLK.N
HsFlag-NUFIP_Ti_2	2.5603	0.1394	1218.55	1218.5	2899.1	1	379.3	77.8	1 K.LSMKPEPLFR.S
HsFLAG-FLJ20729_	4.5887	0.3471	1531.02	1531.792	5861.3	1	1368.5	80.8	18 R.SVGNTIDPVILFQK.M
HsFLAG-FLJ20729_	4.9787	0.3724	1678.47	1679.089	6936.9	1	1500.8	71.4	2 K.MGVGKLEMYVLNPVK.S
HsFLAG-Lin9_Ti_20	5.4948	0.2566	3834.54	3837.364	4682.4	1	356.9	22.8	11 K.AEFILPNGQEVDLPISYLTSVSSLIVWHPANPAEK.I
HsFLAG-ARP6_Ti_1	5.0887	0.4237	2022.71	2023.293	3499.7	1	496.8	64.7	27 R.VLFPGNSTQYNILEGLEK.L
HsFLAG-FLJ20729_	4.7387	0.3543	2026.24	2023.293	6424.1	1	1967.6	54.4	1 R.VLFPGNSTQYNILEGLEK.L
HsFLAG-ARP5_Ti_1	5.0768	0.4177	1539.65	1539.818	9526.9	1	2067.9	83.3	2 K.HLDFLKQPLATQK.D
HsFLAG-ARP6_Ti_2	4.0582	0.2969	1254.88	1254.469	4154.7	4	638.7	72.7	7 K.DLTGQVPTPVVK.Q
HsFLAG-BC014022_	3.4606	0.3814	1366.47	1366.644	3988.6	1	415.9	62.5	12 R.ESLKPAAKPLPSK.S
HsFLAG-FLJ20309_	3.0856	0.2792	909.41	909.117	6948	1	1311.9	93.8	2 K.PAAKPLPSK.S
HsFLAG-Lin9_Ti_20	3.0747	0.2831	1490.64	1491.731	4820.2	1	566.3	66.7	1 K.VNHVEKPPKVESK.E
HsH2AZ-FLAG_293_	3.5248	0.1704	1491.38	1491.731	7763.8	1	1030.6	70.8	4 K.VNHVEKPPKVESK.E
HsFLAG-p53-DNA-D	3.1615	0.321	1687.96	1687.931	6993.1	1	836.3	64.3	2 K.DKPVKTETKPSVTEK.E
HsFLAG-ARP5_Ti_1	2.552	0.0818	1698.72	1699.001	8003.5	8	910.4	61.5	1 K.KEDKTPIKKEEKPK.K
HsFLAG-p53-DNA-D	4.8664	0.392	2627.38	2626.044	10238.5	1	1448.9	31.7	2 K.AAEAVAAAVGTGATTAAVMAAAGIAAIGPAK.E
HsH2AZ-FLAG_293_	4.6089	0.3125	1652.62	1652.796	5894.8	1	1445	80.8	4 K.DFEELKAEEVDVTK.D
HsFLAG-FLJ20729_	3.596	0.1947	1700.44	1699.896	3823.6	1	765.1	76.9	2 K.DIKPQLELIEDEEK.L
HsFLAG-FLJ20729_	3.4095	0.2924	1940.47	1941.229	7351.2	1	771.5	56.7	1 K.DIKPQLELIEDEEKLK.E
HsFLAG-p53-DNA-D	5.2042	0.3593	3328.34	3328.782	5274.7	1	459.2	25.9	2 K.DIKPQLELIEDEEKLKETEPVEAYVIQK.E
HsFLAG-Lin9_Ti_20	4.2952	0.3229	1647.4	1647.909	5261.4	1	1220.8	80.8	2 K.LKETEPVEAYVIQK.E
HsFLAG-FLJ20729_	3.3864	0.4223	1406.18	1406.576	7510.5	1	1113.8	77.3	4 K.ETEPVEAYVIQK.E
HsFlag-DPCD_Ti_20	3.9665	0.3213	2561.84	2562.537	7001.9	1	838	30.7	4 K.AETEEAEEPEEDGEEHVCVSASK.H
HsFLAG-Lin9_Ti_20	4.8823	0.3374	2562.28	2562.537	5028.3	1	709.7	47.7	3 K.AETEEAEEPEEDGEEHVCVSASK.H
HsFLAG-ARP5_Ti_1	3.7763	0.3713	2120.48	2120.194	7306	1	736.3	52.8	1 K.HSPTEDEESAKAEADAYIR.E
HsH2AZ-FLAG_293_	6.2651	0.4149	1941.53	1942.089	8590.3	1	2766.9	72.2	9 K.AAEAGGAEEQYGFLTTPTK.Q
HsFLAG-ARP6_Ti_1	2.5727	0.1971	2743.49	2744.854	5596.2	1	365.7	34.8	1 R.DVMSDETNNEETESPSQEFVNITK.Y
HsFLAG-FLJ20729_	3.6086	0.2158	1521.48	1519.651	4444	3	453.6	57.1	2 K.PADVTPLNGFSEGSK.T
HsFLAG-FLJ20729_	3.7255	0.4147	2029.73	2030.124	4882.2	1	466.4	50	4 K.DYNASASTISPPSSMEEDK.F
HsFLAG-ARP6_Ti_1	2.3298	0.2765	971.29	972.006	6566.3	2	500.3	71.4	1 R.DAYCSEVK.A
HsH2AZ-FLAG_293_	2.896	0.2825	1023.91	1023.085	4144.6	2	780.3	83.3	1 K.DSISAVSSEK.V
HsFLAG-ARP6_Ti_1	3.7948	0.2581	1423.33	1423.606	3954	2	561.3	65.4	7 K.SPSLSPSPPSPLEK.T
HsFlag-DPCD_Ti_20	3.5551	0.2551	1348.82	1349.527	7414.7	1	931.3	68.2	6 R.SVNFSLTPNEIK.V
HsFLAG-Lin9_Ti_20	3.0333	0.2003	3125.84	3124.305	8526.7	1	406.2	28.6	2 K.VSAEAEVAPVSPEVTQEVVEEHCASPEDK.T
HsFLAG-FLJ20729_	3.7743	0.2762	2965.76	2967.172	3893.9	1	524.5	30.6	2 K.TLEVVSPSQSVTGSAGHTPYYQSPTDEK.S
HsFLAG-Lin9_Ti_20	3.5537	0.398	2966.99	2967.172	7785.6	1	665.5	35.2	2 K.TLEVVSPSQSVTGSAGHTPYYQSPTDEK.S
HsFLAG-Lin9_Ti_20	4.0493	0.4162	2711.91	2713.059	5918.4	1	782.6	43.8	1 K.SSHLPTEVIEKPPAVPVSFEFSDAK.D
HsFLAG-p53-DNA-D	5.5783	0.3517	2713.42	2713.059	6263.1	1	1179.2	36.5	8 K.SSHLPTEVIEKPPAVPVSFEFSDAK.D
HsFLAG-p53-DNA-D	6.3277	0.3854	3355.41	3356.67	5738.6	1	988	33.6	14 K.SSHLPTEVIEKPPAVPVSFEFSDAKDENER.A
HsFLAG-FLJ20729_	3.5951	0.3469	2014.41	2015.196	5917.1	1	1023.5	63.9	3 R.ASVSPMDEPVPDSESPIEK.V

	HsFLAG-ARP6_Ti_1	6.3359	0.5603	2114.21	2114.27	6926.7	1	2672.7	78.9	10	R.SPPLIGSESAYESFLSADDK.A
	HsFLAG-FLJ20729_	4.5372	0.4386	2385.37	2385.562	7299.9	1	716	45.2	3	K.QGSPDQVSPVSEMTSTSLYQDK.Q
	HsFLAG-ARP6_Ti_1	4.1967	0.3033	1714.02	1712.854	4290.3	1	593	64.3	8	K.STDFAPIKEDFGQEK.K
	HsFLAG-Lin9_Ti_20	5.7391	0.4916	2077.73	2077.271	9507.4	1	2511.9	72.2	1	K.KTDDVEAMSSQPALALDER.K
	HsFlag-NUFIP_Ti_2	5.4251	0.4481	2053.62	2054.307	7265	1	1620.6	66.7	9	R.KLGDVSPTQIDVSQFGSFK.E
	HsARP6-FLAG_Ti_1	3.2424	0.2827	1345.05	1345.507	8410.7	1	1188.2	72.7	2	R.DMSLYASLTSEK.V
	HsFLAG-ARP6_Ti_1	3.5627	0.4124	1903.36	1904.037	4959.5	1	483.3	50	3	R.ESSPLYSPTFSDSTSAVK.E
	HsFLAG-ARP6_Ti_1	5.5246	0.5094	2409.56	2410.525	5960	1	1608.6	63.6	8	K.TATCHSSSSPPIDAASAEPYGFR.A
	HsFLAG-Lin9_Ti_20	3.9203	0.2804	2410.09	2410.525	7284.5	1	873.8	33	2	K.TATCHSSSSPPIDAASAEPYGFR.A
	HsFLAG-ARP6_Ti_1	5.4608	0.3859	1854.52	1854.137	9232.2	1	1467.4	60	11	R.ASVLFDTMQHHLALNR.D
	HsFlag-NUFIP_Ti_2	4.2141	0.3355	1854.54	1854.137	4468.3	1	904.5	48.3	2	R.ASVLFDTMQHHLALNR.D
	HsFLAG-Lin9_Ti_20	3.5991	0.3274	1990.71	1991.121	7787.5	4	506	46.9	4	K.TPGDFSYAYQKPEETTR.S
	HsFLAG-ARP6_Ti_1	3.514	0.3117	1771.34	1769.726	5825.6	1	891.9	65.4	1	R.SPDEEDYDYESYEK.T
	HsH2AZ-FLAG_293_	4.1042	0.3889	1491.3	1491.551	6411.3	1	1339.1	73.1	1	K.SPSDSGYSYETIGK.T
	HsH2AZ-FLAG_293_	4.6838	0.3733	1659.23	1659.744	7634.8	1	2424.9	84.6	5	K.TPEDGDYSYEIIEK.T
	HsH2AZ-FLAG_293_	4.0645	0.2738	1575.61	1575.626	6581.5	1	1029.1	65.4	7	R.TPEEGGYSYDISEK.T
	HsARP6-FLAG_Ti_1	3.0615	0.3014	1546.92	1545.643	4825.8	1	296.2	53.8	3	K.TTSPPEVSGYSYEK.T
	HsFLAG-Lin9_Ti_20	4.7448	0.3505	3550.94	3551.626	6983.4	1	642.8	24.2	1	R.RLLDDISNGYDDSEDGGHTLGDPSYSYETTEK.I
	HsFLAG-FLJ20729_	4.6642	0.3184	3394.65	3395.438	8982.9	1	1184.5	28.3	2	R.LLDDISNGYDDSEDGGHTLGDPSYSYETTEK.I
	HsFLAG-p53-DNA-D	4.1438	0.4795	1926.61	1927.028	4746.1	1	521.4	56.2	10	K.ITSFPESEGYSYETSTK.T
	HsARP6-FLAG_Ti_1	4.163	0.41	1666.16	1666.702	7515.7	1	1018	65.4	6	R.TPDTSTYCYETAEK.I
	HsFLAG-Lin9_Ti_20	5.0469	0.4827	2315.84	2316.403	6886.8	1	1514.8	63.2	6	R.TPQASTYSYETSDLCYTAEK.K
	HsFLAG-Lin9_Ti_20	4.0985	0.3509	1717.75	1716.815	7407	1	949.7	65.4	4	R.QDVDLCLVSSCEYK.H
	HsFLAG-p53-DNA-D	5.0889	0.3897	4449.99	4451.844	7026.7	1	654.3	22	9	GK.Q
	HsFLAG-FLJ20729_	4.3522	0.3714	1360.94	1361.541	4871	1	872.7	67.9	14	K.PLTQSGGAPPPPGGK.Q
	HsFLAG-p53-DNA-D	3.3074	0.3513	1364.7	1365.659	5675.7	1	769	65.4	2	K.SKPLAASPKPAGLK.E
	HsFLAG-ARP6_Ti_1	3.1565	0.1671	1365.26	1365.659	4615.2	1	567.5	65.4	8	K.SKPLAASPKPAGLK.E
	HsFLAG-p53-DNA-D	2.156	0.1947	1142.57	1143.326	6539	1	661.6	65	2	K.AAKPTTTPEVK.A
	HsFLAG-Lin9_Ti_20	3.373	0.1866	2628.81	2629.939	4234.4	2	189.3	34.8	3	K.SSAVPPGLPVYLDLCYIPNHSNSK.N
	HsFLAG-ARP6_Ti_2	2.5269	0.2611	997.56	998.123	4776.7	8	489.9	78.6	1	K.NVDVEFFK.R
	HsFLAG-ARP6_Ti_2	5.2105	0.3695	1928.26	1929.007	7609.4	1	1462.4	61.8	7	R.SSYYVVSGNDPAAEEPSR.A
	HsFLAG-p53-DNA-D	2.6195	0.214	1028.53	1029.222	9506.2	3	847.8	66.7	3	R.AVLDALLEGK.A
	HsFLAG-Lin9_Ti_20	3.5493	0.1875	1029.31	1029.222	3853.7	2	851.4	83.3	3	R.AVLDALLEGK.A
gi|4826760|re	13	218	46.70%	415	45672	5.6	heterogeneous nuclear ribonucleoprotein F [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.7297	0.4413	3753.46	3754.039	6288.4	1	614.2	25.8	8	R.GLPWSCSVEDVQNFLSDCTIHDGAAGVHFIYTR.E
*	HsFLAG-ARP6_Ti_1	3.483	0.3329	1711.24	1710.792	6411.3	1	1279.5	70	1	R.QSGEAFVELGSEDDVK.M
*	HsFLAG-TIP49b_Ti_	4.1175	0.4777	1631.59	1631.658	7476.9	1	1200.2	66.7	18	K.HSGPNSADSANDGFVR.L
*	HsFLAG-Lin9_Ti_20	4.0416	0.2426	3690.84	3690.194	6680	3	395.9	19.7	3	R.GLPFGCTKEEIVQFFSGLEIVPNGITLPVDPEGK.I
*	HsFLAG-Lin9_Ti_20	3.4972	0.1849	2830.73	2829.219	4755.5	1	400.9	38	2	K.EEIVQFFSGLEIVPNGITLPVDPEGK.I
*	HsFLAG-p53-DNA-D	5.6326	0.4087	1868.52	1869.081	8614.7	1	2252.8	71.9	66	K.ITGEAFVQFASQELAEK.A
*	HsFLAG-ARP6_Ti_1	7.8967	0.5084	3476.73	3476.711	8113.5	1	2105.6	33.9	15	R.MRPGAYSTGYGGYEEYSGLSDGYGFTTDLFGR.D
*	HsFLAG-ARP6_Ti_1	4.0927	0.2922	2212.98	2213.352	5498.8	1	654.5	34.7	2	R.YGDSEFTVQSTTGHCVHMR.G
*	HsFLAG-p53-DNA-D	4.1657	0.3196	2212.98	2213.352	7408.4	1	1142.4	52.8	1	R.YGDSEFTVQSTTGHCVHMR.G

	HsH2AZ-FLAG_293_	5.0454	0.3774	1997.32	1998.202	8397.3	1	1161	59.4	53	K.ATENDIYNFFSPLNPVR.V
	HsYL1_Ti_102.2959.	5.4927	0.2675	1998.86	1998.202	7998.6	1	1939.6	48.4	8	K.ATENDIYNFFSPLNPVR.V
	HsFLAG-TCF3_Ti_1	2.9392	0.214	1092.51	1093.228	6901.6	1	869.9	72.2	12	R.VHIEIGPDGR.V
	HsFLAG-ARP6_Ti_1	3.664	0.2731	1093.44	1093.228	6216	1	1638.1	88.9	29	R.VHIEIGPDGR.V
gi|5803076|re	6	23	46.50%	185	21418	4.9	chromobox homolog 1 (HP1 beta homolog Drosophila) [Homo sapiens]				
*	HsFlag-NUFIP_Ti_11	2.8199	0.1721	2238.25	2238.45	9173.3	1	661.3	50	1	K.KKVEEVLEEEEEEYVVEK.V
*	HsFlag-NUFIP_Ti_1	6.3636	0.3429	2109.67	2110.276	8654.2	1	2663.5	81.2	14	K.KVEEVLEEEEEEYVVEK.V
*	HsFlag-NUFIP_Ti_1	4.7123	0.3195	3428.65	3428.567	5808.1	1	911.8	30.4	3	K.GFSDEDNTWEPEENLDCPDLIAEFLQSQK.T
	HsFlag-NUFIP_Ti_1	2.8706	0.2148	1714.77	1714.045	8801.6	1	611.6	53.3	1	R.IIGATDSSGELMFLMK.W
*	HsFLAG-ARP6_Ti_1	2.7166	0.1141	1159.84	1159.238	4535.1	3	771.3	75	1	K.NSDEADLVPAK.E
*	HsFlag-NUFIP_Ti_11	3.8387	0.2182	1526.95	1527.683	7167	3	909.4	68.2	3	K.CPQVVISFYEER.L
gi|29893564|r	19	177	46.30%	462	51803	9.4	microspherule protein 1 isoform 1 [Homo sapiens]				
gi|59799166|r	19	177	45.10%	475	53001	9.5	microspherule protein 1 isoform 2 [Homo sapiens]				
	HsFLAG-FLJ20309_	2.5182	0.1378	1071.98	1073.235	4782.8	3	585.1	75	1	R.ASSQALGTIPK.R
	HsFLAG-ARP5_Ti_1	3.9839	0.2335	1609.42	1609.817	7963	1	2144.3	80.8	2	R.KKFDDELVESSLAK.S
	HsFLAG-FLJ20309_	4.9034	0.2927	1481.48	1481.643	7205.5	1	2417.8	87.5	23	K.KFDDELVESSLAK.S
	HsFLAG-FLJ20309_	4.575	0.4613	1685.45	1685.961	4477.1	1	675.2	61.8	12	K.APSTPVPPSPAPAPGLTK.R
	HsFLAG-FLJ20309_	4.0193	0.2719	1468.61	1468.736	7002.8	1	1496.4	81.8	8	R.WYALLYDPVISK.L
	HsFLAG-FLJ20309_	2.176	0.2192	1405.63	1406.625	2176.9	5	131.1	58.3	1	R.QLHPEAIAAIQSK.A
	HsFLAG-FLJ20309_	3.4494	0.149	1406.35	1406.625	4641.8	1	705.2	79.2	6	R.QLHPEAIAAIQSK.A
	HsFLAG-ARP5_Ti_1	3.8229	0.1925	1464.31	1464.702	6787.4	1	944.5	66.7	2	K.ALFSKAEEQLLSK.V
	HsFLAG-FLJ20309_	3.8867	0.3677	2030.67	2030.245	4702.4	1	534.2	52.9	8	K.VGSTSQPTLETFQDLLHR.H
	HsFlag-FLJ90652_2	3.5833	0.2181	1226.2	1226.482	7571.6	2	1552.4	83.3	1	K.ALQAHWQLMK.Q
	HsFLAG-FLJ20309_	4.9282	0.3104	1836.56	1836.095	9430	1	2362.5	75	10	K.QYYLLEDQTVQPLPK.G
	HsFLAG-FLJ20309_	5.7663	0.5126	1982.56	1982.065	8013.7	1	2455.2	76.5	23	K.GDQVLNFSDAEDLIDDSK.L
	HsFLAG-FLJ20309_	3.6202	0.2103	2223.78	2223.398	4539.8	2	565.6	35.5	1	K.GDQVLNFSDAEDLIDDSKLK.D
	HsFLAG-FLJ20309_	5.5876	0.3946	2224.2	2223.398	10133.2	1	2770.5	68.4	6	K.GDQVLNFSDAEDLIDDSKLK.D
	HsFLAG-FLJ20309_	5.3057	0.3546	1801.72	1800.963	10726.9	1	2448.8	73.3	46	K.DNQIDVDLSLEGPAWK.I
	HsFLAG-FLJ20436_	3.5641	0.3536	1353.77	1354.421	6100.2	1	1355.3	81.8	7	K.NNGDFFIANEGR.R
	HsFLAG-ARP5_Ti_1	2.8426	0.281	1731.6	1732.002	4652.9	2	363.7	50	1	R.RPIYIDGRPVLCGSK.W
	HsFLAG-FLJ20309_	3.8986	0.3416	1403.39	1402.591	7117.2	1	1227.7	79.2	12	R.LSNNSVVEIASLR.F
	HsFLAG-ARP5_Ti_1	5.1799	0.413	1675.33	1676.055	6850.2	1	1865.4	84.6	7	R.FVFLINQDLIALIR.A
gi|4506457|re	8	31	46.10%	317	36876	4.4	reticulocalbin 2, EF-hand calcium binding domain [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.272	0.302	2266.17	2266.357	6368.3	1	372	41.2	1	K.NSDDTVTWDEYNIQMYDR.V
*	HsFLAG-ARP6_Ti_1	4.713	0.4343	2343.29	2344.45	8628.7	1	1609.7	60.5	2	R.VIDFDENTALDDAEEESFRK.L
*	HsFLAG-ARP6_Ti_1	4.3448	0.4594	1819.25	1818.937	6037.5	1	1355.9	70	13	K.NGDGFVSLEEFLGDYR.W
*	HsFLAG-TCF3_Ti_1	4.6957	0.4444	1943.7	1943.12	5021.1	1	1041.1	73.3	4	R.WDPTANEDPEWILVEK.D
*	HsFLAG-TCF3_Ti_1	4.9504	0.3123	4514.52	4513.937	9618.7	1	622.9	20.5	2	K.K
*	HsFLAG-Lin9_Ti_20	5.7947	0.4392	2771.09	2771.007	6512.4	1	1131.9	52.2	1	K.KLSEEEILENPDLFLTSEATDYGR.Q
*	HsFLAG-Lin9_Ti_20	5.4002	0.3769	2772.01	2771.007	11501.2	1	1951.3	34.8	7	K.KLSEEEILENPDLFLTSEATDYGR.Q
*	HsFLAG-TCF3_Ti_1	2.7604	0.1328	1595.51	1595.665	5863.9	2	425.4	59.1	1	R.QLHDDYFYHDEL.-
gi|15082258|r	7	40	45.90%	183	20811	5.3	chromobox homolog 3 [Homo sapiens]				
gi|89038889|r	7	40	45.90%	183	20811	5.3	PREDICTED: similar to chromobox homolog 3 [Homo sapiens]				

gi|20544151|r	7	40	45.90%	183	20811	5.3	chromobox homolog 3 [Homo sapiens]				
	HsFlag-NUFIP_Ti_1	4.3125	0.3387	1662.52	1662.834	5539.3	1	887.7	69.2	2	K.KVEEAEPEEFVVEK.V
	HsFLAG-p53-DNA-D	3.6481	0.098	3700.25	3698.944	11792	3	730.8	22.5	1	K.WKGFTDADNTWEPEENLDCPELIEAFLNSQK.A
	HsFlag-NUFIP_Ti_1	5.6695	0.4255	3383.95	3384.557	8761.9	1	922.7	26.8	7	K.GFTDADNTWEPEENLDCPELIEAFLNSQK.A
	HsFlag-NUFIP_Ti_1	2.8706	0.2148	1714.77	1714.045	8801.6	1	611.6	53.3	1	R.IIGATDSSGELMFLMK.W
	HsFLAG-ARP6_Ti_1	2.7364	0.1325	1175.28	1176.266	7574.1	1	930.4	70	1	K.DSDEADLVLAK.E
	HsFLAG-ARP6_Ti_1	4.4268	0.2221	1176.19	1176.266	5715.6	1	1346.9	85	2	K.DSDEADLVLAK.E
	HsFlag-NUFIP_Ti_1	4.4119	0.1679	1525.57	1525.711	7777.5	1	1543.6	77.3	26	K.CPQIVIAFYEER.L
gi|11136628|r	7	27	45.80%	225	24764	4.7	eukaryotic translation elongation factor 1 beta 2 [Homo sapiens]				
gi|4503477|re	7	27	45.80%	225	24764	4.7	eukaryotic translation elongation factor 1 beta 2 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	5.5752	0.3747	1606.11	1604.8	6601.3	1	2138.9	85.7	14	K.SPAGLQVLNDYLADK.S
	HsFLAG-TCF3_Ti_1	3.8814	0.272	3446.61	3447.792	4222.8	2	233.2	21	1	K.SYIEGYVPSQADVAVFEAVSSPPPADLCHALR.W
	HsFLAG-FLJ20309_	2.2092	0.0972	726.49	726.938	3544.8	2	369.7	75	6	K.KPALVAK.S
	HsFlag-VPS71_Ti_1	5.4857	0.1175	2851.62	2851.164	5465.8	1	1362.4	41.3	2	K.SSILLDVKPWDDETDMAKLEECVR.S
	HsFlag-VPS71_Ti_1	2.7007	0.3733	1347.71	1348.498	5679.8	1	386.5	50	1	R.SIQADGLVWGSSK.L
	HsARP6-FLAG_Ti_1	3.1041	0.1913	1475.33	1475.648	7720.8	1	1139.3	77.3	1	K.KLQIQCVVEDDK.V
	HsFlag-VPS71_Ti_1	3.6688	0.1914	1348.34	1347.474	4763.4	1	872.7	80	2	K.LQIQCVVEDDK.V
gi|4503571|re	13	106	45.60%	434	47169	7.4	enolase 1 [Homo sapiens]				
*	HsH2AZ-FLAG_293_	3.8993	0.276	1407.24	1407.563	5406.7	1	1113.4	79.2	3	R.GNPTVEVDLFTSK.G
	HsH2AZ-FLAG_293_	5.1206	0.3787	1805.83	1806.026	3207.6	1	636.4	67.6	5	R.AAVPSGASTGIYEALELR.D
*	HsFLAG-p53-DNA-D	2.7268	0.1623	1089.53	1089.234	6500.6	9	732.9	75	2	K.KLNVTEQEK.I
*	HsFLAG-ARP6_Ti_1	6.1831	0.3129	3014.14	3013.383	8871.3	1	1922.7	33.6	16	R.HIADLAGNSEVILPVPAFNVINGGSHAGNK.L
*	HsFlag-VPS71_Ti_1	4.1844	0.3069	1910.94	1909.315	5108.3	1	716.1	59.4	3	K.LAMQEFMILPVGAANFR.E
*	HsFLAG-FLJ20729_	3.5655	0.1616	1144.44	1144.316	6413.2	3	1022.5	77.8	10	R.IGAEVYHNLK.N
*	HsH2AZ-FLAG_293_	4.9245	0.3956	1962.29	1962.08	6759.2	1	1478.1	63.9	4	K.DATNVGDEGGFAPNILENK.E
*	HsFLAG-ARP6_Ti_1	2.9894	0.3155	1541.55	1541.805	9914.9	1	1245.1	65.4	1	K.VVIGMDVAASEFFR.S
*	HsFlag-VPS71_Ti_1	1.9685	0.133	1072.58	1073.191	5674.4	6	440.9	56.2	1	R.SGKYDLDFK.S
*	HsH2AZ-FLAG_293_	4.633	0.3402	1426.21	1426.609	4420.2	1	1058	86.4	14	R.YISPDQLADLYK.S
*	HsFLAG-p53-DNA-D	6.4829	0.2642	2989.06	2987.251	8646.9	1	2274.7	39.6	6	K.SFIKDYPVVSIEDPFDQDDWGAWQK.F
*	HsFLAG-ARP6_Ti_1	5.8762	0.2101	2511.99	2511.663	5110.1	1	1038.4	57.5	15	K.DYPVVSIEDPFDQDDWGAWQK.F
	HsH2AZ-FLAG_293_	5.0674	0.403	2354.25	2354.582	6671.8	1	1036.5	50	26	R.SGETEDTFIADLVVGLCTGQIK.T
gi|11321585|r	10	27	45.30%	340	37377	6	guanine nucleotide-binding protein, beta-1 subunit [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	5.9829	0.4082	2016.43	2017.169	8719.1	1	2264.4	69.4	2	K.ACADATLSQITNNIDPVGR.I
	HsFLAG-ARP6_Ti_1	3.6129	0.315	1338.83	1337.496	4764.8	1	1256	90	1	K.IYAMHWGTDSR.L
	HsFLAG-ARP6_Ti_1	2.4153	0.3245	1017.38	1018.155	4835	1	383.5	61.1	1	R.LLVSASQDGK.L
	HsFLAG-ARP6_Ti_1	3.3869	0.1904	1354.3	1354.546	5425.3	1	892.9	80	3	K.LIIWDSYTTNK.V
	HsFLAG-ARP6_Ti_1	2.2605	0.1278	805.5	805.999	5457.6	1	635.6	83.3	1	K.VHAIPLR.S
*	HsFLAG-ARP6_Ti_1	3.2814	0.4156	1524.58	1524.606	6240.9	2	617.9	62.5	2	R.ELAGHTGYLSCCR.F
*	HsFLAG-ARP6_Ti_1	5.7665	0.3889	3522.89	3523.642	9188.7	1	1039.3	26.6	3	R.QTFTGHESDINAICFFPNGNAFATGSDDATCR.L
*	HsFLAG-ARP6_Ti_1	5.1731	0.4949	2127.28	2128.355	7676.1	1	2921.4	76.5	8	R.LLLAGYDDFNCNVWDALK.A
	HsFLAG-ARP6_Ti_1	2.9143	0.2593	1010.1	1010.098	5766.2	1	890.7	83.3	3	R.AGVLAGHDNR.V
	HsFLAG-ARP6_Ti_1	5.2606	0.5327	2416.35	2417.659	6569.6	1	1462.5	61.4	3	R.VSCLGVTDDGMAVATGSWDSFLK.I
gi|20357529|r	10	19	45.30%	340	37331	6	guanine nucleotide-binding protein, beta-2 subunit [Homo sapiens]				

*	HsFLAG-ARP6_Ti_1	5.0372	0.4292	1933.91	1933.092	8986.4	1	1982.7	66.7	2	K.ACGDSTLTQITAGLDPVGR.I
	HsFLAG-ARP6_Ti_1	3.6129	0.315	1338.83	1337.496	4764.8	1	1256	90	1	K.IYAMHWGTDSR.L
	HsFLAG-ARP6_Ti_1	2.4153	0.3245	1017.38	1018.155	4835	1	383.5	61.1	1	R.LLVSASQDGK.L
	HsFLAG-ARP6_Ti_1	3.3869	0.1904	1354.3	1354.546	5425.3	1	892.9	80	3	K.LIIWDSYTTNK.V
	HsFLAG-ARP6_Ti_1	2.2605	0.1278	805.5	805.999	5457.6	1	635.6	83.3	1	K.VHAIPLR.S
	HsFLAG-ARP6_Ti_1	2.5532	0.1303	1549.49	1550.644	3866.5	1	385	70.8	1	R.ELPGHTGYLSCCR.F
*	HsFLAG-ARP6_Ti_1	5.8125	0.4161	3511.32	3511.708	7030.5	1	1115.5	30.6	2	R.QTFIGHESDINAVAFFPNGYAFTTGSDDATCR.L
*	HsFLAG-ARP6_Ti_1	4.8884	0.518	2159.36	2160.415	8200.4	1	2102.4	70.6	2	R.LLLAGYDDFNCNIWDAMK.G
	HsFLAG-ARP6_Ti_1	2.9143	0.2593	1010.1	1010.098	5766.2	1	890.7	83.3	3	R.AGVLAGHDNR.V
	HsFLAG-ARP6_Ti_1	5.2606	0.5327	2416.35	2417.659	6569.6	1	1462.5	61.4	3	R.VSCLGVTDDGMAVATGSWDSFLK.I
gi|24234688|r	24	121	45.20%	679	73681	6.2	heat shock 70kDa protein 9B precursor [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.5022	0.1468	2080.03	2079.339	9689.8	4	447.7	37.5	1	K.GAVVGIDLGTTNSCVAVMEGK.Q
*	HsFlag-FLJ20643_Ti	2.854	0.1629	959.51	959.047	4139	1	773.3	87.5	2	K.VLENAEGAR.T
*	HsFLAG-ARP6_Ti_1	3.586	0.4219	1450.81	1451.576	4733.8	1	727.6	69.2	1	R.TTPSVVAFTADGER.L
*	HsFLAG-ARP6_Ti_1	2.0004	0.1418	715.24	715.929	3971.5	5	468.9	83.3	1	R.LVGMPAK.R
*	HsFLAG-Lin9_Ti_20	5.169	0.4443	1725.19	1725.902	10197	1	1920.1	71.4	18	K.RQAVTNPNNTFYATK.R
*	HsFLAG-ARP6_Ti_1	3.4882	0.3361	1343.74	1342.411	7164.5	1	1215.6	75	2	R.ASNGDAWVEAHGK.L
*	HsFLAG-p53-DNA-D	3.6127	0.2506	1554.02	1554.888	6032.2	1	1303.8	76.9	6	K.LYSPSQIGAFVLMK.M
*	HsFLAG-p53-DNA-D	3.3963	0.3433	1593.21	1593.795	10112.2	1	1645.9	73.1	1	K.MKETAENYLGHTAK.N
*	HsFLAG-ARP6_Ti_1	3.7642	0.3853	1334.4	1334.428	6980.1	1	689.1	68.2	2	K.ETAENYLGHTAK.N
	HsFLAG-KIAA0515_	2.6001	0.1788	1695.38	1695.872	3084.9	3	390.6	60.7	2	K.NAVITVPAYFNDSQR.Q
*	HsFLAG-ARP6_Ti_1	4.0951	0.2386	1243.38	1243.406	5380.5	6	1153.8	81.8	4	K.DAGQISGLNVLR.V
*	HsFLAG-ARP6_Ti_1	6.7269	0.5222	2252.33	2252.613	7224.4	1	2613.4	72.5	19	K.VIAVYDLGGGTFDISILEIQK.G
*	HsFLAG-ARP6_Ti_1	5.4052	0.5142	2055.7	2057.181	4929.5	1	1284	69.4	22	K.STNGDTFLGGEDFDQALLR.H
*	HsFLAG-ARP6_Ti_1	2.9896	0.1161	1019.18	1019.143	4429.4	1	953.2	100	1	K.RETGVDLTK.D
*	HsFLAG-ARP6_Ti_1	4.6388	0.3364	1363.52	1362.569	6648.5	1	1716.7	86.4	8	R.AQFEGIVTDLIR.R
*	HsFLAG-ARP6_Ti_1	4.4673	0.4029	1447.99	1447.69	6126.9	1	1532.4	76.9	1	K.SDIGEVILVGGMTR.M
*	HsFLAG-ARP8_Ti_2	2.5246	0.0896	1291.62	1291.45	5008.9	6	319.6	60	1	K.VQQTVQDLFGR.A
*	HsFLAG-ARP6_Ti_1	3.9853	0.2574	1292.47	1291.45	8046.7	1	1566.2	85	7	K.VQQTVQDLFGR.A
*	HsFLAG-ARP6_Ti_1	3.9634	0.4456	1673.6	1674.897	8459	1	1611.7	71.4	1	K.VQQTVQDLFGRAPSK.A
*	HsFlag-NUFIP_Ti_11	3.9151	0.2937	1594.39	1593.953	5050.9	1	933.3	71.4	13	K.LLGQFTLIGIPPAPR.G
*	HsFLAG-ARP8_Ti_2	4.9593	0.4288	2420.1	2419.709	12274.9	1	2353.6	59.5	4	R.EQQIVIQSSGGLSKDDIENMVK.N
*	HsFLAG-ARP6_Ti_1	5.9711	0.2458	2144.28	2143.376	8816	1	2454.2	48.6	2	K.ERVEAVNMAEGIIHDTETK.M
*	HsFLAG-ARP6_Ti_1	4.3902	0.3586	1855.21	1854.992	5676.4	1	1541.9	82.1	1	K.MEEFKDQLPADECNK.L
*	HsFLAG-KIAA0515_	3.2296	0.294	1232.55	1232.379	4553.1	1	595.3	77.3	1	R.QAASSLQQASLK.L
gi|40254869|r	20	187	45.10%	499	55442	5.8	pre-mRNA processing factor 31 homolog [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	4.7305	0.4015	1608.27	1606.791	5402.7	1	954	67.9	4	K.ASEVMGPVEAAPEYR.V
*	HsFLAG-TCF3_Ti_1	2.9148	0.0861	2391.82	2391.727	9391.3	4	461.8	35	1	R.VIVDANNLTVEIENELNIIHK.F
*	HsH2AZ-FLAG_293_	4.1427	0.1359	2392.48	2391.727	3203.8	1	607	38.8	5	R.VIVDANNLTVEIENELNIIHK.F
*	HsARP6-FLAG_Ti_1	3.9775	0.2119	2032.79	2033.335	5179.4	2	1048.9	45.3	5	K.RFPELESLVPNALDYIR.T
*	HsFlag-DPCD_Ti_20	5.149	0.4152	2032.92	2033.335	6485.2	1	1007.7	65.6	43	K.RFPELESLVPNALDYIR.T
*	HsFLAG-p53-DNA-D	4.2878	0.2978	1876.71	1877.147	5013.7	1	601.5	60	5	R.FPELESLVPNALDYIR.T
*	HsFlag-VPS71_Ti_1	4.9452	0.3502	1907.65	1906.291	3941	1	1185.8	69.4	23	R.MSFIAPNLSIIIGASTAAK.I

*	HsARP6-FLAG_Ti_1	4.039	0.273	1261.3	1261.522	4778.3	1	1251.2	87.5	4	K.IMGVAGGLTNLSK.M
*	HsFlag-VPS71_Ti_1	3.2213	0.2649	1261.59	1261.522	5207.3	1	511.9	62.5	2	K.IMGVAGGLTNLSK.M
*	HsFLAG-ARP6_Ti_1	4.5993	0.2925	1477.15	1475.774	8107.5	1	1499.3	79.2	14	K.MPACNIMLLGAQR.K
*	HsFLAG-p53-DNA-D	6.3496	0.5013	3517.03	3517.963	7508.5	1	1945.9	35.5	2	R.KTLSGFSSTSVLPHTGYIYHSDIVQSLPPDLR.R
*	HsFlag-NUFIP_Ti_11	5.8024	0.4572	3390.86	3389.789	7359.1	1	1358.6	30.8	17	K.TLSGFSSTSVLPHTGYIYHSDIVQSLPPDLR.R
*	HsFLAG-FLJ20309_	3.7653	0.3766	1235.34	1236.28	7977.6	1	1251.3	85	5	R.VDSFHESTEGK.V
*	HsFlag-VPS71_Ti_1	3.2198	0.2843	1352.62	1351.499	5984	1	1176.6	85	7	K.VGYELKDEIER.K
*	HsH2AZ-FLAG_293_	2.8463	0.1031	1419.46	1419.667	3852.5	1	451	70.8	5	K.QVKPLPAPLDGQR.K
*	HsFlag-VPS71_Ti_1	3.2333	0.3466	2673.46	2673.91	7346.6	1	762.6	41.3	1	R.MSFGEIEEDAYQEDLGFSLGHLGK.S
*	HsFlag-VPS71_Ti_1	5.5543	0.4441	2675.82	2673.91	6516.6	1	1036.6	34.8	8	R.MSFGEIEEDAYQEDLGFSLGHLGK.S
*	HsH2AZ-FLAG_293_	5.5968	0.4423	2602.26	2603.889	5449.2	1	643.1	42	29	R.SSGTASSVAFTPLQGLEIVNPQAAEK.K
*	HsFLAG-FLJ20729_	3.8886	0.2242	2604.93	2603.889	8265.3	1	738.6	26	3	R.SSGTASSVAFTPLQGLEIVNPQAAEK.K
*	HsARP6-FLAG_Ti_1	2.9447	0.2946	1224.06	1223.429	3547	1	503.8	77.8	4	K.YFSSMAEFLK.V
gi|5174715|re	15	191	45.10%	364	40594	6.5	transcription factor-like 1 [Homo sapiens]				
*	HsYL1_Ti_104.0870.	2.1724	0.2336	1116.59	1117.247	3684.9	1	363.5	60	3	R.KVNTPAGSSQK.A
*	HsYL1_Ti_104.0862.	2.8467	0.2797	1117.72	1117.247	5252.2	1	1062.8	85	4	R.KVNTPAGSSQK.A
*	HsH2AZ-FLAG_293_	4.4291	0.3799	1629.46	1629.764	4427.5	1	1447	85.7	9	K.ALLPLELQDDGSDSR.K
*	HsYL1-FLAG_Ti_205	4.1512	0.2883	1757.39	1757.938	6083.4	1	881.1	66.7	58	K.ALLPLELQDDGSDSRK.S
*	HsH2AZ-FLAG_293_	3.3366	0.2365	1963.53	1964.198	8343.1	1	780.5	53.3	5	R.KGPHCERPLTQEELLR.E
*	HsFLAG-TIP49b_Ti_	3.5891	0.2328	1834.72	1836.024	8614.5	1	855.8	57.1	17	K.GPHCERPLTQEELLR.E
*	HsFLAG-TIP49b_Ti_	2.0681	0.1344	987.47	988.129	4962.3	1	419.3	78.6	2	K.ITEELNLR.S
*	HsFlag-VPS71_Ti_1	2.8918	0.1242	988.38	988.129	3862.7	6	756.8	92.9	1	K.ITEELNLR.S
*	HsYL1_Ti_105.1550.	3.9006	0.2837	1456.11	1454.577	6549.2	2	905.7	68.2	34	R.SLETYERLEADK.K
*	HsYL1_Ti_106.2318.	4.4467	0.3951	2320.06	2319.672	8663.9	1	1228.3	52.4	7	K.CPGPIITYHSVTVPLVGEPGPK.E
*	HsYL1-FLAG_Ti_206	5.8213	0.395	3209.45	3209.497	6102.4	1	866.8	29	6	K.EENVDIEGLDPAPSVSALTPHAGTGPVNPPAR.C
*	HsH2AZ-FLAG_293_	4.2636	0.3113	2618.15	2617.877	6042.8	1	701.9	42.9	30	R.TFITFSDDATFEEWFPQGRPPK.V
*	HsFlag-VPS71_Ti_1	2.5301	0.2421	1598.69	1598.811	6906.4	3	385.8	54.2	1	R.EVCPVTHRPALYR.D
*	HsH2AZ-FLAG_293_	3.8529	0.233	1920.42	1920.175	4272.3	4	396.5	50	3	R.PALYRDPVTDIPYATAR.A
*	HsH2AZ-FLAG_293_	3.7285	0.3053	1319.37	1319.457	4110.8	1	1012.3	81.8	11	R.DPVTDIPYATAR.A
gi|16507237|r	27	218	44.80%	654	72333	5.2	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa) [Homo sapiens]				
	HsFlag-FLJ90652_2	4.2425	0.3965	1568.34	1567.739	5067.9	1	1159.1	80.8	12	R.ITPSYVAFTPEGER.L
	HsFLAG-ARP6_Ti_1	4.4719	0.4248	1678.88	1678.796	5407.6	1	1303.3	78.6	14	K.NQLTSNPENTVFDAK.R
	HsFLAG-ARP6_Ti_1	3.7141	0.2789	1431.43	1431.545	4991.3	1	1246.9	86.4	3	R.TWNDPSVQQDIK.F
	HsFLAG-ARP6_Ti_1	3.637	0.2894	1605.62	1605.831	5433.8	1	1357.9	78.6	2	K.TKPYIQVDIGGGQTK.T
	HsFlag-FLJ90652_2	4.4201	0.3183	1537.4	1537.811	5511.5	1	1734.4	88.5	10	K.TFAPEEISAMVLTK.M
	HsFlag-VPS71_Ti_1	2.6074	0.246	1537.5	1537.811	8170.8	1	685.9	57.7	1	K.TFAPEEISAMVLTK.M
	HsFLAG-ARP6_Ti_1	5.1932	0.3055	2016.36	2017.295	5163.4	1	1099.7	64.7	7	K.KVTHAVVTVPAYFNDAQR.Q
	HsFLAG-ARP6_Ti_1	4.9662	0.4247	1889.59	1889.121	4433.6	1	1301.9	78.1	15	K.VTHAVVTVPAYFNDAQR.Q
	HsFLAG-ARP6_Ti_1	4.3982	0.3629	1889.9	1889.121	5678.5	1	1054.9	46.9	2	K.VTHAVVTVPAYFNDAQR.Q
	HsFLAG-ARP6_Ti_1	3.222	0.359	1218.78	1218.414	5732.6	1	921.3	77.3	1	K.DAGTIAGLNVMR.I
	HsFLAG-Lin9_Ti_20	5.2508	0.4465	1660.49	1660.908	5331.5	1	1768.4	80	50	R.IINEPTAAAIAYGLDK.R
	HsYL1_Ti_103.1894.	3.7558	0.2757	1818.9	1817.095	5057.2	1	693.7	62.5	2	R.IINEPTAAAIAYGLDKR.E
	HsFLAG-ARP6_Ti_1	2.8047	0.0885	904.14	904.115	3584.3	4	594.5	91.7	1	R.VMEHFIK.L

	HsFLAG-TIP49b_Ti_	3.336	0.2643	1155.12	1154.274	7185.7	1	1004	83.3	12	K.RALSSQHQAR.I
	HsFLAG-ARP6_Ti_1	5.956	0.5117	2166.48	2166.303	5976.8	1	1719	73.5	13	R.IEIESFYEGEDFSETLTR.A
	HsFLAG-ARP6_Ti_1	4.0561	0.3206	1513.58	1513.752	6056.3	1	1234	77.3	7	R.AKFEELNMDLFR.S
	HsFLAG-ARP6_Ti_1	5.144	0.3191	1589.59	1589.786	7954.8	1	2844.4	82.1	9	K.KSDIDEIVLVGGSTR.I
	HsFLAG-p53-DNA-D	2.3343	0.1163	758.44	758.893	4419.6	8	488.1	83.3	1	R.NTVVPTK.K
	HsTIP60_Ti_103.185	5.1489	0.4695	1837.58	1838.024	8399.6	1	2292.5	75	12	K.SQIFSTASDNQPTVTIK.V
	HsFLAG-p53-DNA-D	2.9197	0.231	1192.48	1192.357	6882.2	1	982.3	83.3	8	K.VYEGERPLTK.D
	HsFlag-NUFIP_Ti_1	5.2239	0.4249	1935.7	1935.19	5644.8	1	1308.4	67.6	5	K.DNHLLGTFDLTGIPPAPR.G
	HsFLAG-KIAA0515_	2.5	0.2671	1316.25	1317.438	3617.5	1	341.1	70	1	R.NELESYAYSLK.N
	HsFLAG-ARP6_Ti_1	3.646	0.1958	1316.8	1317.438	5342.7	3	1372.3	90	5	R.NELESYAYSLK.N
	HsFLAG-ARP6_Ti_1	5.5772	0.419	1976.37	1976.106	7894.2	1	2696	86.7	6	K.IEWLESHQDADIEDFK.A
	HsFLAG-ARP5_Ti_1	3.3458	0.1581	1655.36	1654.988	9557.4	1	1135.9	65.4	2	K.KKELEEIVQPIISK.L
	HsFlag-VPS71_Ti_1	4.3377	0.2314	1398.6	1398.64	5835.4	1	1174.4	81.8	10	K.ELEEIVQPIISK.L
	HsFLAG-ARP6_Ti_1	5.6138	0.5424	2176.25	2177.283	7709.6	1	1500	62.5	7	K.LYGSAGPPPTGEEDTAEKDEL.-
gi|34932414|r	21	225	44.80%	471	54232	8.9	non-POU domain containing, octamer-binding [Homo sapiens]				
*	HsFLAG-FLJ20729_	3.331	0.3673	1860.03	1861.12	3525.7	4	305.1	53.3	4	R.LFVGNLPPDITEEEMR.K
*	HsFLAG-FLJ20309_	3.2046	0.1522	903.04	901.053	6357.8	3	1107.4	92.9	2	K.AGEVFIHK.D
*	HsFLAG-p53-DNA-D	2.9549	0.0838	1143.55	1144.316	6995.6	3	924.2	72.2	1	K.AGEVFIHKDK.G
*	HsFlag-VPS71_Ti_1	3.6723	0.1269	1145.45	1144.316	7345.2	4	1068.2	77.8	2	K.AGEVFIHKDK.G
*	HsFLAG-p53-DNA-D	5.5402	0.449	1814.22	1814.15	6446.3	1	1722.6	76.7	10	R.TLAEIAKVELDNMPLR.G
*	HsFLAG-Lin9_Ti_20	2.9738	0.1979	1248.49	1249.378	5908.7	1	470.9	70	4	R.FACHSASLTVR.N
*	HsFLAG-TIP49b_Ti_	3.152	0.3121	1250.28	1249.378	6197	1	973.5	80	5	R.FACHSASLTVR.N
*	HsFLAG-Lin9_Ti_20	4.7699	0.4136	2669.74	2669.951	10218.3	1	2360.4	38.6	14	R.NLPQYVSNELLEEAFSVFGQVER.A
*	HsFLAG-p53-DNA-D	6.0426	0.4214	2670.13	2669.951	7234	1	1812.9	61.4	95	R.NLPQYVSNELLEEAFSVFGQVER.A
	HsFlag-VPS71_Ti_1	2.2093	0.2393	886.64	887.024	5875.5	7	596.8	78.6	3	R.AVVIVDDR.G
*	HsFlag-VPS71_Ti_1	3.3548	0.3784	1232.55	1232.425	6513.6	1	1416.1	81.8	15	K.GIVEFSGKPAAR.K
*	HsFlag-NUFIP_Ti_1	6.4244	0.4098	3638.51	3638.988	8018	1	1420.1	29.8	14	R.CSEGSFLLTTFPRPVTVEPMDQLDDEEGLPEK.L
	HsFlag-VPS71_Ti_1	4.3893	0.3752	1696.31	1696.874	3791.7	1	805.1	80.8	10	R.FAQPGSFEYEYAMR.W
*	HsFlag-VPS71_Ti_1	2.0073	0.2284	1180.57	1181.416	5319.3	2	367.3	62.5	1	R.HEHQVMLMR.Q
*	HsFLAG-p53-DNA-D	3.1488	0.2082	1181.62	1181.416	5071.6	1	944.1	93.8	2	R.HEHQVMLMR.Q
	HsFlag-VPS71_Ti_1	4.3042	0.3003	1541.67	1541.722	8958.4	1	1251.1	72.7	14	R.RMEELHNQEVQK.R
	HsFlag-VPS71_Ti_1	3.4632	0.2114	1384.7	1385.535	6737.3	1	1568	90	2	R.MEELHNQEVQK.R
*	HsFlag-VPS71_Ti_1	4.3414	0.4787	1539.72	1539.844	7170.3	1	1644.2	75	2	R.MGQMAMGGAMGINNR.G
*	HsFLAG-UTX1_Ti_2	5.3508	0.4734	2163.52	2164.444	6807.2	1	1681	64.3	13	R.FGQAATMEGIGAIGGTPPAFNR.A
*	HsFlag-DPCD_Ti_20	4.1429	0.1642	2163.71	2164.444	9300.8	1	1413.7	36.9	6	R.FGQAATMEGIGAIGGTPPAFNR.A
	HsFlag-VPS71_Ti_1	2.432	0.1594	1072.53	1073.194	3753.9	2	502.2	65	6	R.AAPGAEFAPNK.R
gi|4506005|re	13	117	44.60%	327	37187	6.2	protein phosphatase 1, catalytic subunit, beta isoform 1 [Homo sapiens]				
gi|46249376|r	13	117	44.60%	327	37187	6.2	protein phosphatase 1, catalytic subunit, beta isoform 1 [Homo sapiens]				
	HsFlag-NUFIP_Ti_1	5.6621	0.4071	2196.86	2197.623	6879.7	1	1530.1	63.9	15	K.SREIFLSQPILLELEAPLK.I
	HsFlag-NUFIP_Ti_1	5.5555	0.2355	2197.28	2197.623	5469.5	1	994	41.7	8	K.SREIFLSQPILLELEAPLK.I
	HsFLAG-UTX1_Ti_2	5.8482	0.3752	1954.5	1954.357	3528.8	1	1020.8	78.1	26	R.EIFLSQPILLELEAPLK.I
	HsFlag-NUFIP_Ti_2	3.445	0.3008	1660.61	1661.821	8029.2	2	924.8	65.4	1	K.ICGDIHGQYTDLLR.L
	HsFLAG-UTX1_Ti_2	3.968	0.4278	2582.94	2583.859	3345.1	1	403.7	47.6	4	R.LFEYGGFPPEANYLFLGDYVDR.G

	HsFLAG-UTX1_Ti_2	3.1849	0.2992	1553.73	1552.818	5504.8	1	712.9	70.8	6	K.QSLETICLLLAYK.I
	HsFLAG-p53-DNA-D	2.758	0.1574	1441.48	1440.728	4335.3	1	826.3	80	1	K.IKYPENFFLLR.G
	HsFLAG-UTX1_Ti_2	3.0584	0.3282	1199.35	1199.395	4678.9	1	820	93.8	2	K.YPENFFLLR.G
	HsFlag-NUFIP_Ti_1	5.4504	0.4606	2114.06	2115.32	6688.8	1	1505.3	70.6	19	K.TFTDCFNCLPIAAIVDEK.I
	HsFlag-NUFIP_Ti_1	5.5834	0.4263	2249.12	2249.479	7631.2	1	1500.9	61.1	13	K.IFCCHGGLSPDLQSMEQIR.R
	HsFlag-NUFIP_Ti_1	4.7195	0.3543	2249.42	2249.479	8083.2	1	1565.6	43.1	6	K.IFCCHGGLSPDLQSMEQIR.R
	HsFLAG-p53-DNA-D	4.5257	0.4111	1641.05	1640.792	7920.9	1	2058	80.8	15	R.AHQVVEDGYEFFAK.R
	HsFLAG-Lin9_Ti_20	2.5644	0.0837	1763.29	1762.966	9270.4	3	604.7	50	1	K.YQYGGLNSGRPVTPPR.T
gi|7706254|re	22	112	44.40%	529	59578	8.9	nucleolar protein NOP5/NOP58 [Homo sapiens]				
*	HsFLAG-TIP49a_Ti_	2.7325	0.1487	1245.46	1246.449	4877.4	1	558	66.7	2	K.KLQEVDSLWK.E
*	HsFLAG-TIP49a_Ti_	3.6085	0.2005	1246.86	1246.449	6973.5	1	1195.8	83.3	2	K.KLQEVDSLWK.E
*	HsFLAG-p53-DNA-D	5.6134	0.5378	1914.72	1915.168	7632.2	1	2560.3	79.4	26	K.FQDTAEALAAFTALMEGK.I
*	HsFLAG-TIP49a_Ti_	5.1869	0.3444	1915.16	1915.168	8296	1	1885.5	45.6	2	K.FQDTAEALAAFTALMEGK.I
*	HsFlag-NUFIP_Ti_2	2.9021	0.3307	1250.94	1251.382	5124.4	1	699.6	77.3	4	K.EAHEPLAVADAK.L
*	HsFLAG-TIP49a_Ti_	4.4195	0.4093	1883.72	1883.182	5495.4	1	939	66.7	9	K.LNLSCIHSPVVNELMR.G
*	HsFLAG-TIP49a_Ti_	3.5119	0.1412	1399.57	1399.605	5292.5	4	811.7	75	3	R.SQMDGLIPGVEPR.E
*	HsFLAG-TIP49a_Ti_	4.3009	0.4279	1647.4	1647.914	6190	1	1719.4	82.1	4	R.EMAAMCLGLAHSLSR.Y
*	HsFLAG-TIP49a_Ti_	5.9636	0.3005	1890.65	1890.199	6934.4	1	1702.2	71.9	6	K.VDTMIVQAISLLDDLDK.E
*	HsFLAG-TIP49a_Ti_	4.6796	0.2104	1891.68	1890.199	6805.8	1	1420.7	46.9	2	K.VDTMIVQAISLLDDLDK.E
*	HsFLAG-TIP49a_Ti_	4.0677	0.3645	1549.52	1549.728	8834.4	1	1239	72.7	1	R.EWYGWHFPELGK.I
*	HsFlag-DPCD_Ti_20	2.7029	0.1909	1584.55	1585.792	3008.2	1	473.9	65.4	1	K.LSELLPEEVEAEVK.A
*	HsFLAG-TIP49a_Ti_	3.2585	0.3	1962.45	1960.419	5313.7	1	414.7	44.4	4	R.MMAIAPNVTVMVGELVGAR.L
*	HsFLAG-TIP49a_Ti_	3.3791	0.3146	1320.59	1321.606	4991.6	1	893.8	75	5	R.LIAHAGSLLNLAK.H
*	HsFlag-NUFIP_Ti_11	4.107	0.3559	1321.72	1321.606	5778.4	1	1391.8	83.3	17	R.LIAHAGSLLNLAK.H
*	HsYL1_Ti_104.1462.	3.3755	0.2408	1324.63	1325.508	5337	1	844.1	66.7	6	K.HAASTVQILGAEK.A
*	HsYL1_Ti_104.1463.	3.9694	0.3704	1326.53	1325.508	4703	1	1237.1	83.3	4	K.HAASTVQILGAEK.A
*	HsFLAG-ARP6_Ti_1	4.0626	0.3809	1734.48	1734.993	7148.7	1	1709.8	73.3	4	K.YGLIYHASLVGQTSPK.H
*	HsFLAG-TIP49a_Ti_	4.9649	0.3941	1837.47	1835.896	10126.8	1	2200.9	71.9	3	R.YDAFGEDSSSAMGVENR.A
*	HsSrcap_Ti_201.074	3.0709	0.3164	1630.61	1629.684	6877.7	1	703.2	57.1	1	K.TYDPSGDSTLPTCSK.K
*	HsFLAG-TIP49b_Ti_	4.2822	0.3499	1860.08	1861.059	6773.3	1	822.8	60.7	2	K.RKIEQVDKEDEITEK.K
*	HsFLAG-TIP49a_Ti_	4.5291	0.3377	1704.33	1704.872	8463	1	1903.2	76.9	4	R.KIEQVDKEDEITEK.K
gi|17921989|r	21	460	44.40%	448	49924	5.1	tubulin, alpha 1 [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.8546	0.3066	2415.78	2416.655	9887	1	636.1	42.5	25	R.QLFHPEQLITGKEDAANNYAR.G
	HsSrcap_Ti_204.213	5.0964	0.4219	2416.38	2416.655	6002.3	1	934.1	37.5	18	R.QLFHPEQLITGKEDAANNYAR.G
	HsScrap_Ti_106.239	2.55	0.1652	1877.45	1876.082	6295.5	1	349.4	53.6	1	R.RNLDIERPTYTNLNR.L
	HsFlag-ZnF-HIT2_Ti_	2.9442	0.2517	1719.52	1719.895	6354.4	3	522.7	57.7	12	R.NLDIERPTYTNLNR.L
	HsFLAG-ARP6_Ti_1	5.0973	0.4595	1487.62	1488.768	7314.4	1	1783.7	80.8	94	R.LISQIVSSITASLR.F
	HsFLAG-Lin9_Ti_20	3.9906	0.2202	1487.96	1488.768	5903.2	1	1035.4	48.1	1	R.LISQIVSSITASLR.F
	HsFLAG-ARP6_Ti_1	5.8116	0.4265	2410.46	2410.689	5990.7	1	1327.4	60	74	R.FDGALNVDLTEFQTNLVPYPR.I
	HsYL1_Ti_106.2380.	4.538	0.4145	1756.22	1758.07	4074.6	1	799.2	70	54	R.IHFPLATYAPVISAEK.A
	HsFLAG-ARP6_Ti_1	5.1723	0.3713	2751.88	2752.037	6388.1	1	727.7	32.6	7	K.AYHEQLSVAEITNACFEPANQMVK.C
	HsYL1_Ti_103.2152.	5.4112	0.353	2751.97	2752.037	8492.5	1	1660.1	52.2	3	K.AYHEQLSVAEITNACFEPANQMVK.C
	HsFLAG-ARP6_Ti_1	3.1777	0.2663	1250.3	1250.43	4496.7	1	907.7	93.8	7	K.YMACCLLYR.G

*	HsSrcap_Ti_202.005	2.4492	0.2131	985.54	986.156	7210.4	1	734.7	72.2	2	K.DVNAAIAAIK.T
	HsSrcap_Ti_205.275	4.3851	0.1572	1742.07	1741.953	8212.2	1	1660.4	51.9	6	K.RSIQFVDWCPTGFK.V
	HsFLAG-ARP6_Ti_1	4.7996	0.4001	1743.87	1741.953	5585.1	1	1005.5	73.1	32	K.RSIQFVDWCPTGFK.V
	HsFLAG-TCF3_Ti_1	3.0532	0.402	1584.47	1585.766	5401	1	539.5	58.3	17	R.SIQFVDWCPTGFK.V
	HsSrcap_Ti_202.297	4.5222	0.2867	1585.72	1585.766	5721.7	1	1065.6	75	43	R.SIQFVDWCPTGFK.V
	HsFLAG-ARP6_Ti_2	4.0719	0.4153	1825.6	1826.103	3498.4	1	615.9	58.8	34	K.VGINYQPPTVVPGGDLAK.V
	HsFLAG-ARP6_Ti_1	6.0682	0.4321	1865.52	1866.108	10861.7	1	2782.2	75	18	R.AVCMLSNTTAIAEAWAR.L
	HsFLAG-ARP6_Ti_1	4.4765	0.3204	1867.57	1866.108	8904.4	1	1596.3	45.3	7	R.AVCMLSNTTAIAEAWAR.L
	HsFLAG-ARP6_Ti_1	3.7547	0.214	2330.07	2331.521	8623.8	3	888.4	34.2	2	R.AFVHWYVGEGMEEGEFSEAR.E
	HsFLAG-ARP6_Ti_1	4.334	0.4395	2330.87	2331.521	6787.1	1	1352.6	57.9	3	R.AFVHWYVGEGMEEGEFSEAR.E
gi|21626466|r	41	432	44.30%	847	94623	6.3	matrin 3 [Homo sapiens]				
gi|62750354|r	41	432	44.30%	847	94623	6.3	matrin 3 [Homo sapiens]				
	HsFLAG-ARP6_Ti_2	3.2763	0.2749	1040.13	1040.121	5942.3	1	1129.5	87.5	7	K.SFQQSSLSR.D
	HsFLAG-UTX1_Ti_2	5.4884	0.3927	2371.44	2372.742	7455.8	1	917.2	45.8	15	R.DLSAAGIGLLAAATQSLSMPASLGR.M
	HsFlag-VPS71_Ti_1	6.1332	0.4876	2371.97	2372.742	6044.1	1	880.6	34.4	17	R.DLSAAGIGLLAAATQSLSMPASLGR.M
	HsFLAG-Lin9_Ti_20	3.1088	0.2671	1092.3	1092.243	3961.5	1	616.6	83.3	7	R.GPLPLSSQHR.G
	HsFLAG-TIP49b_Ti_	3.2761	0.2068	2866.61	2867.151	6354.2	2	327.9	33.3	1	R.GPLPLSSQHRGDADQASNILASFGLSAR.D
	HsFLAG-TIP49b_Ti_	5.884	0.3666	2867.45	2867.151	9832.9	1	1931.8	34.3	6	R.GPLPLSSQHRGDADQASNILASFGLSAR.D
	HsFlag-VPS71_Ti_1	5.8029	0.4744	1794.88	1793.931	8546.6	1	1770	67.6	26	R.GDADQASNILASFGLSAR.D
	HsFLAG-Lin9_Ti_20	4.0939	0.2691	1480.21	1480.571	7272.1	4	1124	77.3	5	R.DLDELSRYPEDK.I
	HsFLAG-p53-DNA-D	5.0834	0.298	3081.86	3082.521	7141	1	1068.2	33	10	R.DLDELSRYPEDKITPENLPQILLQLK.R
	HsFLAG-Lin9_Ti_20	4.3798	0.2484	1620.25	1620.973	5362.9	1	1071.1	50	2	K.ITPENLPQILLQLK.R
	HsFLAG-Lin9_Ti_20	3.2105	0.304	1621.05	1620.973	3772.8	1	450.9	69.2	22	K.ITPENLPQILLQLK.R
	HsFLAG-TIP49b_Ti_	4.0842	0.3478	1366.48	1366.473	8718.8	1	1304.6	77.3	14	R.RTEEGPTLSYGR.D
	HsH2AZ-FLAG_293_	3.543	0.3765	1210.3	1210.286	5880.9	1	1457.3	85	1	R.TEEGPTLSYGR.D
	HsFLAG-p53-DNA-D	2.5418	0.0879	2362.15	2363.462	9704.4	2	466.8	35	1	R.DSFDDRGPSLNPVLDYDHGSR.S
	HsFlag-NUFIP_Ti_2	4.3879	0.2831	2362.76	2363.462	7326.1	1	1381.2	41.2	5	R.DSFDDRGPSLNPVLDYDHGSR.S
	HsFlag-DPCD_Ti_20	3.8934	0.4056	1627.3	1627.754	5356.6	1	851	67.9	13	R.GPSLNPVLDYDHGSR.S
	HsFLAG-TIP49b_Ti_	4.3679	0.3877	2000.14	2001.045	7192.6	1	1335.4	70	8	R.CRDDSFFGETSHNYHK.F
	HsFlag-NUFIP_Ti_2	4.3759	0.328	2000.27	2001.045	8340.8	1	1342	45	7	R.CRDDSFFGETSHNYHK.F
	HsFlag-NUFIP_Ti_2	6.3025	0.3513	1935.67	1936.178	7196.6	2	1645.5	47.1	9	K.RGAPPSSNIEDFHGLLPK.G
	HsFLAG-ARP6_Ti_1	3.245	0.3324	1936.73	1936.178	5925.7	2	406.2	50	5	K.RGAPPSSNIEDFHGLLPK.G
	HsFlag-NUFIP_Ti_2	4.0409	0.3762	1779.26	1779.99	2870	1	395.2	65.6	6	R.GAPPSSNIEDFHGLLPK.G
	HsFlag-NUFIP_Ti_2	5.5063	0.4171	1997.57	1998.178	8835	1	2428.9	75	10	K.GYPHLCSICDLPVHSNK.E
	HsFlag-NUFIP_Ti_2	3.5669	0.2015	1997.84	1998.178	7111.7	1	1125.2	43.8	1	K.GYPHLCSICDLPVHSNK.E
	HsFLAG-TIP49b_Ti_	3.9952	0.3528	1508.84	1509.581	6722.2	1	970	75	17	K.EWSQHINGASHSR.R
	HsYL1_Ti_103.1307.	2.2413	0.1634	1324.57	1325.427	2820.7	1	195	61.5	1	R.GNLGAGNGNLQGPR.H
	HsFlag-VPS71_Ti_1	3.2189	0.2788	1325.58	1325.427	8982.7	1	1199.4	69.2	4	R.GNLGAGNGNLQGPR.H
	HsFLAG-TIP49b_Ti_	2.9129	0.2528	1144.46	1145.365	6089.4	1	677.2	68.8	12	R.VVHIMDFQR.G
	HsFLAG-FLJ20729_	3.0313	0.3788	1145.36	1145.365	4796.6	1	1161.7	93.8	14	R.VVHIMDFQR.G
	HsFlag-NUFIP_Ti_11	6.1565	0.4426	2439.7	2439.903	4931.1	1	851	60	25	R.YQLLQLVEPFGVISNHLILNK.I
	HsFlag-NUFIP_Ti_11	4.7563	0.3991	2440	2439.903	6300.7	1	900.3	36.2	38	R.YQLLQLVEPFGVISNHLILNK.I
	HsYL1_Ti_105.3602.	3.5809	0.2044	3733.05	3735.2	8015.7	3	406.1	18.9	2	K.INEAFIEMATTEDAQAAVDYYTTTPALVFGKPVR.V

	HsFLAG-TIP49b_Ti_	2.5212	0.167	1026.4	1027.166	5332.8	8	562.4	68.8	2	K.KPEGKPDQK.F
	HsFLAG-ARP6_Ti_1	4.806	0.4114	2037.75	2038.311	6562.6	1	1524.9	47.2	6	R.VIHLSNLPHSGYSDSAVLK.L
	HsFLAG-TIP49b_Ti_	5.6359	0.3425	2039.72	2038.311	5332	1	1055.3	66.7	35	R.VIHLSNLPHSGYSDSAVLK.L
	HsFlag-DPCD_Ti_20	4.4425	0.4401	1915.24	1916.049	9223.9	1	2300.7	75	4	K.IEELDQENEAALENGIK.N
	HsMRGBP-FLAG_Ti	4.824	0.4774	2778.97	2778.727	7619.7	1	1481.6	54.3	4	K.DTSENADGQSDENKDDYTIPDEYR.I
	HsFLAG-Lin9_Ti_20	4.2844	0.3729	1970.25	1970.319	6024.8	1	1334.6	45.6	2	R.IGPYQPNVPVGIDYVIPK.T
	HsMRGBP-FLAG_Ti	3.9507	0.3183	1971.58	1970.319	4552.3	1	692.8	58.8	31	R.IGPYQPNVPVGIDYVIPK.T
	HsFLAG-Lin9_Ti_20	3.6723	0.25	1572.12	1574.737	6568.8	1	921.8	70.8	11	K.LCSLFYTNEEVAK.N
	HsFLAG-Lin9_Ti_20	3.6441	0.2961	1472.36	1472.566	6016.2	1	611.1	68.2	6	K.NTHCSSLPHYQK.L
	HsFLAG-TIP49b_Ti_	3.7711	0.3885	1472.42	1472.566	7370.8	1	1223.1	77.3	20	K.NTHCSSLPHYQK.L
gi|14211843|r	5	16	44.30%	122	13895	4.8	short coiled-coil protein [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	5.7242	0.3985	2092.56	2093.388	10112.9	1	2328	67.6	5	R.LINQVLELQHTLEDLSAR.V
*	HsFLAG-TCF3_Ti_1	5.0454	0.3084	2093.68	2093.388	6271.7	1	1658.6	50	4	R.LINQVLELQHTLEDLSAR.V
*	HsFLAG-TCF3_Ti_1	2.6956	0.0978	1146.36	1145.298	5938.2	2	915	83.3	1	R.VDAVKEENLK.L
*	HsFLAG-TCF3_Ti_1	4.677	0.4327	2890.97	2892.164	8820.8	1	1399.4	46	4	K.SENQVLGQYIENLMSASSVFQTTDTK.S
*	HsFLAG-TCF3_Ti_1	6.161	0.4097	2891.59	2892.164	12589.9	1	1585.5	32	2	K.SENQVLGQYIENLMSASSVFQTTDTK.S
gi|14141166|r	10	45	44.20%	362	38222	6.8	poly(rC)-binding protein 2 isoform b [Homo sapiens]				
gi|14141168|r	10	45	43.70%	366	38651	6.8	poly(rC)-binding protein 2 isoform a [Homo sapiens]				
	HsARP6-FLAG_Ti_1	3.1504	0.1495	1290.13	1289.354	6671.6	3	866.9	70	1	R.INISEGNCPER.I
	HsFLAG-Lin9_Ti_20	3.8142	0.3117	1358.8	1359.652	6178	1	712.3	66.7	3	R.IITLAGPTNAIFK.A
	HsFLAG-p53-DNA-D	3.7563	0.2841	1359.12	1359.652	4604	1	1031.7	83.3	15	R.IITLAGPTNAIFK.A
	HsFLAG-ARP6_Ti_1	4.229	0.2884	3353.91	3353.831	7765.5	1	776.9	25	4	K.AFAMIIDKLEEDISSSMTNSTAASRPPVTLR.L
	HsFLAG-Lin9_Ti_20	3.4935	0.3709	1429.07	1429.666	3637.5	3	395.4	65.4	1	R.LVVPASQCGSLIGK.G
	HsFLAG-Lin9_Ti_20	4.6761	0.4043	2089.82	2091.257	7514.3	1	1044	52.6	7	R.ESTGAQVQVAGDMLPNSTER.A
	HsFLAG-Lin9_Ti_20	4.065	0.421	1715.07	1714.022	3460.1	1	517.1	63.3	10	R.AITIAGIPQSIIECVK.Q
	HsFLAG-FLJ20729_	4.3205	0.4615	2430.73	2430.769	4966.5	1	632.9	34.1	2	K.GVTIPYRPKPSSSPVIFAGGQDR.Y
	HsFLAG-ARP6_Ti_1	3.9872	0.4442	2205.8	2206.547	9661.6	1	709.1	42.5	1	R.QVTITGSAASISLAQYLINVR.L
	HsFLAG-p53-DNA-D	2.0012	0.2148	1012.45	1013.064	6156.7	2	416.5	60	1	R.LSSETGGMGSS.-
gi|5902076|re	13	76	44.00%	248	27745	10.4	splicing factor, arginine/serine-rich 1 (splicing factor 2, alternate splicing factor) [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	3.5644	0.3301	1258.46	1257.475	4329.5	1	750.7	80	9	R.IYVGNLPPDIR.T
*	HsH2AZ-FLAG_293_	2.6651	0.137	1028.25	1029.134	6056.2	8	612.3	78.6	2	K.DIEDVFYK.Y
*	HsFlag-NUFIP_Ti_1	4.4245	0.298	1722.02	1721.913	6524.5	1	1811.8	51.8	4	R.RGGPPFAFVEFEDPR.D
*	HsFlag-NUFIP_Ti_1	4.5453	0.4353	1565.47	1565.725	4993.7	1	1110.4	73.1	25	R.GGPPFAFVEFEDPR.D
*	HsFlag-NUFIP_Ti_1	4.0372	0.2715	2541.67	2542.723	4586.7	2	346.5	38.6	11	R.GGPPFAFVEFEDPRDAEDAVYGR.D
*	HsFlag-NUFIP_Ti_1	2.0609	0.1989	995.48	996.021	3620.8	1	510.9	75	1	R.DAEDAVYGR.D
*	HsFLAG-ARP6_Ti_1	2.1911	0.3042	1123.38	1124.108	2694.8	5	309.1	68.8	2	R.DGYDYDGYR.L
*	HsFLAG-ARP6_Ti_1	3.0876	0.3576	1124.2	1124.108	4127.7	1	1013.3	87.5	2	R.DGYDYDGYR.L
*	HsFlag-NUFIP_Ti_1	3.3671	0.3036	1669.61	1669.918	2975.1	7	275.4	53.3	2	R.VVVSGLPPSGSWQDLK.D
*	HsFLAG-ARP6_Ti_1	3.792	0.4251	1418.27	1418.469	5696.7	1	833.2	72.7	4	R.EAGDVCYADVYR.D
*	HsARP6-FLAG_Ti_1	3.0675	0.1031	1079.15	1079.198	5323.3	1	1006.8	83.3	4	R.DGTGVVEFVR.K
*	HsFLAG-p53-DNA-D	1.81	0.1737	1112.33	1113.274	4728.6	4	320.5	62.5	1	R.KEDMTYAVR.K
*	HsFLAG-ARP6_Ti_1	3.5358	0.2676	1165.98	1163.232	5070.7	1	1133.6	94.4	9	R.SHEGETAYIR.V
gi|25453472|r	10	38	43.80%	281	31122	5	eukaryotic translation elongation factor 1 delta isoform 2 [Homo sapiens]				

gi|25453474|r	10	38	19.00%	647	71408	6.4	eukaryotic translation elongation factor 1 delta isoform 1 [Homo sapiens]				
	HsFlag-VPS71_Ti_1	4.4888	0.4058	1529.32	1527.695	7655.2	1	1537.7	76.9	1	R.FYEQMNGPVAGASR.Q
	HsFLAG-ARP6_Ti_1	5.1818	0.4938	2185.99	2186.3	7722.2	1	987.9	47.8	7	K.SLAGSSGPGASSGTSGDHGELVVR.I
	HsFLAG-TCF3_Ti_1	4.1002	0.1851	1300.45	1300.498	6408.6	1	1425.9	81.8	6	R.GVVQELQQAISK.L
	HsFlag-VPS71_Ti_1	2.8505	0.1426	1423.58	1424.618	4652	7	222.1	50	1	R.ATAPQTQHVSPMR.Q
	HsFLAG-ARP6_Ti_1	3.3714	0.2141	1423.79	1424.618	5879.6	1	832.5	66.7	7	R.ATAPQTQHVSPMR.Q
	HsFLAG-FLJ20309_	2.2092	0.0972	726.49	726.938	3544.8	2	369.7	75	6	K.KPALVAK.S
	HsFlag-VPS71_Ti_1	4.3908	0.2963	1375.45	1374.58	8237.1	1	2270	87.5	2	R.SIQLDGLVWGASK.L
	HsARP6-FLAG_Ti_1	3.1041	0.1913	1475.33	1475.648	7720.8	1	1139.3	77.3	1	R.KLQIQCVVEDDK.V
	HsFlag-VPS71_Ti_1	3.6688	0.1914	1348.34	1347.474	4763.4	1	872.7	80	2	K.LQIQCVVEDDK.V
	HsFlag-VPS71_Ti_1	6.2851	0.4534	3176.18	3176.547	8861	1	2146.7	34.3	5	K.VGTDLLEEEITKFEEHVQSVDIAAFNKI.-
gi|14043070|r	20	160	43.50%	372	38747	9.1	heterogeneous nuclear ribonucleoprotein A1 isoform b [Homo sapiens]				
gi|4504445|re	20	160	50.60%	320	34196	9.2	heterogeneous nuclear ribonucleoprotein A1 isoform a [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.0406	0.1578	1300.51	1300.411	5352.9	1	844.5	80	5	K.SESPKEPEQLR.K
	HsFLAG-p53-DNA-D	3.2219	0.1513	1428.09	1428.585	5677.4	2	801.4	77.3	2	K.SESPKEPEQLRK.L
	HsFLAG-p53-DNA-D	3.8687	0.1704	1913.4	1914.166	7228.4	8	888.5	39.1	1	R.KLFIGGLSFETTDESLR.S
	HsFlag-VPS71_Ti_1	5.1633	0.3583	1786.14	1785.992	6484.5	1	1954.1	83.3	48	K.LFIGGLSFETTDESLR.S
	HsFlag-VPS71_Ti_1	5.0503	0.4516	2521.98	2522.761	7244.9	1	1189.9	55	2	R.SHFEQWGTLTDCVVMRDPNTK.R
	HsFLAG-p53-DNA-D	4.0844	0.1983	2522.3	2522.761	6421.6	1	686	33.8	2	R.SHFEQWGTLTDCVVMRDPNTK.R
	HsFLAG-p53-DNA-D	5.3975	0.5236	2148.33	2149.383	10346	1	1878.8	60.5	7	R.GFGFVTYATVEEVDAAMNAR.P
	HsFlag-VPS71_Ti_1	4.819	0.4507	2511.61	2511.814	7887.6	1	891.3	45.5	4	R.GFGFVTYATVEEVDAAMNARPHK.V
	HsFLAG-p53-DNA-D	3.6762	0.3178	2939.29	2939.275	6079.2	1	609.8	27.9	1	R.GFGFVTYATVEEVDAAMNARPHKVDGR.V
	HsFLAG-ARP5_Ti_1	3.2256	0.1205	1437.74	1438.583	5828.9	1	515.7	62.5	2	R.EDSQRPGAHLTVK.K
	HsFLAG-p53-DNA-D	3.6907	0.1927	1220.14	1219.439	7676.3	1	1667.5	88.9	3	K.IEVIEIMTDR.G
	HsFLAG-Lin9_Ti_20	5.2831	0.3359	1856.33	1856.989	7657.7	1	1774.9	50	1	K.RGFAFVTFDDHDSVDK.I
	HsFLAG-Lin9_Ti_20	4.3543	0.3782	1858.18	1856.989	9098.4	1	913.1	60	12	K.RGFAFVTFDDHDSVDK.I
	HsFLAG-p53-DNA-D	4.428	0.2888	1700.46	1700.802	5988	1	1476.1	78.6	18	R.GFAFVTFDDHDSVDK.I
	HsFlag-VPS71_Ti_1	3.9174	0.2864	1486.86	1486.553	7688.4	1	1598.8	81.8	14	K.YHTVNGHNCEVR.K
	HsFLAG-Lin9_Ti_20	2.9389	0.1647	1613.63	1614.727	7325.1	1	1020.3	70.8	1	K.YHTVNGHNCEVRK.A
	HsFlag-VPS71_Ti_1	2.7146	0.3137	1375.54	1376.468	7140	1	628.8	57.7	5	R.SSGPYGGGGQYFAK.P
	HsFlag-VPS71_Ti_1	3.9291	0.3126	1377.7	1376.468	4784.6	1	826	73.1	2	R.SSGPYGGGGQYFAK.P
	HsFLAG-ARP6_Ti_1	4.2724	0.4124	1629.4	1629.772	7173.5	1	1307.5	66.7	23	R.SSGPYGGGGQYFAKPR.N
	HsFLAG-p53-DNA-D	4.7302	0.4736	1695.6	1695.656	7009.5	1	873.8	55.9	7	R.NQGGYGGSSSSSSYGSGR.R
gi|22202633|r	6	20	43.50%	154	17328	6.3	prefoldin 5 isoform alpha [Homo sapiens]				
	HsFLAG-p53-DNA-D	6.0367	0.4147	2064.65	2064.3	8124.5	1	2348.4	76.5	7	K.NQLDQEVEFLSTSIAQLK.V
	HsFLAG-p53-DNA-D	5.5785	0.297	2065.17	2064.3	7744.6	1	2256	51.5	3	K.NQLDQEVEFLSTSIAQLK.V
*	HsFLAG-p53-DNA-D	4.3908	0.4341	1634.68	1634.971	3193.8	1	623.9	71.4	2	K.ELLVPLTSSMYVPGK.L
*	HsFLAG-p53-DNA-D	4.2011	0.3709	3802.25	3803.405	5271.7	1	314.8	20.5	1	K.ELLVPLTSSMYVPGKLHDVEHVLIDVGTGYYVEK.T
	HsFLAG-p53-DNA-D	5.9323	0.378	2186.47	2187.457	9500.7	1	2025	61.1	5	K.LHDVEHVLIDVGTGYYVEK.T
	HsFLAG-p53-DNA-D	5.3571	0.3776	1485.5	1485.724	6429.3	1	1674.4	78.6	2	K.IQQLTALGAAQATAK.A
gi|11968182|r	10	20	43.40%	152	17719	11	ribosomal protein S18 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.1027	0.1301	948.22	948.194	2976.8	1	824.8	93.8	1	K.IAFAITAIK.G
	HsFlag-NUFIP_Ti_11	3.0149	0.1657	1014.24	1014.219	7361.6	1	973.6	92.9	2	R.RYAHVVLR.K

	HsFlag-NUFIP_Ti_10	2.6196	0.2233	858.99	858.031	4609.3	1	712.6	91.7	1	R.YAHVVLR.K
	HsFlag-NUFIP_Ti_10	2.0378	0.1339	903.57	904.051	4335.5	2	431.4	71.4	1	R.KADIDLTK.R
*	HsFLAG-ARP6_Ti_1	4.1065	0.3422	1404.29	1404.476	6003.1	1	1533.6	86.4	4	K.RAGELTEDEVER.V
*	HsFlag-NUFIP_Ti_10	3.5203	0.2353	1247.59	1248.289	6146.9	1	905.9	75	2	R.AGELTEDEVER.V
*	HsFlag-NUFIP_Ti_10	3.4238	0.2061	1072.43	1072.311	6258.1	3	1063.1	87.5	1	R.VITIMQNPR.Q
	HsFlag-NUFIP_Ti_10	1.9671	0.1171	1060.66	1061.228	3291.3	7	238.1	64.3	1	K.IPDWFLNR.Q
	HsFLAG-ARP6_Ti_1	2.9088	0.1132	1061.31	1061.228	4158.4	2	657.6	92.9	6	K.IPDWFLNR.Q
	HsFLAG-TCF3_Ti_10	3.3146	0.3239	1321.52	1322.461	5926.2	1	566.8	63.6	1	K.YSQVLANGLDNK.L
gi|4506695|re	8	36	43.40%	145	16060	10.3	ribosomal protein S19 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_10	3.3123	0.1893	1135.34	1135.222	7084.5	1	1096.1	87.5	2	K.DVNQQEFVR.A
*	HsFlag-NUFIP_Ti_10	2.1942	0.1127	1072.67	1073.234	8746.1	1	863.7	75	1	K.VPEWVDTVK.L
*	HsFLAG-p53-DNA-D	3.46	0.3757	1970.75	1970.151	4466.2	1	501.5	53.6	2	K.HKELAPYDENWFYTR.A
*	HsFlag-NUFIP_Ti_10	4.0246	0.3891	1704.47	1704.836	4913.9	1	732.6	75	9	K.ELAPYDENWFYTR.A
*	HsFlag-NUFIP_Ti_10	2.7035	0.3098	1133.46	1132.282	4767.1	1	728.5	77.8	1	R.NGVMPSHFSR.G
*	HsFlag-NUFIP_Ti_10	3.2476	0.0982	1127.64	1127.373	6510.3	1	1385.1	88.9	14	R.RVLQALEGLK.M
*	HsFLAG-p53-DNA-D	2.189	0.1351	942.52	943.091	9789.8	1	670.3	61.1	2	R.IAGQVAAANK.K
*	HsFLAG-p53-DNA-D	3.2545	0.2951	944.05	943.091	5562.2	1	878.2	83.3	5	R.IAGQVAAANK.K
gi|74136883|r	35	153	43.00%	825	90585	6	heterogeneous nuclear ribonucleoprotein U isoform a [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.6714	0.1313	1203.28	1203.422	8106.9	6	1133.8	77.8	4	K.VSELKEELKK.R
	HsFLAG-FLJ20729_	4.8069	0.3769	3128.35	3128.311	8146.3	1	1040.6	27.4	5	R.LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGR.S
	HsFLAG-p53-DNA-D	3.5121	0.318	1716.12	1715.947	5790	1	646.8	50	9	K.SSGPTSLFAVTVAPPGAR.Q
*	HsFLAG-p53-DNA-D	3.7853	0.407	2154.43	2154.304	5923.6	2	372.5	41.3	2	K.KAEGGGGGGRPGAPAAGDGKTEQK.G
	HsFLAG-p53-DNA-D	3.5659	0.2137	2546.51	2546.718	6853.7	1	699.2	32.9	1	R.PREDHGRGYFEYIEENKYSR.A
	HsSrcap_Ti_202.223	2.6717	0.2987	1291.34	1292.387	8590.8	1	654.3	66.7	2	R.GYFEYIEENK.Y
	HsFLAG-Lin9_Ti_20	4.3457	0.3532	1293.29	1292.387	8915.7	1	1333.9	77.8	11	R.GYFEYIEENK.Y
	HsFLAG-p53-DNA-D	4.1626	0.4118	1697.87	1698.829	6853.7	1	1087.5	75	8	R.GYFEYIEENKYSR.A
	HsFlag-VPS71_Ti_10	2.5369	0.2163	2032.15	2032.321	9376.8	1	682.5	44.4	1	R.LSASSLTMESFAFLWAGGR.A
	HsFLAG-Lin9_Ti_20	2.9738	0.1931	996.27	997.096	7751.1	4	1087	85.7	1	K.DIDIHEVR.I
	HsFLAG-Lin9_Ti_20	3.4817	0.4053	2843.24	2843.98	9965	1	600.7	34.8	3	K.FDENDVITCFANFESDEVELSYAK.N
	HsFLAG-Lin9_Ti_20	2.4706	0.2981	1048.39	1049.172	4533.7	8	233.8	61.1	1	K.NGQDLGVAFK.I
	HsFLAG-Lin9_Ti_20	3.2219	0.1975	1049.33	1049.172	8492.1	1	1133.2	83.3	2	K.NGQDLGVAFK.I
	HsFLAG-Lin9_Ti_20	6.1426	0.3588	3040.84	3041.414	10440.7	1	2201	37	2	K.EVLAGRPLFPHVLCHNCAVEFNFGQK.E
	HsFLAG-Lin9_Ti_20	4.2536	0.3608	2415.48	2415.689	5433.7	1	1093.5	40.8	2	R.PLFPHVLCHNCAVEFNFGQK.E
	HsFLAG-Lin9_Ti_20	3.9027	0.3138	2416.29	2415.689	11331.9	1	1475.2	52.6	2	R.PLFPHVLCHNCAVEFNFGQK.E
	HsFLAG-p53-DNA-D	5.2469	0.3326	2726.06	2726.058	7238.1	2	602.9	29.8	16	K.EKPYFPIPEEYTFIQNVPLEDR.V
	HsFLAG-Lin9_Ti_20	3.6017	0.1424	2727.06	2726.058	5694.6	1	874	52.4	4	K.EKPYFPIPEEYTFIQNVPLEDR.V
	HsFlag-VPS71_Ti_10	4.6269	0.3975	2467.91	2468.768	4834.9	1	657.4	52.6	7	K.PYFPIPEEYTFIQNVPLEDR.V
	HsFLAG-FLJ20729_	4.1581	0.3646	1706.28	1706.035	8412.2	1	1159.5	60	2	K.KDCEVVMMIGLPGAGK.T
	HsFLAG-FLJ20729_	3.814	0.299	1577.48	1577.861	8355.6	1	1531.8	67.9	2	K.DCEVVMMIGLPGAGK.T
	HsFLAG-p53-DNA-D	4.1722	0.2862	2188.64	2188.463	8734.8	1	847.5	47.4	1	K.HAAENPGKYNILGTNTIMDK.M
	HsFLAG-FLJ20729_	3.6121	0.2541	1383.36	1383.603	5657.8	1	1646.8	86.4	5	K.YNILGTNTIMDK.M
	HsFLAG-p53-DNA-D	2.0216	0.1131	783.52	784.022	7544.4	1	737.8	83.3	1	K.MMVAGFK.K
	HsSrcap_Ti_204.194	4.9388	0.3509	1804.81	1805.004	4556.2	1	779	66.7	13	K.RNFILDQTNVSAAAQR.R

	HsFLAG-p53-DNA-D	5.3142	0.3075	1649.64	1648.816	7998.9	1	3267.4	89.3	12	R.NFILDQTNVSAAAQR.R
	HsFLAG-p53-DNA-D	3.3018	0.2814	1130.3	1130.316	5406	1	1295.7	93.8	2	K.MCLFAGFQR.K
	HsFlag-VPS71_Ti_1(	3.0535	0.3036	1423.58	1423.572	4959.1	1	816.9	72.7	5	K.AVVVCPKDEDYK.Q
	HsFLAG-Lin9_Ti_20	3.5467	0.4232	2605.69	2603.851	6912.2	1	513.9	40.5	4	K.GNFTLPEVAECFDEITYVELQK.E
	HsFLAG-p53-DNA-D	2.8634	0.106	1266.63	1267.422	7387.8	5	662.3	66.7	1	K.LLEQYKEESK.K
	HsFLAG-p53-DNA-D	3.6232	0.1822	1267.47	1267.422	7839.9	3	1240.5	83.3	4	K.LLEQYKEESK.K
	HsFLAG-p53-DNA-D	3.9145	0.2282	1394.96	1395.596	9660.9	1	1504.5	80	3	K.LLEQYKEESKK.A
	HsFLAG-Lin9_Ti_20	5.2866	0.4897	2212.15	2213.333	9677.9	1	1617.1	61.8	10	K.NQSQGYNQWQQGQFWGQK.P
	HsFLAG-p53-DNA-D	4.0413	0.3322	3659.67	3660.864	9522.7	1	670.3	24.1	3	K.NQSQGYNQWQQGQFWGQKPWSQHYHQGYY.-
	HsFLAG-Lin9_Ti_20	3.2864	0.3231	1466.39	1466.555	9169.6	1	1221.7	75	2	K.PWSQHYHQGYY.-
gi|33286418|r	16	46	42.90%	531	57937	7.8	pyruvate kinase 3 isoform 1 [Homo sapiens]				
	HsFlag-VPS71_Ti_1(	4.4192	0.3855	1360.9	1360.519	7391.4	2	1262.3	75	3	R.NTGIICTIGPASR.S
	HsFlag-VPS71_Ti_1(	4.227	0.4227	1884.61	1885.046	7849.9	1	1023.8	60	2	R.LNFSHGTHEYHAETIK.N
	HsFlag-VPS71_Ti_1(	4.3665	0.3714	2465.98	2466.794	4031.4	1	332.6	40.9	6	R.TATESFASDPILYRPVAVALDTK.G
	HsFlag-VPS71_Ti_1(	2.752	0.3092	1119.93	1119.26	7890	5	728.8	65	2	K.GSGTAEVELKK.G
	HsFlag-VPS71_Ti_1(	4.6883	0.3172	1470.61	1469.6	6337.6	1	1489.6	90	2	K.CDENILWLDYK.N
	HsH2AZ-FLAG_293_	4.2933	0.3682	1780.32	1780.929	7349.3	1	1936.2	70.6	3	K.GADFLVTEVENGGSLGSK.K
	HsFLAG-ARP6_Ti_1	5.5277	0.4773	1765.11	1766.048	4590.9	1	1037.8	67.6	9	K.KGVNLPGAAVDLPAVSEK.D
	HsFLAG-p53-DNA-D	4.7037	0.3492	2477.47	2478.849	10005.2	1	1540.2	34.8	1	K.KGVNLPGAAVDLPAVSEKDIQDLK.F
	HsFlag-FLJ90652_2	3.3152	0.4024	1637.32	1637.874	5731.6	1	869.7	62.5	1	K.GVNLPGAAVDLPAVSEK.D
	HsFlag-VPS71_Ti_1(	3.8713	0.4065	1878.13	1878.262	6515.9	1	1206.9	65.6	1	R.AGKPVICATQMLESMIK.K
	HsFlag-VPS71_Ti_1(	4.3743	0.1831	3496.91	3496.791	6176.7	1	661.3	24.2	2	R.AEGSDVANAVLDGADCIMLSGETAKGDYPLEAVR.M
*	HsH2AZ-FLAG_293_	3.2855	0.3664	1932.83	1933.171	10004.3	1	989.2	56.7	3	R.EAEAAIYHLQLFEELR.R
*	HsFlag-VPS71_Ti_1(	3.4427	0.2051	2331.83	2332.616	4557.7	1	393.1	40.9	1	R.RLAPITSDPTEATAVGAVEASFK.C
*	HsFLAG-ARP6_Ti_1	5.6955	0.4802	2176.2	2176.428	5237.7	1	1816.2	73.8	7	R.LAPITSDPTEATAVGAVEASFK.C
	HsFLAG-KIAA0515_	1.8576	0.0812	840.79	841.041	3029.5	1	189.9	64.3	2	R.APIIAVTR.N
	HsFlag-VPS71_Ti_1(	2.9372	0.2286	1645.57	1643.75	8996.4	1	1136.3	69.2	1	K.DPVQEAWAEDVDLR.V
gi|5453617|re	10	44	42.90%	154	17536	9.4	zinc finger, HIT domain containing 1 [Homo sapiens]				
*	HsFLAG-TIP49a_Ti_	4.1765	0.343	2551.01	2550.744	7129.8	1	634.8	28.4	2	R.QLEALENDNFQDDPHAGLPQLGK.R
*	HsFlag-VPS71_Ti_1(	4.3684	0.3034	2551.11	2550.744	4452	1	457.1	45.5	11	R.QLEALENDNFQDDPHAGLPQLGK.R
*	HsH2AZ-FLAG_293_	4.8242	0.2674	2706.67	2706.932	9255.7	1	1037.9	29.3	2	R.QLEALENDNFQDDPHAGLPQLGKR.L
*	HsFlag-VPS71_Ti_1(	4.0653	0.2459	1479.87	1478.558	5961.3	1	1585.9	83.3	8	K.RLPQFDDDADTGK.K
*	HsVPS71-FLAG_Ti_	4.7803	0.3728	1607.57	1606.732	5674.6	1	1578.6	84.6	12	K.RLPQFDDDADTGKK.K
*	HsFlag-VPS71_Ti_1(	5.1109	0.1762	1607.8	1606.732	6083.1	1	1575.9	55.8	3	K.RLPQFDDDADTGKK.K
*	HsVPS71-FLAG_Ti_	2.8153	0.3248	1323.54	1322.371	6240.9	1	1336.9	86.4	2	R.LPQFDDDADTGK.K
*	HsVPS71-FLAG_Ti_	3.5786	0.2386	1450.63	1450.545	8109	1	1079.3	66.7	2	R.LPQFDDDADTGKK.K
*	HsFLAG-TIP49b_Ti_	4.4627	0.3825	2294.42	2294.433	5740.6	1	1094.4	60.5	1	R.PFCAVCGFPSPYTCVSCGAR.Y
*	HsFlag-VPS71_Ti_1(	2.345	0.2125	1101.67	1102.158	3327.6	1	232.2	75	1	R.CLGTHQETR.C
gi|7657381|re	12	66	42.50%	504	55181	6.6	PRP19/PSO4 pre-mRNA processing factor 19 homolog [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.18	0.1432	2715.28	2715.974	7392.7	1	595.3	37	1	K.YIAENGTDPINNQPLSEEQLIDIK.V
*	HsFLAG-p53-DNA-D	5.0571	0.3776	2033.43	2033.309	7930.6	1	1184.1	59.4	6	K.ALQDEWDAVMLHSFTLR.Q
*	HsFLAG-FLJ20729_	3.768	0.4305	1799.4	1799.907	8518.6	1	1164.9	64.3	14	R.QELSHALYQHDAACR.V
*	HsFlag-NUFIP_Ti_2(	2.9351	0.0948	1601.69	1598.834	4031.3	1	344.6	57.7	6	K.TVPEELVKPEELSK.Y

*	HsFlag-NUFIP_Ti_20	4.4114	0.2967	2901.82	2902.243	11046.6	1	1097.7	27.8	3	R.QVASHVGLHSASIPGILALDLCPSDTNK.I
*	HsFLAG-p53-DNA-D	4.9665	0.3524	2602.11	2602.95	9410.9	1	2025.1	38	7	K.KVTSVVFHPSQDLVFSASPDATIR.I
*	HsFlag-NUFIP_Ti_20	5.2905	0.4184	2473.76	2474.776	4408	1	791.1	52.3	9	K.VTSVVFHPSQDLVFSASPDATIR.I
*	HsFlag-NUFIP_Ti_20	3.9097	0.1983	2475.57	2474.776	8024.9	3	696.8	29.5	2	K.VTSVVFHPSQDLVFSASPDATIR.I
*	HsFLAG-Lin9_Ti_20	3.4797	0.338	1615.74	1615.839	3840.8	1	603.9	73.1	10	R.IWSVPNASCVQVVR.A
*	HsFlag-NUFIP_Ti_20	3.8357	0.3013	3475.35	3475.738	8256.7	1	978.3	25	1	K.VTDETSGCSLTCAQFHPDGLIFGTGTMDSQIK.I
*	HsFlag-NUFIP_Ti_20	6.1909	0.3472	3604.6	3603.88	11201.5	1	1480.5	25.7	5	R.TNVANFPGHSGPITSIAFSENGYYLATAADDSSVK.L
*	HsFlag-NUFIP_Ti_20	3.8413	0.2399	1320.94	1321.473	7248.9	2	1356.4	85	2	K.TLQLDNNFEVK.S
gi|10835063|r	13	138	42.50%	294	32575	4.8	nucleophosmin 1 isoform 1 [Homo sapiens]				
gi|40353734|r	13	138	47.20%	265	29465	4.6	nucleophosmin 1 isoform 2 [Homo sapiens]				
	HsFLAG-ARP5_Ti_1	5.1118	0.3152	2573.97	2574.726	8825.2	1	1338.7	38.8	2	K.ADKDYHFKVDNDENEHQLSLR.T
	HsH2AZ-FLAG_293_	3.9554	0.3085	2260.89	2260.384	7768.7	1	1491	47.1	1	K.DYHFKVDNDENEHQLSLR.T
	HsFLAG-p53-DNA-D	5.4611	0.3233	2261.19	2260.384	9169	1	2091.2	70.6	5	K.DYHFKVDNDENEHQLSLR.T
	HsFlag-VPS71_Ti_1	2.4938	0.2372	1568.62	1569.628	5358.7	3	306.9	45.8	2	K.VDNDENEHQLSLR.T
	HsFLAG-p53-DNA-D	3.9301	0.3163	1569.6	1569.628	10906.1	1	1067.5	62.5	17	K.VDNDENEHQLSLR.T
	HsFLAG-p53-DNA-D	5.7756	0.4204	2930.96	2931.287	10844.9	1	1469.7	40.7	4	R.TVSLGAGAKDELHIVEAEAMNYEGSPIK.V
	HsFlag-VPS71_Ti_1	6.6085	0.3152	2931.25	2931.287	12352.1	1	2636.9	34.3	20	R.TVSLGAGAKDELHIVEAEAMNYEGSPIK.V
	HsFLAG-FLJ20729_	4.7012	0.2618	2145.95	2146.377	7356	1	1445.4	58.3	1	K.DELHIVEAEAMNYEGSPIK.V
	HsFlag-NUFIP_Ti_20	5.0046	0.3682	2228.96	2228.655	7564.4	1	970	50	49	K.MSVQPTVSLGGFEITPPVVLR.L
	HsFlag-VPS71_Ti_1	4.561	0.2731	2229.08	2228.655	6095.4	2	822.8	36.2	3	K.MSVQPTVSLGGFEITPPVVLR.L
	HsVPS71-FLAG_Ti_	6.534	0.4967	3725.63	3725.288	10538.8	1	2755.2	33.9	6	K.LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEK.A
	HsFLAG-TCF3_Ti_1	2.9034	0.2619	933.35	932.018	9077.3	8	1145.5	81.2	2	K.GPSSVEDIK.A
	HsFLAG-FLJ20729_	4.7746	0.2209	1820.16	1821.017	7298.9	1	1976	76.9	26	R.MTDQEAIQDLWQWR.K
gi|5453854|re	9	58	42.40%	356	37526	7.1	poly(rC) binding protein 1 [Homo sapiens]				
	HsARP6-FLAG_Ti_1	3.1504	0.1495	1290.13	1289.354	6671.6	3	866.9	70	1	R.INISEGNCPER.I
*	HsTIP60_Ti_106.263	2.6537	0.1144	1388.55	1389.678	8084.1	7	523.9	54.2	2	R.IITLTGPTNAIFK.A
*	HsMRGBP-FLAG_Ti_	3.7983	0.217	1389.58	1389.678	5660.5	2	701.6	66.7	24	R.IITLTGPTNAIFK.A
*	HsFlag-VPS71_Ti_1	4.0523	0.1808	3382.6	3380.856	7663.7	1	1190.1	28.3	3	K.AFAMIIDKLEEDINSSMTNSTAASRPPVTLR.L
*	HsFlag-VPS71_Ti_1	3.8784	0.431	1444.36	1443.693	4458.4	2	453.6	65.4	9	R.LVVPATQCGSLIGK.G
	HsFLAG-Lin9_Ti_20	4.6761	0.4043	2089.82	2091.257	7514.3	1	1044	52.6	7	R.ESTGAQVQVAGDMLPNSTER.A
*	HsFLAG-FLJ20729_	3.1247	0.3733	1674.49	1673.913	3404.1	1	470.6	63.3	5	R.AITIAGVPQSVTECVK.Q
*	HsFlag-NUFIP_Ti_20	3.5963	0.296	2607.96	2607.875	8753.5	1	974.5	29.2	1	R.QQSHFAMMHGGTGFAGIDSSSPEVK.G
*	HsFlag-VPS71_Ti_1	5.0623	0.5064	2178.51	2178.494	7193	1	1219.7	57.5	6	R.QVTITGSAASISLAQYLINAR.L
gi|4501955|re	39	253	42.30%	1014	113135	8.9	poly (ADP-ribose) polymerase family, member 1 [Homo sapiens]				
*	HsFLAG-FLJ20729_	3.6535	0.2828	1455.06	1455.788	7660.4	2	1124.8	66.7	1	R.MAIMVQSPMFDGK.V
*	HsFLAG-FLJ20729_	2.6879	0.36	1185.27	1186.307	8438.5	1	725.4	65	4	K.TLGDFAAEYAK.S
*	HsFLAG-p53-DNA-D	3.7407	0.3835	1186.34	1186.307	3761.1	1	1098.6	90	7	K.TLGDFAAEYAK.S
*	HsFLAG-p53-DNA-D	1.9552	0.1411	1193.3	1194.344	5089.3	7	373.3	62.5	1	R.WYHPGCFVK.N
*	HsFLAG-p53-DNA-D	4.4173	0.2913	2025.24	2025.228	5811.6	8	578.8	37.5	2	K.NREELGFRPEYSASQLK.G
*	HsFLAG-p53-DNA-D	3.551	0.2959	2025.69	2025.228	4939.7	1	397.5	53.1	8	K.NREELGFRPEYSASQLK.G
*	HsFLAG-p53-DNA-D	2.5424	0.2622	1080.4	1081.211	6238.8	9	457.4	61.1	1	K.GFSLLATEDK.E
*	HsFLAG-Lin9_Ti_20	3.2508	0.2325	1081.27	1081.211	7742.7	1	1290.9	83.3	1	K.GFSLLATEDK.E
*	HsFLAG-ARP5_Ti_1	4.724	0.3736	1650.21	1650.913	7703.1	1	1995	78.6	5	K.GFSLLATEDKEALKK.Q

*	HsFLAG-p53-DNA-D	4.0503	0.1991	1517.52	1517.636	7271.6	1	1015.4	65.4	7	K.RKGDEVDGVDEVAK.K
*	HsFLAG-FLJ20729_	4.1024	0.3401	1702.16	1700.932	5300.2	1	754.7	65.4	2	K.AQNDLIWNIKDELK.K
*	HsFLAG-p53-DNA-D	3.5792	0.2951	1828.14	1829.106	8292.8	1	954.8	60.7	1	K.AQNDLIWNIKDELKK.V
*	HsARP6-FLAG_Ti_1	2.5558	0.251	1401.17	1400.531	5598.8	4	431	58.3	2	K.QQVPSGESAILDR.V
*	HsFlag-VPS71_Ti_1	3.954	0.2854	2529.5	2528.855	3833.5	1	420.8	43.2	1	R.VADGMVFGALLPCEECSGQLVFK.S
*	HsFLAG-FLJ20729_	4.5121	0.4899	1738.18	1738.814	8245.2	1	2045.8	78.6	4	K.SDAYYCTGDVTAWTK.C
*	HsFLAG-p53-DNA-D	5.0483	0.4315	3768.28	3770.203	5964.3	1	778.5	25	2	R.IFPPETSASVAATPPPSTASAPAAVNSSASADKPLSNMK.I
*	HsFLAG-Lin9_Ti_20	5.5069	0.4786	1625.4	1625.773	8928	1	2219.1	78.6	22	R.VVSEDFLQDVSASTK.S
*	HsFlag-NUFIP_Ti_1	6.346	0.4733	2138.73	2139.502	8174.5	1	1912	66.7	33	K.SLQELFLAHILSPWGAEVK.A
*	HsFLAG-Lin9_Ti_20	5.5545	0.1908	2139.65	2139.502	6952.5	1	1704.7	45.8	20	K.SLQELFLAHILSPWGAEVK.A
*	HsFLAG-p53-DNA-D	6.1643	0.4481	3187.91	3187.709	10410.1	1	1581.4	31.2	1	K.SLQELFLAHILSPWGAEVKAEPVEVVAPR.G
*	HsFLAG-Lin9_Ti_20	2.8942	0.1523	1066.98	1067.23	3827.8	2	463.8	72.2	2	K.AEPVEVVAPR.G
*	HsFLAG-p53-DNA-D	4.5578	0.4005	1990.47	1990.137	7125.4	1	1187.6	60.5	4	K.GGAAVDPDSGLEHSAHVLEK.G
*	HsARP6-FLAG_Ti_1	4.6971	0.3151	1363.52	1362.652	5321.1	1	1585.1	91.7	15	K.VFSATLGLVDIVK.G
*	HsFlag-VPS71_Ti_1	5.3597	0.3588	2044.91	2045.253	6390.7	1	2114.6	81.2	19	K.KFYPLEIDYGQDEEAVK.K
*	HsFLAG-Lin9_Ti_20	3.9523	0.2273	2044.99	2045.253	5340.5	2	839.9	42.2	1	K.KFYPLEIDYGQDEEAVK.K
*	HsFLAG-p53-DNA-D	4.6091	0.3122	2172.65	2173.427	8538.9	1	1969.7	67.6	1	K.KFYPLEIDYGQDEEAVKK.L
*	HsFLAG-p53-DNA-D	4.464	0.2787	2173.25	2173.427	6797.1	1	1365.8	44.1	2	K.KFYPLEIDYGQDEEAVKK.L
*	HsFLAG-p53-DNA-D	2.1174	0.2507	957.53	958.146	4409.1	3	373	68.8	5	K.KLTVNPGTK.S
*	HsFLAG-p53-DNA-D	3.0281	0.1668	1366.52	1366.687	4297.9	1	568.9	72.7	3	K.SKLPKPVQDLIK.M
*	HsFLAG-p53-DNA-D	6.4772	0.423	3493.88	3493.812	9932.9	1	1994.3	33.9	14	K.RQIQAAYSILSEVQQAVSQGSSDSQILDLSNR.F
*	HsFLAG-p53-DNA-D	6.3012	0.3302	3338.62	3337.625	9343.9	1	1756.5	33.3	5	R.QIQAAYSILSEVQQAVSQGSSDSQILDLSNR.F
*	HsFlag-NUFIP_Ti_1	3.2731	0.2714	1468.91	1469.741	5621	6	410.2	59.1	8	R.FYTLIPHDFGMK.K
*	HsFLAG-FLJ20309_	4.0038	0.3344	1495.34	1495.719	4968.8	1	1016.9	80.8	21	K.KPPLLNNADSVQAK.V
*	HsFLAG-p53-DNA-D	5.4667	0.4344	2107.05	2107.47	8754.2	1	1942.2	67.6	5	K.VEMLDNLLDIEVAYSLLR.G
*	HsFLAG-p53-DNA-D	5.3189	0.4267	1826.23	1826.868	5529.9	1	1293.5	68.8	1	R.GGSDDSSKDPIDVNYEK.L
*	HsFLAG-p53-DNA-D	3.7162	0.0955	1531.72	1531.663	9109.8	3	1414.9	70.8	1	K.VVDRDSEEAEIIR.K
*	HsFLAG-FLJ20729_	2.5344	0.1721	1660.71	1659.837	5126.7	1	508.7	61.5	1	K.VVDRDSEEAEIIRK.Y
*	HsFLAG-FLJ20729_	4.599	0.3711	1378.43	1378.571	7563.4	1	1653.6	83.3	18	R.TTNFAGILSQGLR.I
*	HsFLAG-p53-DNA-D	2.6896	0.2403	1130.4	1131.332	8274.2	1	949.1	72.2	2	K.GIYFADMVSK.S
gi|4503481|re	16	80	42.10%	437	50119	6.7	eukaryotic translation elongation factor 1 gamma [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.9977	0.4196	1348.38	1348.545	8345	1	2199.4	83.3	3	K.ALIAAQYSGAQVR.V
	HsFlag-VPS71_Ti_1	3.4037	0.1264	1119.44	1119.39	3273.9	3	755.9	88.9	2	R.ILGLLDAYLK.T
	HsFLAG-FLJ20729_	3.6858	0.4155	2008.51	2009.403	8371.3	1	801	53.1	2	R.VTLADITVVCTLLWLYK.Q
	HsFlag-VPS71_Ti_1	4.1316	0.3	1609.89	1610.822	6576.4	1	1586.8	81.8	8	R.WFLTCINQPQFR.A
	HsFLAG-ARP6_Ti_1	5.1437	0.4402	2357.31	2358.502	5626.3	1	808.9	54.8	7	K.AAAPAPEEEMDECEQALAAEPK.A
	HsFlag-VPS71_Ti_1	2.9486	0.1479	925.31	925.075	3563.8	5	747.7	92.9	5	K.DPFAHLPK.S
	HsFlag-VPS71_Ti_1	2.5267	0.1651	1085.55	1086.23	8691	1	672.5	68.8	1	K.STFVLDEFK.R
	HsFlag-VPS71_Ti_1	2.9035	0.1986	1086.69	1086.23	4856.4	1	775.4	81.2	2	K.STFVLDEFK.R
	HsFLAG-p53-DNA-D	2.7754	0.1934	1242.55	1242.417	6681.3	2	777.8	72.2	1	K.STFVLDEFKR.K
	HsFLAG-BC014022_	3.9502	0.282	2589.47	2590.851	5166.6	4	422.8	30	1	R.KYSNEDTLSVALPYFWEHFDK.D
	HsFLAG-ARP6_Ti_1	4.4679	0.4029	2461.6	2462.677	7024.2	1	1335.3	42.1	6	K.YSNEDTLSVALPYFWEHFDK.D
	HsFlag-FLJ90652_2	4.4263	0.3159	2462.93	2462.677	5650.2	1	593.6	44.7	12	K.YSNEDTLSVALPYFWEHFDK.D

	HsFlag-VPS71_Ti_1(	5.2782	0.5543	2550.96	2551.901	8541.5	1	1415.9	55	6	R.FPEELTQTFMSCNLITGMFQR.L
	HsFLAG-ARP6_Ti_1	4.8393	0.3873	2688.59	2688.912	4725.7	1	619.2	50	15	R.GQELAFPLSPDWQVDYESYTWR.K
*	HsFlag-VPS71_Ti_1(	3.8261	0.2676	1575.15	1573.743	3332.4	1	599.2	73.1	6	R.KLDPGSEETQTLVR.E
	HsFlag-VPS71_Ti_1(	3.7857	0.2408	1686.62	1685.836	7272.8	1	1255.3	69.2	3	R.EYFSWEGAFQHVGK.A
gi|4507555|re	17	74	41.60%	694	75492	7.7	thymopoietin isoform alpha [Homo sapiens]				
	HsFLAG-KIAA0515_	2.5085	0.142	1700.23	1698.874	4238.1	8	409.2	53.3	1	K.SELVANNVTLPAGEQR.K
	HsFLAG-p53-DNA-D	4.7959	0.3471	1719.67	1719.981	7762.8	1	1475.9	73.1	9	K.DVYVQLYLQHLTAR.N
	HsFLAG-UTX1_Ti_2(	3.7274	0.3961	1252.53	1252.416	6178.6	1	1455	81.8	21	R.NRPPLPAGTNSK.G
	HsFlag-NUFIP_Ti_2(	5.4352	0.4378	2571.48	2571.72	7444.5	1	1550	36	8	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S
	HsFLAG-p53-DNA-D	4.1052	0.2686	2688.36	2689.887	10107.3	1	620.4	34.1	1	R.QEDKDDLDVTELTNEDLLDQLVK.Y
	HsFlag-Ies6_293_Ti_	4.6388	0.3556	2190.38	2189.378	7580	1	1027.3	55.6	3	K.DDLDVTELTNEDLLDQLVK.Y
	HsARP6-FLAG_Ti_1	3.1637	0.357	1330.97	1331.514	3923.2	1	937.3	75	6	K.YGVNPGPIVGTTR.K
	HsFLAG-FLJ20729_	2.5442	0.253	1647.67	1648.767	4565.1	1	1021.1	73.3	1	R.SSTPLPTISSSAENTR.Q
*	HsFlag-VPS71_Ti_1(	3.9223	0.264	1287.65	1286.384	4811.3	1	1065.1	81.8	2	R.SHISDQSPLSSK.R
*	HsFLAG-Lin9_Ti_20	3.8372	0.3956	2139.9	2140.398	5555.3	1	679.7	52.6	6	K.ALEESESSQLISPPLAQAIR.D
*	HsFLAG-FLJ20729_	5.1548	0.4987	2319.16	2320.579	5094	1	937.4	54.8	3	R.DSGSFVAFQNIPGSELMSSFAK.T
*	HsFLAG-Lin9_Ti_20	4.8097	0.4581	1656.17	1655.932	9066.2	1	1390.1	63.3	5	K.TVVSHSLTTLGLEVAK.Q
*	HsFLAG-FLJ20729_	3.2818	0.296	1832.58	1834.079	6157.9	1	526	50	2	K.IDASELSFPFHESILK.V
*	HsFLAG-Lin9_Ti_20	3.9152	0.2627	3896.11	3894.214	5283.3	1	800.1	27.1	1	K.VDDEILGFISEATPLGGIQAASTESCNQQLDLALCR.A
*	HsFlag-VPS71_Ti_1(	4.8072	0.3955	2035.02	2035.307	8769.9	1	1831.3	60.5	2	R.AYEAAASALQIATHTAFVAK.A
*	HsFLAG-Lin9_Ti_20	2.6037	0.2344	1067.54	1068.261	5694.6	1	832.8	77.8	2	R.THQALGILSK.T
*	HsFLAG-FLJ20309_	3.1718	0.3494	1953.95	1954.063	9711.3	1	731.3	50	1	K.TYDAASYICEAAFDEVK.M
gi|21040371|r	20	70	41.50%	427	49130	5.7	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39 isoform 1 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	3.0073	0.2799	1296.63	1297.413	4711.8	2	221.9	54.5	3	K.GSYVSIHSSGFR.D
	HsFLAG-FLJ20729_	3.6241	0.3653	1296.99	1297.413	6359.8	1	982	72.7	7	K.GSYVSIHSSGFR.D
	HsFLAG-Lin9_Ti_20	2.6521	0.1748	1243.61	1244.52	3979.5	1	468.9	77.8	1	R.DFLLKPELLR.A
	HsFlag-NUFIP_Ti_1(	3.2269	0.1338	1244.76	1244.52	4710.6	2	906.8	83.3	2	R.DFLLKPELLR.A
	HsFLAG-FLJ20729_	6.4447	0.4235	3653	3654.027	6880.9	1	1503.5	33.1	11	R.AIVDCGFEHPSEVQHECIPQAILGMDVLCQAK.S
	HsFLAG-Lin9_Ti_20	3.0334	0.2796	1292.53	1293.434	4011	1	344.4	68.2	1	K.NCPHVVVGTPGR.I
	HsFLAG-Lin9_Ti_20	3.7331	0.4048	1294.37	1293.434	7962.6	1	1293.8	72.7	4	K.NCPHVVVGTPGR.I
	HsFLAG-Lin9_Ti_20	2.974	0.2034	1162.4	1163.238	5671.2	2	798.3	81.2	1	K.HFVLDECDK.M
*	HsFlag-VPS71_Ti_1(	3.1569	0.3406	1832.46	1832.05	5669.5	1	804.6	64.3	1	K.FMQDPMEVFVDDETK.L
	HsFLAG-Lin9_Ti_20	3.2061	0.3726	1462.54	1463.72	5019	2	426	59.1	2	K.LTLHGLQQYYVK.L
	HsFLAG-Lin9_Ti_20	3.5535	0.2277	1462.54	1463.72	6395.9	1	1144.6	54.5	1	K.LTLHGLQQYYVK.L
	HsFLAG-p53-DNA-D	3.4387	0.3284	1464.78	1463.72	6416.1	1	1051.3	77.3	8	K.LTLHGLQQYYVK.L
*	HsFLAG-Lin9_Ti_20	4.3755	0.4408	2294.69	2296.702	8589.3	1	1289.9	52.6	2	R.CMALAQLLVEQNFPAIAIHR.G
*	HsFLAG-FLJ20729_	4.5924	0.3713	2296.48	2296.702	7131.2	1	750.3	32.9	2	R.CMALAQLLVEQNFPAIAIHR.G
	HsFLAG-FLJ20729_	3.868	0.3173	1260.58	1260.525	6371.3	1	891.1	75	4	R.RILVATNLFGR.G
	HsFLAG-Lin9_Ti_20	2.2326	0.1198	1104.68	1104.338	5498.1	2	339.8	66.7	2	R.ILVATNLFGR.G
	HsFLAG-Lin9_Ti_20	3.4027	0.2346	1105.14	1104.338	6349.5	1	1134.3	83.3	7	R.ILVATNLFGR.G
	HsFLAG-Lin9_Ti_20	4.8327	0.4231	1480.33	1480.615	7594.8	1	2068.7	84.6	6	K.GLAITFVSDENDAK.I
	HsFLAG-Lin9_Ti_20	3.7762	0.3725	1480.73	1480.615	8409.7	1	923.6	61.5	4	K.GLAITFVSDENDAK.I
*	HsFLAG-Lin9_Ti_20	4.3415	0.221	3535.32	3536.874	9513.3	1	1483	28.4	1	K.ILNDVQDRFEVNVAELPEEIDISTYIEQSR.-

gi|4758138|re	22	94	41.40%	614	69148	8.9	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 [Homo sapiens]				
*	HsFlag-DPCD_Ti_20	3.2958	0.2532	1419.54	1419.62	7432	1	1293.9	85	1	K.WNLDELPKFEK.N
*	HsFlag-NUFIP_Ti_2	3.8621	0.3098	1390.29	1390.498	7384.4	1	1283.7	80	9	K.NFYQEHPDLAR.R
*	HsFLAG-FLJ20309_	3.2958	0.2603	1253.38	1253.357	9365.4	1	1605.9	88.9	3	R.RTAQEVETYR.R
*	HsFLAG-FLJ20729_	3.9676	0.3743	2280.75	2281.634	6402.9	1	748.3	50	1	K.PVLNFYEANFPANVMDVIAR.Q
*	HsFlag-DPCD_Ti_20	5.6373	0.4736	3360.23	3360.766	9553.9	1	1579.7	30.5	2	R.QNFTEPTAIQAQGWPVALSGLDMVGVAQTGSGK.T
	HsFLAG-FLJ20729_	3.68	0.1617	1369.4	1369.57	8205	1	1337	70.8	10	R.GDGPICLVLAPTR.E
*	HsFLAG-Lin9_Ti_20	5.4316	0.3968	1793.46	1793.94	9690.1	1	2098.9	75	8	R.ELAQQVQQVAAEYCR.A
	HsFLAG-Lin9_Ti_20	3.4493	0.2586	1173.24	1173.321	5889.8	4	1103.1	80	1	R.GVEICIATPGR.L
*	HsFLAG-Lin9_Ti_20	2.3909	0.2523	1094.49	1095.247	6275.4	3	584.4	68.8	2	R.LIDFLECGK.T
*	HsFLAG-Lin9_Ti_20	3.2364	0.2181	1095.22	1095.247	3521.4	2	696.4	87.5	1	R.LIDFLECGK.T
	HsFlag-VPS71_Ti_1	3.9446	0.3609	1338.59	1337.595	6421.6	1	1768.7	90	2	R.MLDMGFEPQIR.K
	HsFlag-VPS71_Ti_1	3.4534	0.2605	1350.45	1349.59	5704.3	1	749	80	3	R.QTLMWSATWPK.E
*	HsFLAG-Lin9_Ti_20	4.9428	0.3348	3818.02	3817.213	9500.1	1	1143.8	26.6	2	K.DYIHINIGALELSANHNILQIVDVCHDVEKDEK.L
*	HsFlag-DPCD_Ti_20	2.5611	0.1431	1284.29	1284.432	4219.3	2	459	63.6	1	R.DGWPAMGIHGDK.S
*	HsFLAG-ARP5_Ti_1	3.7464	0.4159	1549.58	1549.814	6393	1	1428.5	75	2	K.HGKAPILIATDVASR.G
	HsFlag-DPCD_Ti_20	3.9001	0.3219	1227.45	1227.447	6409.8	1	1340.3	81.8	24	K.APILIATDVASR.G
	HsFLAG-Lin9_Ti_20	2.3447	0.1664	1227.48	1227.447	4392.5	1	224.8	54.5	1	K.APILIATDVASR.G
	HsFlag-VPS71_Ti_1	3.8816	0.4273	2082.57	2083.39	7258	1	890.5	52.6	1	K.APILIATDVASRGLDVEDVK.F
	HsH2AZ-FLAG_293_	2.0551	0.157	874.29	874.966	5857.2	2	691.2	78.6	1	R.GLDVEDVK.F
*	HsFlag-DPCD_Ti_20	4.598	0.3916	2132.41	2133.281	5941.3	1	757.7	56.2	11	K.FVINYDYPNSSEDYIHR.I
*	HsFLAG-Lin9_Ti_20	2.646	0.2621	1575.74	1575.761	7983.9	1	407.6	46.2	1	K.TGTAYTFFTPNNIK.Q
*	HsFlag-VPS71_Ti_1	3.8136	0.382	1576.66	1575.761	6786.8	1	825.7	61.5	7	K.TGTAYTFFTPNNIK.Q
gi|20127479|r	35	314	41.00%	930	103533	6	RNA binding motif protein 10 isoform 1 [Homo sapiens]				
*	HsMRGBP-FLAG_Ti	3.3071	0.2244	2903.8	2904.746	6719.2	1	746.5	45.5	1	R.DQDYRTEQGEEEEEEEDEEEEEK.A
*	HsFLAG-p53-DNA-D	5.8565	0.3438	2226.4	2227.075	9083.8	1	2272.7	70.6	16	R.TEQGEEEEEEEDEEEEEK.A
*	HsARP6-FLAG_Ti_1	3.3562	0.2855	1360.08	1360.525	3613.8	1	612.2	81.8	4	R.MLPQAATEDDIR.G
	HsFLAG-p53-DNA-D	2.7401	0.1703	1180.62	1181.297	5182.6	1	516.5	70	8	R.GQLQSHGVQAR.E
	HsFlag-NUFIP_Ti_1	3.8075	0.3191	1181.36	1181.297	6403.1	1	1391.2	90	40	R.GQLQSHGVQAR.E
	HsH2AZ-FLAG_293_	4.8317	0.4558	1725.49	1725.901	8956.4	1	2071.3	78.6	39	R.GFAFVEFSHLQDATR.W
	HsFLAG-p53-DNA-D	5.3208	0.3142	1770.7	1770.016	9739.7	1	2077	75	27	R.WMEANQHSLNILGQK.V
	HsFLAG-Lin9_Ti_20	2.4237	0.2055	1288.58	1289.492	4529.7	3	535.4	70	1	K.VSMHYSDPKPK.I
	HsFlag-NUFIP_Ti_1	2.7225	0.1915	1289.42	1289.492	3455.2	6	481.3	75	1	K.VSMHYSDPKPK.I
	HsARP6-FLAG_Ti_1	3.2198	0.2221	1191.73	1192.28	7836.4	2	1294	87.5	4	K.INEDWLCNK.C
	HsH2AZ-FLAG_293_	3.5364	0.2358	1328.72	1329.496	4905.1	1	1266.9	81.8	1	K.SEAEQKLPLGTR.L
	HsFLAG-FLJ20729_	4.0519	0.2898	1198.26	1198.365	5574.7	1	1133.1	90	10	R.LDQQTLPLGGR.E
	HsFLAG-p53-DNA-D	5.1787	0.2824	2827.99	2829.2	7493.1	1	1293.9	33.7	23	R.NLNPHSTMDSILGALAPYAVLSSSNVR.V
	HsFlag-NUFIP_Ti_1	5.7653	0.444	2828.92	2829.2	7664.5	1	1639.8	51.9	21	R.NLNPHSTMDSILGALAPYAVLSSSNVR.V
*	HsFLAG-Lin9_Ti_20	5.7372	0.4469	3446.71	3448.086	7035.3	1	1296	30.6	2	R.GFAFIQLSTIVEAAQLLQILQALHPPLTIDGK.T
	HsARP6-FLAG_Ti_1	2.1201	0.1228	921.42	922.069	7145.1	4	554.9	71.4	3	K.TINVEFAK.G
	HsFLAG-FLJ20729_	4.3579	0.4022	2534.99	2535.701	8876	1	1308.7	34	2	K.GDPTGAGPEASLEPGADSVSMQAFSR.A
	HsFlag-FLJ90652_2	5.5311	0.3203	2536.28	2535.701	5205.1	1	937.9	54	12	K.GDPTGAGPEASLEPGADSVSMQAFSR.A
	HsFLAG-ARP6_Ti_2	7.5476	0.5384	3768.67	3770.119	11301.2	1	2813.9	31.8	8	R.AQPGAAPGIYQQSAEASSSQGTAANSQSYTIMSPAVLK.S

	HsFlag-Ies6_293_Ti_	3.9275	0.3663	1516.18	1516.651	4696.4	1	800	76.9	13	R.TYVPALEQSADGHK.E
	HsFLAG-p53-DNA-D	4.4336	0.3003	2187.06	2187.371	8227.7	1	1028.4	52.5	1	R.TYVPALEQSADGHKETGAPSK.E
	HsFLAG-ARP5_Ti_1	3.7954	0.3767	2503.21	2501.712	3932.3	1	829.8	39.1	2	R.TYVPALEQSADGHKETGAPSKEGK.E
	HsARP6-FLAG_Ti_1	2.6535	0.1861	1149.16	1149.292	3711.7	2	627.6	83.3	2	K.NSFQPISSLR.D
	HsFlag-DPCD_Ti_20	4.2484	0.3178	1439.35	1439.562	8141.1	1	2470	84.6	10	R.ESATADAGYAILEK.K
	HsFlag-NUFIP_Ti_2(	2.9015	0.2106	1047.48	1048.19	5598.6	1	512.9	75	4	R.HQQLSGLHK.Q
	HsFlag-DPCD_Ti_20	2.9624	0.083	1048.03	1048.19	8150.5	8	743.5	75	1	R.HQQLSGLHK.Q
	HsFLAG-p53-DNA-D	3.8299	0.1603	1639.61	1639.806	7054.3	1	1027	69.2	2	R.RAHLSENELEALEK.N
	HsFLAG-Lin9_Ti_20	3.4231	0.2285	1482.79	1483.618	5679.1	1	724.4	62.5	1	R.AHLSENELEALEK.N
	HsH2AZ-FLAG_293_	4.4575	0.4333	1483.58	1483.618	5074	1	1377	87.5	20	R.AHLSENELEALEK.N
	HsFLAG-ARP5_Ti_1	3.8399	0.1632	2359.45	2360.616	4438.1	1	889.6	40.8	3	R.AHLSENELEALEKNDMEQMK.Y
	HsFLAG-p53-DNA-D	5.3946	0.4197	1856.14	1857.03	6839	1	2051.8	75	2	R.KYGGISTASVDFEQPTR.D
	HsFLAG-Lin9_Ti_20	4.5126	0.4349	1727.96	1728.856	8285.9	1	1389.9	63.3	15	K.YGGISTASVDFEQPTR.D
	HsH2AZ-FLAG_293_	3.1781	0.2426	1093.12	1091.123	4757.1	1	780	80	6	R.DGLGSDNIGSR.M
	HsFLAG-FLJ20729_	2.5255	0.2164	1314.49	1313.497	4499.2	3	442.7	63.6	1	K.QGIVTPIEAQTR.V
	HsFlag-ZnF-HIT2_Ti_	3.4101	0.4467	1366.16	1366.424	5424	1	1221.5	79.2	8	R.GSSYGVTSTESYK.E
gi|27436946|r	30	64	41.00%	664	74140	7	lamin A/C isoform 1 precursor [Homo sapiens]				
	HsFlag-VPS71_Ti_1(	2.1536	0.2683	1359.62	1360.467	4088.3	3	128.4	46.2	1	R.SGAQASSTPLSPTR.I
	HsFlag-VPS71_Ti_1(	4.1003	0.18	1360.65	1360.467	6247	1	928	69.2	4	R.SGAQASSTPLSPTR.I
	HsFLAG-p53-DNA-D	4.6882	0.2397	1630.74	1630.752	9789	1	2304.5	83.3	2	R.LQEKEDLQELNDR.L
	HsFlag-VPS71_Ti_1(	3.103	0.1755	1132.47	1132.172	6394.6	1	969.7	87.5	1	K.EDLQELNDR.L
	HsFlag-VPS71_Ti_1(	3.0851	0.2256	1090.5	1090.178	6661.7	2	1241.2	88.9	2	R.SLETENAGLR.L
	HsFlag-VPS71_Ti_1(	2.2948	0.0874	1148.57	1149.243	4221.8	9	281.3	61.1	1	R.ITESEEVVSR.E
	HsFlag-VPS71_Ti_1(	3.4394	0.2194	1149.49	1149.243	6260.5	1	1264	88.9	4	R.ITESEEVVSR.E
	HsFlag-VPS71_Ti_1(	2.2801	0.2719	1165.61	1166.233	4990.3	6	366.9	55	1	K.AAYEAELGDAR.K
	HsFlag-VPS71_Ti_1(	3.4773	0.2975	1172.56	1172.327	6022.3	1	1386.2	90	1	K.KEGDLIAAQAR.L
	HsFlag-VPS71_Ti_1(	1.8584	0.1021	1043.54	1044.153	2789.8	9	281.9	66.7	1	K.EGDLIAAQAR.L
	HsFlag-VPS71_Ti_1(	3.1647	0.1097	1002.63	1003.141	4922.9	4	523.1	75	2	K.DLEALLNSK.E
	HsFlag-VPS71_Ti_1(	2.8896	0.2939	1120.36	1120.245	4877.2	7	475.5	65	1	K.EAALSTALSEK.R
	HsFlag-VPS71_Ti_1(	3.326	0.1583	1340.68	1339.494	3277.7	4	490.5	75	2	K.RTLEGELHDLR.G
	HsFlag-VPS71_Ti_1(	2.1662	0.1149	901.62	902.035	6089	1	505	62.5	1	K.LEAALGEAK.K
	HsFlag-VPS71_Ti_1(	3.9555	0.3264	1510.81	1510.745	7789.7	1	1178.7	72.7	1	R.LQTMKEELDFQK.N
	HsFlag-VPS71_Ti_1(	1.9905	0.125	887.49	888.009	3806.9	6	310.2	71.4	1	R.LVEIDNGK.Q
	HsFlag-VPS71_Ti_1(	4.9804	0.4732	1753.98	1753.869	5325.1	1	1308.5	73.3	6	R.NSNLVGAAHEELQQSR.I
	HsFlag-VPS71_Ti_1(	3.9408	0.135	1701.68	1700.976	6107.6	2	1229.9	48.2	2	R.IRIDSLSAQLSQLQK.Q
	HsFlag-VPS71_Ti_1(	5.4745	0.3853	1701.77	1700.976	8985.5	1	2218.9	78.6	6	R.IRIDSLSAQLSQLQK.Q
	HsFlag-VPS71_Ti_1(	2.8258	0.2669	1430.62	1431.629	5384.4	1	628.4	62.5	2	R.IDSLSAQLSQLQK.Q
	HsFlag-VPS71_Ti_1(	4.0817	0.19	1431.66	1431.629	8408.4	1	1506.2	75	2	R.IDSLSAQLSQLQK.Q
	HsFlag-VPS71_Ti_1(	2.5089	0.0803	1052.86	1052.209	5177.3	7	686.1	85.7	1	K.EREMAEMR.A
	HsFLAG-p53-DNA-D	4.622	0.2877	1894.72	1895.135	8276.9	1	1935.5	75	4	R.MQQQLDEYQELLDIK.L
	HsFlag-VPS71_Ti_1(	2.9584	0.3826	1203.49	1204.276	10934	1	1251.5	70	2	R.VAVEEVDEEGK.F
	HsYL1_Ti_101.1451.	3.9583	0.3743	1204.45	1204.276	5515.6	1	1476.4	90	4	R.VAVEEVDEEGK.F
	HsFlag-VPS71_Ti_1(	4.8029	0.4061	2534.45	2534.877	7915.1	1	1261	47.9	4	K.AGQVVTIWAAGAGATHSPPTDLVWK.A

	HsFlag-VPS71_Ti_1	3.3998	0.2348	1364.69	1364.426	5400.3	2	657.8	68.2	1	K.AQNTWGCGNSLR.T
	HsFlag-VPS71_Ti_1	3.7332	0.2836	1494.76	1492.687	7803.7	1	1124.7	69.2	1	R.TALINSTGEEVAMR.K
	HsYL1-FLAG_Ti_20	5.3062	0.4644	2365.71	2366.504	5597.3	1	1258.7	53.8	2	K.ASASGSGAQVGGPISSGSSASSVTVTR.S
	HsYL1-FLAG_Ti_20	3.7677	0.4226	2367.85	2366.504	8411.7	1	1193.6	31.7	1	K.ASASGSGAQVGGPISSGSSASSVTVTR.S
gi|4506901|re	7	63	40.90%	164	19330	11.6	splicing factor, arginine/serine-rich 3 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_2	2.8919	0.1552	1250.82	1249.369	6620	5	1030.9	72.7	1	K.VYVGNLGNNGNK.T
*	HsFLAG-p53-DNA-D	4.7049	0.3335	1877.51	1878.052	7604.7	1	1310.9	62.5	3	K.VYVGNLGNNGNKTELER.A
*	HsFlag-NUFIP_Ti_1	3.0193	0.3527	1044.35	1044.198	5145.9	1	1183.2	93.8	7	R.AFGYYGPLR.S
	HsFLAG-ARP6_Ti_2	3.9808	0.2277	1621.89	1622.777	5591.6	1	1081.1	76.9	35	R.NPPGFAFVEFEDPR.D
*	HsFLAG-UTX1_Ti_2	3.15	0.1968	2322.14	2321.511	5073	2	369.8	45	6	R.NPPGFAFVEFEDPRDAADAVR.E
*	HsARP6-FLAG_Ti_1	3.2187	0.2243	1131.24	1131.274	7163.5	1	1008.3	77.8	4	R.VRVELSNGEK.R
*	HsFLAG-FLJ20309_	3.2808	0.1802	1124.37	1124.247	6681.2	1	1208	88.9	7	R.NRGPPPSWGR.R
gi|14277700|r	8	37	40.90%	132	14515	7.2	ribosomal protein S12 [Homo sapiens]				
gi|89034991|r	8	37	40.90%	132	14598	6.9	PREDICTED: similar to ribosomal protein S12 [Homo sapiens]				
gi|51468838|r	8	37	40.90%	132	14598	6.9	PREDICTED: similar to ribosomal protein S12 [Homo sapiens]				
	HsFlag-NUFIP_Ti_1	2.3792	0.1985	1066.71	1067.233	5574.3	4	487.9	61.1	6	K.TALIHDGLAR.G
	HsFlag-NUFIP_Ti_1	2.6363	0.166	1067.53	1067.233	5103	6	770.1	77.8	2	K.TALIHDGLAR.G
	HsFlag-NUFIP_Ti_11	4.1687	0.376	2291.75	2292.547	5968.6	1	1094.5	61.1	1	K.RQAHLCVLASNCDEPMYVK.L
	HsFlag-NUFIP_Ti_11	5.2725	0.3439	2291.75	2292.547	10072.9	1	1982	45.8	2	K.RQAHLCVLASNCDEPMYVK.L
	HsFlag-NUFIP_Ti_1	3.8555	0.3648	2136.65	2136.36	8818.7	1	777.3	50	2	R.QAHLCVLASNCDEPMYVK.L
	HsFLAG-ARP6_Ti_1	4.8198	0.1209	1751.34	1752.03	7470.9	1	1662.7	75	12	K.LVEALCAEHQINLIK.V
	HsFlag-NUFIP_Ti_1	3.2132	0.3059	1189.76	1190.394	5456.5	1	707	72.2	3	K.KLGEWVGLCK.I
	HsFlag-NUFIP_Ti_1	3.5234	0.3303	1190.63	1190.394	5208.3	1	1103.3	88.9	9	K.KLGEWVGLCK.I
gi|38201714|r	12	58	40.80%	326	36092	9.2	ELAV-like 1 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.9851	0.3803	2164.71	2163.453	4795.5	1	641.5	61.8	5	R.TNLIVNYLPQNMTQDELR.S
*	HsFLAG-FLJ20729_	4.1253	0.3683	1353.41	1354.5	6086.5	1	1512.9	83.3	8	R.SLFSSIGEVESAK.L
*	HsFLAG-Lin9_Ti_20	2.5616	0.3188	1353.49	1354.5	8433.6	1	827.5	58.3	1	R.SLFSSIGEVESAK.L
*	HsFLAG-Lin9_Ti_20	4.3752	0.2735	1783.26	1784.024	6375.9	1	1436.1	45.3	2	K.VAGHSLGYGFVNYVTAK.D
*	HsFLAG-Lin9_Ti_20	4.6822	0.3917	1783.45	1784.024	7570.2	1	1568.2	65.6	5	K.VAGHSLGYGFVNYVTAK.D
*	HsFLAG-FLJ20729_	2.7624	0.1926	1336.34	1336.531	5806.3	1	1139.2	77.3	1	K.VSYARPSSEVIK.D
*	HsFLAG-FLJ20729_	4.4955	0.2531	1219.37	1219.383	8688.7	1	1990.9	90	2	K.DANLYISGLPR.T
*	HsFLAG-FLJ20729_	4.1365	0.3403	1189.21	1189.354	6916.4	1	1439.4	85	7	R.VLVDQTTGLSR.G
*	HsFLAG-FLJ20729_	5.1818	0.2771	2769.5	2770.028	5149.5	1	653.2	31	3	K.RSEAEEAITSFNGHKPPGSSEPITVK.F
*	HsFlag-DPCD_Ti_20	4.7286	0.3396	1569.17	1569.804	9044.4	1	1694.7	73.1	20	K.NVALLSQLYHSPAR.R
*	HsFLAG-Lin9_Ti_20	3.5741	0.2627	1569.2	1569.804	3357.6	2	719.2	51.9	1	K.NVALLSQLYHSPAR.R
*	HsFLAG-Lin9_Ti_20	2.9728	0.2243	1234.4	1234.363	6305.4	2	894.8	75	3	R.FGGPVHHQAQR.F
gi|7706326|re	4	8	40.80%	125	14585	9.4	splicing factor 3B, 14 kDa subunit [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	4.1783	0.2939	1417.06	1417.617	6547.2	1	1368.6	81.8	2	K.ITAEEMYDIFGK.Y
*	HsARP6-FLAG_Ti_1	3.8848	0.2974	1592.53	1591.758	7404.9	1	1264.9	65.4	4	R.GTAYVVYEDIFDAK.N
*	HsFlag-DPCD_Ti_20	3.5847	0.2813	1665.88	1664.707	7003.3	1	1130.2	73.1	1	K.NACDHLSGFNVCNR.Y
*	HsFLAG-Lin9_Ti_20	3.9669	0.2339	1388.44	1388.609	7581.3	1	1572.3	85	1	R.YLVVLYYNANR.A
gi|88988849|r	18	42	40.70%	703	75909	8.9	PREDICTED: similar to antiquitin [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	5.0051	0.4232	2193.85	2193.612	7022.9	1	1447.2	63.9	2	R.PAAFMSTLLINQPQYAWLK.E

	HsFLAG-TCF3_Ti_1	3.3565	0.1918	1906.5	1906.069	6073.6	1	736.4	56.2	1	R.GEVITTYCPANNEPIAR.V
	HsFLAG-TCF3_Ti_1	2.9498	0.1128	1340.5	1340.43	5708.5	2	583.2	72.7	1	R.QASVADYEETVK.K
	HsFLAG-TCF3_Ti_1	4.0738	0.3709	1474.6	1474.799	7171.1	1	1483.2	76.9	2	K.IQVLGSLVSLEMGK.I
	HsFLAG-TCF3_Ti_1	3.2581	0.2411	2683.11	2684.969	11249.5	1	757.8	37	3	K.ILVEGVGEVQEYVDICDYAVGLSR.M
	HsFLAG-TCF3_Ti_1	2.758	0.2282	1169.5	1170.412	6139.2	6	420.2	60	1	R.MIGGPILPSER.S
	HsFLAG-TCF3_Ti_1	3.5036	0.1533	1171.58	1170.412	5588.2	1	1294.9	90	2	R.MIGGPILPSER.S
	HsFLAG-TCF3_Ti_1	3.3907	0.3712	1346.25	1345.579	5735.3	1	938.7	73.1	2	K.GAPTTSLISVAVTK.I
	HsFLAG-TCF3_Ti_1	4.9525	0.4131	1451.44	1451.663	6761	1	1797.9	80.8	4	R.VNLLSFTGSTQVGK.Q
	HsFLAG-TCF3_Ti_1	2.4456	0.2649	1451.68	1451.663	5804	2	340.4	53.8	2	R.VNLLSFTGSTQVGK.Q
	HsFLAG-TCF3_Ti_1	6.0133	0.3744	3702.96	3702.199	8230.4	1	1491.9	28.5	2	R.SLLELGGNNAIIAFEDADLSLVVPSALFAAVGTAGQR.C
	HsFLAG-TCF3_Ti_1	4.147	0.3895	1708.59	1708.914	7913.3	1	1445.3	73.1	2	R.LFIHESIHDEVVNR.L
	HsFLAG-TCF3_Ti_1	4.082	0.3784	1906.93	1908.167	4233.2	1	629.4	59.4	5	R.VGNPWDPNVLYGPLHTK.Q
	HsFLAG-TCF3_Ti_1	4.9239	0.1905	1910.1	1908.167	4979.1	1	888.1	46.9	2	R.VGNPWDPNVLYGPLHTK.Q
	HsFLAG-TCF3_Ti_1	3.592	0.3662	1609.66	1608.893	8205.4	1	1025.3	60.7	2	K.QAVSMFLGAVEEAKK.E
	HsFLAG-TCF3_Ti_1	4.9047	0.4476	4060.88	4061.645	9390.5	1	803.7	22.2	2	K.VMDRPGNYVEPTIVTGLGHDASIAHTETFAPILYVFK.F
	HsFLAG-TCF3_Ti_1	4.7824	0.3366	1883.53	1884.055	7410.5	1	1612.5	75	2	K.FKNEEEVFAWNNEVK.Q
	HsFLAG-TCF3_Ti_1	5.2927	0.3629	2508.2	2507.683	4319.9	1	673.9	50	5	K.GSDCGIVNVNIPTSGAEIGGAFGGEK.H
gi|4506605|re	7	56	40.70%	140	14865	10.5	ribosomal protein L23 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.9124	0.4684	1969.64	1971.227	4205.6	1	693	55.3	27	R.ISLGLPVGAVINCADNTGAK.N
*	HsFLAG-ARP6_Ti_1	5.1692	0.4547	1844.01	1844.241	8001	1	2307.2	73.5	16	R.LNRLPAAGVGDMVMATVK.K
*	HsFLAG-ARP6_Ti_1	5.0206	0.3615	1845.07	1844.241	5954.5	1	2546.5	57.4	7	R.LNRLPAAGVGDMVMATVK.K
*	HsFLAG-ARP6_Ti_1	3.8157	0.3839	1460.45	1460.79	6057.7	1	1890	85.7	2	R.LPAAGVGDMVMATVK.K
*	HsFlag-NUFIP_Ti_11	2.792	0.3117	1018.94	1019.278	4599	4	482.2	75	2	K.KVHPAVVIR.Q
*	HsFLAG-TIP49b_Ti_	1.8524	0.1141	890.54	891.104	5827.9	1	549	78.6	1	K.VHPAVVIR.Q
*	HsFLAG-ARP6_Ti_1	3.1181	0.3206	901.26	901.051	4130.9	1	1037.1	88.9	1	K.GSAITGPVAK.E
gi|23111018|r	32	295	40.50%	852	94370	6.7	RNA binding motif protein 10 isoform 2 [Homo sapiens]				
	HsFLAG-p53-DNA-D	2.7401	0.1703	1180.62	1181.297	5182.6	1	516.5	70	8	R.GQLQSHGVQAR.E
	HsFlag-NUFIP_Ti_1	3.8075	0.3191	1181.36	1181.297	6403.1	1	1391.2	90	40	R.GQLQSHGVQAR.E
	HsH2AZ-FLAG_293_	4.8317	0.4558	1725.49	1725.901	8956.4	1	2071.3	78.6	39	R.GFAFVEFSHLQDATR.W
	HsFLAG-p53-DNA-D	5.3208	0.3142	1770.7	1770.016	9739.7	1	2077	75	27	R.WMEANQHSLNILGQK.V
	HsFLAG-Lin9_Ti_20	2.4237	0.2055	1288.58	1289.492	4529.7	3	535.4	70	1	K.VSMHYSDPKPK.I
	HsFlag-NUFIP_Ti_1	2.7225	0.1915	1289.42	1289.492	3455.2	6	481.3	75	1	K.VSMHYSDPKPK.I
	HsARP6-FLAG_Ti_1	3.2198	0.2221	1191.73	1192.28	7836.4	2	1294	87.5	4	K.INEDWLCNK.C
	HsH2AZ-FLAG_293_	3.5364	0.2358	1328.72	1329.496	4905.1	1	1266.9	81.8	1	K.SEAEQKLPLGTR.L
	HsFLAG-FLJ20729_	4.0519	0.2898	1198.26	1198.365	5574.7	1	1133.1	90	10	R.LDQQTLPLGGR.E
	HsFLAG-p53-DNA-D	5.1787	0.2824	2827.99	2829.2	7493.1	1	1293.9	33.7	23	R.NLNPHSTMDSILGALAPYAVLSSSNVR.V
	HsFlag-NUFIP_Ti_1	5.7653	0.444	2828.92	2829.2	7664.5	1	1639.8	51.9	21	R.NLNPHSTMDSILGALAPYAVLSSSNVR.V
*	HsFLAG-Lin9_Ti_20	4.8046	0.3357	3349.29	3348.954	5586.7	1	812.9	30	4	R.GFAFIQLSTIEAAQLLQILQALHPPLTIDGK.T
	HsARP6-FLAG_Ti_1	2.1201	0.1228	921.42	922.069	7145.1	4	554.9	71.4	3	K.TINVEFAK.G
	HsFLAG-FLJ20729_	4.3579	0.4022	2534.99	2535.701	8876	1	1308.7	34	2	K.GDPTGAGPEASLEPGADSVSMQAFSR.A
	HsFlag-FLJ90652_2	5.5311	0.3203	2536.28	2535.701	5205.1	1	937.9	54	12	K.GDPTGAGPEASLEPGADSVSMQAFSR.A
	HsFLAG-ARP6_Ti_2	7.5476	0.5384	3768.67	3770.119	11301.2	1	2813.9	31.8	8	R.AQPGAAPGIYQQSAEASSSQGTAANSQSYTIMSPAVLK.S
	HsFlag-Ies6_293_Ti_	3.9275	0.3663	1516.18	1516.651	4696.4	1	800	76.9	13	R.TYVPALEQSADGHK.E

	HsFLAG-p53-DNA-D	4.4336	0.3003	2187.06	2187.371	8227.7	1	1028.4	52.5	1	R.TYVPALEQSADGHKETGAPSK.E
	HsFLAG-ARP5_Ti_1	3.7954	0.3767	2503.21	2501.712	3932.3	1	829.8	39.1	2	R.TYVPALEQSADGHKETGAPSKEGK.E
	HsARP6-FLAG_Ti_1	2.6535	0.1861	1149.16	1149.292	3711.7	2	627.6	83.3	2	K.NSFQPISSLR.D
	HsFlag-DPCD_Ti_20	4.2484	0.3178	1439.35	1439.562	8141.1	1	2470	84.6	10	R.ESATADAGYAILEK.K
	HsFlag-NUFIP_Ti_2	2.9015	0.2106	1047.48	1048.19	5598.6	1	512.9	75	4	R.HQQLSGLHK.Q
	HsFlag-DPCD_Ti_20	2.9624	0.083	1048.03	1048.19	8150.5	8	743.5	75	1	R.HQQLSGLHK.Q
	HsFLAG-p53-DNA-D	3.8299	0.1603	1639.61	1639.806	7054.3	1	1027	69.2	2	R.RAHLSENELEALEK.N
	HsFLAG-Lin9_Ti_20	3.4231	0.2285	1482.79	1483.618	5679.1	1	724.4	62.5	1	R.AHLSENELEALEK.N
	HsH2AZ-FLAG_293_	4.4575	0.4333	1483.58	1483.618	5074	1	1377	87.5	20	R.AHLSENELEALEK.N
	HsFLAG-ARP5_Ti_1	3.8399	0.1632	2359.45	2360.616	4438.1	1	889.6	40.8	3	R.AHLSENELEALEKNDMEQMK.Y
	HsFLAG-p53-DNA-D	5.3946	0.4197	1856.14	1857.03	6839	1	2051.8	75	2	R.KYGGISTASVDFEQPTR.D
	HsFLAG-Lin9_Ti_20	4.5126	0.4349	1727.96	1728.856	8285.9	1	1389.9	63.3	15	K.YGGISTASVDFEQPTR.D
	HsH2AZ-FLAG_293_	3.1781	0.2426	1093.12	1091.123	4757.1	1	780	80	6	R.DGLGSDNIGSR.M
	HsFLAG-FLJ20729_	2.5255	0.2164	1314.49	1313.497	4499.2	3	442.7	63.6	1	K.QGIVTPIEAQTR.V
	HsFlag-ZnF-HIT2_Ti_	3.4101	0.4467	1366.16	1366.424	5424	1	1221.5	79.2	8	R.GSSYGVTSTESYK.E
gi|13654237|	124	711	40.40%	4128	469093	7.1	protein kinase, DNA-activated, catalytic polypeptide [Homo sapiens]				
	HsFlag-VPS71_Ti_1	3.1564	0.1969	1104.55	1104.205	4645.3	1	1004.4	88.9	1	R.LQETLSAADR.C
	HsFLAG-ARP6_Ti_1	3.4156	0.348	1267.07	1267.44	6775.3	1	1188.7	77.3	2	R.CGAALAGHQLIR.G
*	HsYL1_Ti_103.2394.	2.2289	0.1184	995.91	996.279	4933	1	542.8	68.8	1	K.IPALDLLIK.L
*	HsFlag-VPS71_Ti_1	4.9831	0.3646	2859.06	2859.27	5206.6	1	1588.6	42.7	6	K.VYELLGLLGEVHPSEMINNAENLFR.A
*	HsFlag-VPS71_Ti_1	3.0001	0.2689	1248.68	1248.44	5800.7	9	600.1	65	3	K.TQMTSAVREPK.L
*	HsYL1_Ti_104.1712.	2.5984	0.1812	970.73	971.194	7066.3	1	875.1	75	10	K.LPVLAGCLK.G
*	HsARP6-FLAG_Ti_1	2.5794	0.1694	971.23	971.194	4773.7	6	851.5	81.2	1	K.LPVLAGCLK.G
	HsFLAG-ARP6_Ti_1	3.4483	0.3049	1240.19	1240.408	5303.3	1	862	80	3	K.GLSSLLCNFTK.S
	HsFLAG-FLJ20729_	3.4904	0.2367	1090.48	1090.271	8161.7	4	1063	83.3	3	K.RYAVPSAGLR.L
	HsFLAG-p53-DNA-D	3.1573	0.3197	1278.35	1278.535	5137.7	1	527.8	68.2	1	K.KAALSALESFLK.Q
	HsARP6-FLAG_Ti_1	2.6896	0.2787	1150.62	1150.36	5945.8	1	1047.9	80	1	K.AALSALESFLK.Q
	HsFlag-VPS71_Ti_1	4.6649	0.4004	1709.82	1709.015	6948.1	1	2076.1	87.5	1	K.LQYFMEQFYGIIR.N
	HsFLAG-Lin9_Ti_20	3.0104	0.2447	1496.71	1497.704	4200.8	1	268.9	58.3	1	R.NCISTVVHQGLIR.I
	HsFlag-FLJ90652_2	4.1712	0.3847	1497.19	1497.704	10300.3	1	1686.9	75	6	R.NCISTVVHQGLIR.I
	HsFlag-VPS71_Ti_1	5.8917	0.4717	4322.47	4321.774	10178.5	1	1708.5	26.4	1	R.HLLSSDQMMDSILADEAFFSVNSSSESLNHLLYDEFVK.S
	HsARP6-FLAG_Ti_1	3.8115	0.3091	1619.74	1618.796	9750.5	1	1265.6	62.5	5	K.DFSAFINLVEFCR.E
	HsYL1_Ti_102.1448.	1.8945	0.1846	926.84	927.045	4732	1	442.6	78.6	1	K.YFEGVSPK.S
	HsFLAG-Lin9_Ti_20	3.5113	0.0991	3201.21	3202.684	8747.1	5	589.1	25	1	K.QYKDELLASCLTFLLSLPHNIIELDVR.A
	HsFlag-VPS71_Ti_1	4.3449	0.5036	2823.49	2824.203	6840.8	1	1195	47.9	3	K.LGLSYTPLAEVGLNALEEWSIYIDR.H
	HsFLAG-ARP6_Ti_1	2.9148	0.2172	1176.94	1176.274	6813.4	1	1060.3	83.3	1	K.NNWEVSALSR.A
	HsYL1-FLAG_Ti_20	4.9663	0.3643	1576.58	1575.716	6424.5	1	1306	76.9	3	K.NLSSNEAISLEEIR.I
	HsFlag-VPS71_Ti_1	3.1254	0.4037	1443.65	1444.733	4751.1	1	368.7	53.8	2	R.VVQMLGSLGGQINK.N
	HsFlag-VPS71_Ti_1	5.1522	0.1853	1444.64	1444.733	7862.3	1	2028.7	84.6	19	R.VVQMLGSLGGQINK.N
	HsYL1_Ti_106.2268.	2.7473	0.1267	1093.7	1093.317	5598.8	3	774.1	87.5	1	K.RLSFAVPFR.E
	HsFLAG-p53-DNA-D	3.4665	0.3077	1705.08	1705.111	5308.8	1	1261.6	76.9	3	R.EMKPVIFLDVFLPR.V
	HsFlag-VPS71_Ti_1	4.5739	0.4276	1316.52	1316.629	7374.2	1	1732.8	85	3	K.PVIFLDVFLPR.V
	HsVPS71-FLAG_Ti_	2.8424	0.2979	1176.73	1176.312	8318.3	1	871.6	70	1	R.VTELALTASDR.Q

	HsFLAG-p53-DNA-D	4.6937	0.4194	1937.23	1938.378	6834.2	1	1415.1	65.6	12	K.VAACELLHSMVMFMLGK.A
	HsFLAG-ARP6_Ti_1	3.9465	0.358	2067.47	2068.37	4524.7	1	788.1	63.9	2	K.ATQMPEGGQGAPPMYQLYK.R
	HsFlag-VPS71_Ti_1	2.4189	0.2337	1176.57	1177.266	5118.2	4	371.8	61.1	1	R.LACDVDQVTR.Q
	HsFlag-VPS71_Ti_1	3.4514	0.2887	1178.73	1177.266	5894.8	1	1494.4	94.4	1	R.LACDVDQVTR.Q
	HsFLAG-FLJ20729_	3.9892	0.3433	2275.74	2275.673	7316.8	1	706.9	50	7	R.QLYEPLVMQLIHWFTNNK.K
*	HsFLAG-Lin9_Ti_20	4.6992	0.3315	2946.18	2946.324	8007	1	984.6	40.4	3	K.KFESQDTVALLEAILDGIVDPVDSTLR.D
	HsFLAG-p53-DNA-D	2.7201	0.2388	1530.94	1530.813	5522.1	2	681.3	70.8	1	K.RLYSLALHPNAFK.R
	HsFLAG-Lin9_Ti_20	3.8855	0.3579	1374.1	1374.626	7855.5	1	1814.1	81.8	7	R.LYSLALHPNAFK.R
	HsFLAG-p53-DNA-D	3.5594	0.2787	1530.49	1530.813	6622.1	1	1028.1	75	2	R.LYSLALHPNAFKR.L
	HsYL1_Ti_103.1928.	3.4673	0.2255	1339.68	1339.537	4709.1	1	865.5	77.3	3	R.LGASLAFNNIYR.E
	HsFlag-VPS71_Ti_1	3.9839	0.4009	2048.54	2048.159	8824.4	1	893.9	50	3	K.SLGTIQQCCDAIDHLCR.I
	HsFlag-VPS71_Ti_1	5.5792	0.3974	3880.61	3881.384	8246.6	1	1436.2	26.4	8	K.DVLKEEGVSFLINTFEGGGCGQPSGILAQPTLLYLR.G
	HsFLAG-Lin9_Ti_20	5.1073	0.4657	1815.79	1816.105	5611.3	1	1473.6	73.5	14	R.TVGALQVLGTEAQSSLLK.A
	HsFlag-VPS71_Ti_1	5.0433	0.4681	2077.07	2077.446	6030.8	1	1251.4	63.9	13	K.AVAFFLESIAMHDIIAAEK.C
	HsFLAG-ARP6_Ti_1	3.7921	0.229	1968.65	1969.26	8317.7	1	798.5	50	1	R.IMEFTTTLLNTSPEGWK.L
	HsFlag-VPS71_Ti_1	4.7321	0.2615	3770.99	3770.37	5396.2	8	353.9	22	1	R.VLVQTLCEPASIGFNIGDVQVMAHLPDVCVNLMK.A
	HsFlag-VPS71_Ti_1	4.5945	0.3123	2563.98	2563.79	7346.7	1	1080.5	47.7	8	K.ITAQSIEELCAVNLYGPDAQVDR.S
	HsYL1_Ti_102.1270.	1.9614	0.2325	919.8	919.075	7237.9	3	769	75	2	R.LAAVVSACK.Q
	HsFLAG-FLJ20729_	5.9348	0.4696	3143.93	3144.598	8878	1	2133	36.6	6	R.AGLLHNILPSQSTDLHHSVGTELLSLVYK.G
	HsARP6-FLAG_Ti_1	2.5897	0.3164	2052.33	2053.332	8987.7	2	745.7	47.2	1	K.QLASGLLELAFAFGGLCER.L
	HsYL1_Ti_102.3251.	4.4206	0.4037	1991.65	1991.264	9459.7	1	1666.1	64.7	9	K.NLDLAVLELMQSSVDNTK.M
	HsYL1_Ti_105.1760.	2.0448	0.14	1210.55	1211.45	4744.4	1	384.9	66.7	1	K.LATTILQHWK.K
	HsFLAG-ARP6_Ti_1	3.3526	0.2598	1212.14	1211.45	7120.3	1	945.4	77.8	14	K.LATTILQHWK.K
	HsFlag-VPS71_Ti_1	4.9829	0.3023	2339.02	2337.678	3514.6	1	849.1	61.9	1	K.GQAVTLLPFFTSLTGGSLEELR.R
	HsFLAG-ARP6_Ti_1	4.0509	0.3221	1768.36	1769.115	7145.1	1	1103.3	64.3	3	R.VLEQLIVAHFPMQSR.E
	HsFlag-VPS71_Ti_1	5.4343	0.3444	2712.98	2710.183	7593.9	1	1293.1	35.2	1	K.FLDALELSQSPMLLELMTEVLCR.E
	HsFLAG-p53-DNA-D	4.2634	0.3802	1895.75	1896.084	6891.2	1	1288	67.9	3	R.EQQHVMEELFQSSFR.R
	HsYL1_Ti_106.2890.	3.4127	0.3821	2233.69	2232.526	5832.6	1	708.9	55.6	1	R.RGSCVTQVGLLESVYEMFR.K
	HsYL1_Ti_103.3694.	3.889	0.367	2076.74	2076.338	5075.9	1	912.2	61.8	1	R.GSCVTQVGLLESVYEMFR.K
	HsFLAG-Lin9_Ti_20	3.4965	0.0851	1696.33	1696.981	7548	2	1181.3	67.9	3	R.EFFSTIVVDAIDVLK.S
	HsTIP60_Ti_102.175	3.2242	0.3364	1397.33	1397.525	9034	1	1191	72.7	2	K.LNESTFDTQITK.K
	HsFlag-VPS71_Ti_1	2.0937	0.144	1022.76	1023.177	4372.1	1	461.6	68.8	2	R.LPKDDVHAK.E
	HsYL1_Ti_104.0882.	2.84	0.1425	1023.42	1023.177	3580.4	1	1032.1	93.8	1	R.LPKDDVHAK.E
	HsFLAG-ARP6_Ti_1	5.7435	0.4816	2047.02	2048.226	8240.3	1	2080.2	70.6	14	K.INQVFHGSCITEGNELTK.T
	HsFlag-VPS71_Ti_1	3.5245	0.4436	2274.9	2275.461	7249.1	1	997.2	58.3	3	K.LCYDAFTENMAGENQLLER.R
	HsFLAG-FLJ20729_	3.7376	0.416	1620.06	1620.845	7261	1	1663.6	83.3	9	K.FYQGFLFSEKPEK.N
	HsYL1_Ti_103.3372.	4.4801	0.1354	1445.54	1445.742	5733.3	1	1671.3	86.4	34	K.NLLIFENLIDLK.R
	HsYL1_Ti_102.2228.	3.2515	0.4075	1609.46	1609.837	5136.4	1	762.3	66.7	7	R.YNFPVEVEVPMER.K
	HsFlag-VPS71_Ti_1	3.6397	0.3369	1370.94	1370.616	5671.2	1	1193.6	81.8	2	R.HECMAPLTALVK.H
	HsFLAG-Lin9_Ti_20	3.6447	0.4909	1467.66	1468.563	4892.5	1	854.1	73.1	10	R.SLGPPQGEEDSVPR.D
	HsFLAG-ARP6_Ti_1	3.0748	0.2967	1206.61	1206.474	4974.8	2	774.4	80	5	K.LGNPIVPLNIR.L
	HsYL1_Ti_103.1931.	3.3955	0.3107	1680.84	1679.957	6583.1	1	1074.5	69.2	4	K.LVINTEEVFRPYAK.H
	HsARP6-FLAG_Ti_1	4.4738	0.2774	1589.91	1588.888	6384.3	1	1533.2	75	8	K.EVYAAAAEVLGLILR.Y

	HsFLAG-ARP6_Ti_1	4.8965	0.3931	1518.15	1518.714	7517.6	1	2222.5	87.5	9	K.NILEESLCELVAK.Q
	HsFlag-VPS71_Ti_1	4.0647	0.3028	1327.47	1327.67	6381.3	1	1554.7	90	5	R.FMNAVFFLLPK.F
	HsFLAG-ARP6_Ti_1	4.0746	0.417	2085.59	2086.318	7522.6	1	757.1	50	6	R.ELLNPVVEFVSHPSTTCR.E
	HsFLAG-ARP6_Ti_1	4.8837	0.4951	1754.18	1754.758	8071.1	1	1912.7	78.6	1	R.DPESETDNDSQEIFK.L
	HsFLAG-Lin9_Ti_20	6.0493	0.4143	2119.77	2120.497	8814.9	1	1765.9	63.9	31	K.DVLIQGLIDENPGLQLIIR.N
	HsARP6-FLAG_Ti_1	3.7488	0.1585	1219.28	1219.467	4257	2	747.3	80	4	R.LLALNSLYSPK.I
	HsYL1_Ti_102.2174.	5.76	0.4048	2296.05	2296.601	6363.9	1	1103.6	57.5	12	R.STVLTPMFVETQASQGTLQTR.T
	HsFlag-VPS71_Ti_1	5.2335	0.3881	1918.3	1919.018	8493.5	1	1026.6	56.2	13	R.ATQQQHDFTLTQTADGR.S
	HsFlag-VPS71_Ti_1	4.2415	0.1238	3235.16	3236.475	6179.8	1	669.7	25	7	R.SSFDWLTGSSTDPLVDHTSPSSDSLLFAHK.R
	HsFLAG-p53-DNA-D	6.204	0.467	3390.7	3392.663	6292.9	1	934.6	30	1	R.SSFDWLTGSSTDPLVDHTSPSSDSLLFAHKR.S
	HsFlag-VPS71_Ti_1	3.4546	0.1493	1314.59	1313.453	5263.9	1	996.9	81.8	2	K.RLGLPGDEVDNK.V
	HsFLAG-Lin9_Ti_20	3.6398	0.2149	1135.53	1136.293	7382.1	1	1380.1	83.3	3	R.HGDLPDIQIK.H
	HsYL1_Ti_106.2196.	2.354	0.344	1520.63	1521.76	3307.9	1	210.7	53.8	1	K.HSSLITPLQAVAQR.D
	HsFLAG-p53-DNA-D	3.9323	0.2492	1521.04	1521.76	6562.4	1	1074.7	69.2	15	K.HSSLITPLQAVAQR.D
	HsFLAG-ARP6_Ti_1	3.6626	0.3041	1521.26	1521.76	7050.3	1	1361.1	46.2	2	K.HSSLITPLQAVAQR.D
	HsYL1_Ti_106.2351.	3.9572	0.3778	2160.44	2159.537	4656.9	1	512.4	47.4	4	K.HSSLITPLQAVAQRDPIIAK.Q
	HsFLAG-p53-DNA-D	3.641	0.3188	1340.53	1340.605	5145.2	1	986.6	86.4	16	K.QLFSSLFSGILK.E
	HsFlag-VPS71_Ti_1	5.3062	0.3326	2297.83	2298.482	7277.9	1	1727.1	67.6	7	K.DFWELASLDCYNHLAEWK.S
	HsYL1-FLAG_Ti_20	4.7808	0.4106	2242.86	2241.336	6649.6	1	1065.8	57.9	7	K.SLEYCSTASIDSENPPDLNK.I
	HsFLAG-p53-DNA-D	4.0708	0.3767	2236.63	2237.578	7495.1	1	574.4	50	4	K.IWSEPFYQETYLPYMIR.S
	HsFlag-VPS71_Ti_1	5.8271	0.3801	1904.89	1905.199	7633.8	1	2216.3	75	12	K.LLLQGEADQSLLTFIDK.A
	HsFLAG-Lin9_Ti_20	5.457	0.4129	2181.39	2182.522	7428	1	2442.5	72.2	38	K.LQSVQALTEIQEFISFISK.Q
	HsFLAG-p53-DNA-D	3.2144	0.2798	1591.88	1592.795	5346.3	1	714.2	66.7	5	R.LLNTWTNRYPDAK.M
	HsFlag-VPS71_Ti_1	4.2702	0.2592	1735.72	1734.983	4931.8	1	1035.9	76.9	3	K.MDPMNIWDDIITNR.C
	HsYL1-FLAG_Ti_20	3.8478	0.2084	1806.56	1806.983	8895.7	2	1139.1	60.7	1	R.MEVQEQEEDISSLIR.S
	HsFlag-VPS71_Ti_1	4.1535	0.4005	1973.93	1972.133	4835.4	1	782.5	67.9	2	K.TRDDWLVSWVQSYCR.L
	HsFlag-VPS71_Ti_1	4.4792	0.2605	1450.66	1449.61	4898.4	1	1019.5	79.2	4	R.SQGCSEQVLTVLK.T
*	HsTIP60_Ti_104.255	4.714	0.4368	1769.77	1769.946	7034.1	1	1520.6	70	7	K.TVSLLDENNVSSYLSK.N
	HsYL1_Ti_105.2370.	3.0653	0.3507	2009.23	2009.316	7175.1	1	468.7	46.9	1	K.NILAFRDQNILLGTTYR.I
	HsYL1_Ti_102.2186.	5.2947	0.3119	2174.43	2174.376	4542.8	1	660.4	55.3	20	R.IIANALSSEPACLAEIEEDK.A
	HsYL1-FLAG_Ti_20	3.6137	0.3247	1481.52	1481.554	6779.2	2	974.3	69.2	1	R.ILELSGSSSEDSEK.V
*	HsFLAG-p53-DNA-D	5.2116	0.3823	2633.43	2633.912	8828.7	1	1318.7	47.8	2	R.KEEENASVIDSAELQAYPALVVEK.M
*	HsFLAG-Lin9_Ti_20	3.9705	0.1915	2633.79	2633.912	7116.5	2	825.7	30.4	1	R.KEEENASVIDSAELQAYPALVVEK.M
	HsFlag-VPS71_Ti_1	5.4266	0.4281	2178	2178.592	8293.8	1	1247	58.8	11	R.LLQIIERYPEETLSLMTK.E
	HsFlag-VPS71_Ti_1	5.0687	0.4028	2178.73	2178.592	8378	1	2547	51.5	6	R.LLQIIERYPEETLSLMTK.E
	HsFlag-VPS71_Ti_1	4.1927	0.2968	3975.74	3977.373	6066	1	759.7	24.3	6	K.DQAVAVQHSVEEITDNYPQAIVYPFIISSESYSFK.D
	HsFlag-VPS71_Ti_1	5.8434	0.4078	3003.59	3004.41	8429.9	1	1203.7	30.8	16	K.SKLDQGGVIQDFINALDQLSNPELLFK.D
	HsFlag-VPS71_Ti_1	5.2965	0.384	3004.8	3004.41	8063.1	1	1292.3	46.2	4	K.SKLDQGGVIQDFINALDQLSNPELLFK.D
	HsFLAG-p53-DNA-D	5.8528	0.3505	2789.27	2789.158	9035.4	1	2061.3	52.1	7	K.LDQGGVIQDFINALDQLSNPELLFK.D
	HsFLAG-Lin9_Ti_20	4.5163	0.2729	2789.33	2789.158	7850.6	1	1010.2	31.2	2	K.LDQGGVIQDFINALDQLSNPELLFK.D
	HsFlag-VPS71_Ti_1	2.2286	0.2375	788.62	788.925	2602.3	2	143.2	64.3	1	K.APGLGAFR.R
	HsFLAG-p53-DNA-D	3.1557	0.2288	1360.11	1360.552	9338.6	1	1551.9	80	2	K.FIQTFGKEFDK.H
	HsYL1_Ti_102.3170.	5.2157	0.2961	1637.71	1637.932	5796.6	1	1569	84.6	10	K.LSDFNDITNMLLLK.M

	HsFlag-VPS71_Ti_1(	6.5433	0.4405	2396.14	2395.659	8616.7	1	2586.8	46.2	4	R.VEQLFQVMNGILAQDSACSQR.A
	HsYL1_Ti_102.3086.	5.8733	0.4184	2397.02	2395.659	7388.5	1	1701	62.5	5	R.VEQLFQVMNGILAQDSACSQR.A
*	HsFlag-VPS71_Ti_1(	4.7181	0.2933	1630.18	1629.937	6549.9	1	1458.8	76.9	28	R.LGLIEWLENTVTLK.D
	HsYL1_Ti_104.1338.	3.8227	0.3105	1340.95	1339.451	7640.5	1	1027.4	68.2	11	K.GANRTETVTSFR.K
	HsFLAG-p53-DNA-D	2.9051	0.3643	1621.61	1621.953	9990.1	2	667.7	50	1	K.ETGLMYSIMVHALR.A
	HsFLAG-FLJ20729_	4.0691	0.4355	1637.15	1637.888	5477.1	1	1357	82.1	9	R.SDPGLLTNTMDVFVK.E
	HsYL1_Ti_104.1802.	4.9206	0.2972	1561.04	1559.762	8216.8	1	1539.7	69.2	8	K.KGGSWIQEINVAEK.N
	HsFLAG-ARP6_Ti_1	3.5376	0.3083	2121.39	2122.392	3531.1	1	540.9	38.2	1	K.LAGANPAVITCDELLLGHEK.A
	HsFLAG-p53-DNA-D	4.4011	0.3141	2122.77	2122.392	6524.3	1	1231.3	57.9	9	K.LAGANPAVITCDELLLGHEK.A
	HsSrcap_Ti_201.073	3.759	0.2333	1633.38	1632.722	4950.6	1	647.8	64.3	4	R.AQEPESGLSEETQVK.C
	HsFLAG-FLJ20729_	3.2417	0.2553	1605.62	1604.785	6198.3	1	984	73.1	1	K.CLMDQATDPNILGR.T
gi|32455264|r	9	17	40.20%	199	22110	8.1	peroxiredoxin 1 [Homo sapiens]				
gi|4505591|re	9	17	40.20%	199	22110	8.1	peroxiredoxin 1 [Homo sapiens]				
gi|32455266|r	9	17	40.20%	199	22110	8.1	peroxiredoxin 1 [Homo sapiens]				
	HsFLAG-FLJ20729_	2.1531	0.2154	980.42	981.142	5432.3	1	591.3	75	4	K.IGHPAPNFK.A
	HsFLAG-ARP8_Ti_2	3.8271	0.2934	1752.6	1752.082	3975.2	1	556.8	59.4	1	K.KQGGLGPMNIPLVSDPK.R
	HsFlag-VPS71_Ti_1(	3.3492	0.3322	1624.42	1623.908	6283.6	1	898.4	60	2	K.QGGLGPMNIPLVSDPK.R
	HsFLAG-FLJ20729_	2.9201	0.1987	1264.4	1264.467	4976.1	1	688.1	70	2	K.RTIAQDYGVLK.A
	HsFLAG-KIAA0515_	2.9532	0.1804	1212.33	1212.392	5537	2	805.4	80	1	R.QITVNDLPVGR.S
	HsFLAG-KIAA0515_	3.5023	0.2731	1198.25	1197.376	5290.8	1	1130.6	88.9	2	R.LVQAFQFTDK.H
	HsFlag-VPS71_Ti_1(	4.6358	0.3108	2407.06	2407.654	7084.8	1	850	47.6	1	K.HGEVCPAGWKPGSDTIKPDVQK.S
	HsFLAG-TCF3_Ti_1(	5.0195	0.3701	2407.52	2407.654	7497.1	1	2012.8	44	3	K.HGEVCPAGWKPGSDTIKPDVQK.S
	HsFlag-FLJ90652_2!	3.4658	0.208	1285.41	1285.44	8216.9	2	1155	72.7	1	K.PGSDTIKPDVQK.S
gi|10863977|r	2	7	40.00%	95	10835	6.5	LSM2 homolog, U6 small nuclear RNA associated [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.9354	0.2786	2189.82	2191.412	11836.2	1	673.6	41.7	1	K.NDLSICGTLHSVDQYLNIK.L
*	HsH2AZ-FLAG_293_	4.635	0.3373	2145.5	2146.362	4699.9	1	1559.4	72.2	6	R.YVQLPADEVDTQLLQDAAR.K
gi|4885375|re	19	225	39.90%	213	21365	10.9	H1 histone family, member 2 [Homo sapiens]				
	HsFLAG-TCF3_Ti_1(	3.2643	0.3269	1326.71	1327.564	6954.3	2	515.5	50	5	R.KASGPPVSELITK.A
	HsFLAG-TCF3_Ti_1(	4.9006	0.3748	1327.44	1327.564	7126.5	1	2047.7	87.5	16	R.KASGPPVSELITK.A
	HsFLAG-ARP6_Ti_1	4.397	0.2266	1328.74	1327.564	4535.9	1	1145.4	56.2	1	R.KASGPPVSELITK.A
	HsFlag-NUFIP_Ti_1(	3.3729	0.2564	1198.14	1199.39	5929.5	1	866.6	77.3	68	K.ASGPPVSELITK.A
	HsFLAG-FLJ20309_	3.0382	0.2718	1198.52	1199.39	8477.2	3	646.4	59.1	6	K.ASGPPVSELITK.A
	HsFLAG-Lin9_Ti_20	3.0617	0.1302	847.04	846.015	3664.5	3	944	93.8	10	R.SGVSLAALK.K
	HsFLAG-p53-DNA-D	3.6663	0.1223	973.78	974.189	5265.2	3	1165.6	94.4	20	R.SGVSLAALKK.A
	HsFLAG-p53-DNA-D	3.6718	0.3489	1235.52	1236.411	6430.2	1	1295.6	77.3	2	K.KALAAAGYDVEK.N
	HsFLAG-p53-DNA-D	4.871	0.4075	1236.42	1236.411	8171.8	1	2418	90.9	3	K.KALAAAGYDVEK.N
	HsFLAG-p53-DNA-D	4.9255	0.4111	1707.39	1707.884	8048	1	1885.7	70	3	K.KALAAAGYDVEKNNSR.I
	HsFlag-FLJ20643_Ti	3.4651	0.3974	1107.57	1108.236	9933.9	1	1436.6	75	24	K.ALAAAGYDVEK.N
	HsFLAG-ARP6_Ti_2	3.7074	0.3214	1108.09	1108.236	4889.2	1	1195.4	85	40	K.ALAAAGYDVEK.N
	HsFLAG-ARP6_Ti_1	4.1777	0.3647	1579.17	1579.71	7228.5	1	1615.9	75	4	K.ALAAAGYDVEKNNSR.I
	HsVPS71-FLAG_Ti_	3.6461	0.2615	1540.18	1539.729	5699.1	1	976.7	66.7	2	K.GTLVQTKGTGASGSFK.L
	HsFLAG-ARP6_Ti_1	3.3753	0.2545	1167.29	1167.307	7149.1	1	1246.2	77.3	2	K.GTGASGSFKLNK.K
	HsFLAG-p53-DNA-D	2.2696	0.0973	987.61	987.144	3002.7	6	378.2	66.7	1	K.KAASGEAKPK.V

*	HsFlag-NUFIP_Ti_11	2.2448	0.1097	670.43	670.83	3256.3	1	389.7	83.3	1	K.KPVGAAK.K
*	HsFLAG-p53-DNA-D	2.2745	0.179	1085.8	1086.32	5371.5	4	414.8	55	1	K.AKKPAAATVTK.K
*	HsFLAG-TCF3_Ti_1	2.5041	0.3169	886.53	887.067	4294.8	1	514.3	75	16	K.KPAAATVTK.K
gi|59859885|r	8	59	39.70%	295	32854	4.9	ribosomal protein SA [Homo sapiens]				
gi|9845502|re	8	59	39.70%	295	32854	4.9	ribosomal protein SA [Homo sapiens]				
	HsFlag-NUFIP_Ti_1	4.2588	0.3692	1204.09	1204.371	8028.8	1	1826.1	83.3	7	K.FAAATGATPIAGR.F
	HsFlag-NUFIP_Ti_1	4.4753	0.5023	1699.48	1699.907	3408.4	1	560.3	71.4	8	R.FTPGTFTNQIQAAFR.E
	HsFlag-NUFIP_Ti_1	3.0509	0.2708	913.3	913.105	4232	2	978	92.9	1	R.LLVVTDPR.A
	HsFlag-NUFIP_Ti_1	5.5581	0.4986	2997.06	2998.285	6353.2	1	838.2	44.2	10	R.ADHQPLTEASYVNLPTIALCNTDSPLR.Y
	HsFlag-NUFIP_Ti_1	5.9107	0.4253	2997.29	2998.285	8807.5	1	1816.3	36.5	19	R.ADHQPLTEASYVNLPTIALCNTDSPLR.Y
	HsFlag-NUFIP_Ti_1	3.4062	0.1796	1307.4	1307.455	4319.8	1	1167.2	90	4	R.YVDIAIPCNNK.G
	HsFlag-NUFIP_Ti_11	5.1742	0.491	1614.93	1615.954	6401.2	1	1649.8	80.8	5	K.GAHSVGLMWWMLAR.E
	HsFlag-NUFIP_Ti_1	4.3065	0.3128	3580.45	3580.904	5891.4	1	320.2	22.3	5	R.EHPWEVMPDLYFYRDPEEIEKEEQAAAEK.A
gi|46367785|r	13	79	39.50%	390	43483	5.3	hypothetical protein LOC54934 [Homo sapiens]				
*	HsFlag-FLJ90652_2	5.1833	0.4423	2163.94	2164.43	8649.5	1	1985.8	68.4	2	K.KTNPGPVGETLLCQLSSYAK.T
*	HsFlag-FLJ90652_2	3.7518	0.3568	2036.71	2036.256	3280.7	1	711.1	72.2	1	K.TNPGPVGETLLCQLSSYAK.T
*	HsFlag-FLJ90652_2	3.1421	0.129	1292.24	1292.345	9102.6	1	1154	72.7	5	K.TELGSQTPESSR.S
*	HsFLAG-FLJ20436_	4.9105	0.3529	2032.92	2034.008	5781.6	1	1943.5	72.2	2	R.GDPDSEADSIDSDQEDPLK.H
*	HsFLAG-FLJ20436_	3.6118	0.2709	1255.42	1255.456	4037.3	6	691.1	83.3	10	R.LQSLYIDQFK.R
*	HsFLAG-FLJ20436_	2.5692	0.1889	1255.48	1255.456	7946.3	6	577.6	61.1	2	R.LQSLYIDQFK.R
*	HsFlag-FLJ90652_2	5.8026	0.5067	2149.25	2150.48	9305	1	2189.4	65	2	R.KVEHEALGSSLLTGPEGLLAK.E
*	HsFLAG-FLJ20436_	3.2203	0.4445	2022.5	2022.306	7513.5	1	723.2	47.4	4	K.VEHEALGSSLLTGPEGLLAK.E
*	HsFLAG-FLJ20436_	3.3282	0.3308	1058.43	1058.225	4994.1	1	1264.2	93.8	15	R.YGVEALLHR.Q
*	HsFLAG-FLJ20436_	4.9716	0.4323	1573.59	1572.736	7235.6	1	1398.8	71.4	28	R.MLATDGAAQQAHTTR.S
*	HsFLAG-FLJ20436_	2.881	0.148	1096	1095.207	4094.9	1	1334.7	93.8	5	R.CLAFVDDVR.C
*	HsFlag-FLJ90652_2	5.3515	0.45	2013.97	2015.209	11095.5	1	2045.6	73.3	2	R.HCLTHICQDTNQVLFK.C
*	HsFlag-FLJ90652_2	2.7851	0.4026	2185.24	2185.396	7814.8	1	434.1	38.6	1	K.ASAPLSQSGLATANGKPEPTSIS.-
gi|40217847|r	64	254	39.40%	2136	244505	6.1	activating signal cointegrator 1 complex subunit 3-like 1 [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	3.2005	0.3349	1500.22	1500.692	9200.8	1	1053	69.2	2	R.RDEPTGEVLSLVGK.L
*	HsFlag-ZnF-HIT2_Ti_	5.8245	0.2867	2059.43	2057.312	10135.4	1	2096.4	45.8	2	R.RDEPTGEVLSLVGKLEGTR.M
*	HsFlag-ZnF-HIT2_Ti_	3.1803	0.2166	1426.15	1426.532	5682.4	8	582.1	70	1	R.KRDEDRHDINK.M
*	HsFlag-ZnF-HIT2_Ti_	3.8549	0.3204	2227.47	2227.621	7000.3	1	751.8	50	1	K.GYTLLSEGIDEMVGIIYKPK.T
*	HsFLAG-p53-DNA-D	5.1975	0.468	2150.41	2151.424	8847.5	1	1998.7	63.9	26	R.ETYEVLLSFIQAALGDQPR.D
*	HsFlag-ZnF-HIT2_Ti_	4.8369	0.4048	2150.55	2151.424	7502.9	1	1355.4	40.3	13	R.ETYEVLLSFIQAALGDQPR.D
*	HsFlag-ZnF-HIT2_Ti_	5.3757	0.345	1588.44	1587.82	6983.1	1	2464.1	89.3	19	R.DILCGAADEVLAVLK.N
*	HsFlag-ZnF-HIT2_Ti_	3.7203	0.3434	1489.03	1489.623	6529.9	1	1218.4	79.2	3	K.EIDLLLGQTDDTR.Y
*	HsFlag-ZnF-HIT2_Ti_	2.9074	0.2354	1042.47	1043.254	4901	4	636	75	2	R.YHVLVNLGK.K
*	HsFlag-ZnF-HIT2_Ti_	2.6404	0.2825	996.4	997.093	4160	2	507.7	68.8	1	K.KITDYGGDK.E
*	HsFlag-ZnF-HIT2_Ti_	2.6401	0.1695	997.62	997.093	4423.9	6	742	87.5	1	K.KITDYGGDK.E
*	HsFlag-ZnF-HIT2_Ti_	3.5838	0.2387	1158.77	1158.381	5882.9	2	1192.2	88.9	1	K.KADEVLEILK.T
*	HsFLAG-p53-DNA-D	3.4438	0.4608	1934.05	1935.187	8367.3	1	1161.7	64.3	1	K.FLYQLHETEKEDLIR.E
*	HsFlag-ZnF-HIT2_Ti_	3.7079	0.2984	2349.96	2349.605	7083.4	1	813.2	38.2	1	K.FLYQLHETEKEDLIREER.S
*	HsFlag-DPCD_Ti_20	5.1411	0.4849	2179.27	2179.378	10246.2	1	2287.1	65.8	1	R.MDTDLETMDLDQGGEALAPR.Q

*	HsFlag-ZnF-HIT2_Ti_	4.6489	0.2993	2293.35	2293.599	8480.4	1	933.1	35.5	2	R.QVLDLEDLVFTQGSHFMANK.R
*	HsFlag-ZnF-HIT2_Ti_	5.335	0.3288	2293.69	2293.599	6891.9	1	880.2	55.3	2	R.QVLDLEDLVFTQGSHFMANK.R
*	HsFlag-ZnF-HIT2_Ti_	3.1308	0.2534	1236.41	1236.339	3944.7	1	737.8	88.9	3	K.RCQLPDGSFR.R
*	HsFlag-NUFIP_Ti_2	3.8386	0.2707	2921.83	2922.351	7621.7	1	782.6	29	1	K.GYEEVHVPALKPKPFGSEEQLLPVEK.L
*	HsFlag-ZnF-HIT2_Ti_	3.0733	0.318	2922.15	2922.351	7152.5	1	415.8	36	1	K.GYEEVHVPALKPKPFGSEEQLLPVEK.L
*	HsScrap_Ti_102.186	2.0827	0.3085	1117.31	1118.234	7089.3	5	419.4	61.1	1	K.YAQAGFEGFK.T
*	HsFLAG-Lin9_Ti_20	4.6499	0.3088	1944.5	1945.143	8962.6	1	1342.5	55.6	9	R.AALETDENLLLCAPTGAGK.T
	HsFlag-ZnF-HIT2_Ti_	4.5812	0.4214	1281.58	1282.497	7970.8	1	2003.2	86.4	3	R.SLVQEMVGSFGK.R
	HsSrcap_Ti_202.417	4.661	0.4043	2094.69	2094.415	3106.6	1	900.8	77.8	17	R.LIGLSATLPNYEDVATFLR.V
	HsFlag-ZnF-HIT2_Ti_	4.3858	0.3971	2821.23	2822.19	7903.4	1	744	41.3	5	K.GLFYFDNSFRPVPLEQTYVGITEK.K
	HsFLAG-UTX1_Ti_2	5.6592	0.3751	2821.4	2822.19	10070	1	1296.9	32.6	12	K.GLFYFDNSFRPVPLEQTYVGITEK.K
	HsFlag-ZnF-HIT2_Ti_	3.4992	0.3033	1199.48	1199.398	7284.2	3	1333.5	83.3	7	K.NQVLVFVHSR.K
	HsFlag-ZnF-HIT2_Ti_	3.6542	0.3634	1799.71	1800.088	6055.5	1	941	60	2	K.DLLPYGFAIHHAGMTR.V
	HsFlag-ZnF-HIT2_Ti_	4.2348	0.2839	1716.62	1717.036	4287.9	1	563.9	67.9	4	R.WTELGALDILQMLGR.A
	HsFlag-VPS71_Ti_1	5.2983	0.3652	1942.03	1940.265	9674.2	1	1963	64.7	5	K.LPDMLNAEIVLGNVQNAK.D
	HsFlag-ZnF-HIT2_Ti_	3.2966	0.2684	1446.27	1446.6	8082.9	1	955.9	66.7	2	R.SPTLYGISHDDLK.G
	HsFlag-ZnF-HIT2_Ti_	4.8544	0.4061	2341.6	2341.583	8221.5	1	1346.1	37.5	2	R.SPTLYGISHDDLKGDPLLDQR.R
	HsFlag-VPS71_Ti_1	3.97	0.3151	1596.78	1596.929	7252.6	1	1311.2	76.9	1	R.RLDLVHTAALMLDK.N
	HsFlag-ZnF-HIT2_Ti_	3.5283	0.1732	1350.43	1350.517	7811.2	1	1169.5	72.7	5	K.KTGNFQVTELGR.I
	HsFlag-ZnF-HIT2_Ti_	3.2068	0.3482	1222.54	1222.343	8112.7	1	929.8	70	1	K.TGNFQVTELGR.I
	HsFlag-ZnF-HIT2_Ti_	6.2146	0.4972	3571.87	3573.04	7081.7	1	1129.6	31	4	R.IASHYYITNDTVQTYNQLLKPTLSEIELFR.V
	HsFlag-ZnF-HIT2_Ti_	5.0097	0.4404	1699.58	1699.904	9260.6	1	2422.5	84.6	11	R.LYDLNHNEIGELIR.M
	HsARP6-FLAG_Ti_1	3.3164	0.2047	1407.54	1406.668	7085.6	1	987.4	72.7	3	K.LELSVHLQPITR.S
	HsFlag-VPS71_Ti_1	3.3279	0.2043	1721.66	1721.904	4008.4	1	644	69.2	2	K.VELTITPDFQWDEK.V
	HsFlag-ZnF-HIT2_Ti_	5.3994	0.2815	3067.78	3068.544	6281.9	1	864.3	32.3	8	K.YAQDEHLITFFVPVFEPLPPQYFIR.V
	HsSrcap_Ti_205.489	3.7977	0.2724	3070.04	3068.544	5046.9	1	705.3	43.8	3	K.YAQDEHLITFFVPVFEPLPPQYFIR.V
	HsFLAG-p53-DNA-D	3.9309	0.4356	1624.66	1623.815	5927.1	1	1162.6	79.2	5	R.WLSCETQLPVSFR.H
	HsFlag-VPS71_Ti_1	4.4633	0.3654	2120.87	2120.497	6754.3	1	1195.8	61.1	10	K.YPPPTELLDLQPLPVSALR.N
	HsScrap_Ti_102.197	2.6165	0.374	1301.33	1302.383	3434.6	1	298.9	65	2	R.NSAFESLYQDK.F
	HsFLAG-UTX1_Ti_2	4.1336	0.1884	3508.48	3509.856	7589.6	1	680.2	24.2	1	K.FPFFNPIQTQVFNTVYNSDDNVFVGAPTGSGK.T
*	HsFlag-ZnF-HIT2_Ti_	5.6492	0.5402	2639.72	2640.991	9523.1	1	2122.3	62.5	4	R.CVYITPMEALAEQVYMDWYEK.F
	HsARP6-FLAG_Ti_1	2.5271	0.2176	1376.78	1376.59	6200.2	1	890.9	75	1	K.VVLLTGETSTDLK.L
	HsFlag-ZnF-HIT2_Ti_	3.7522	0.3695	1843.51	1843.133	5854.3	1	818.6	60	4	K.GNIIISTPEKWDILSR.R
	HsFlag-ZnF-HIT2_Ti_	3.8888	0.2258	3337.3	3335.751	7687.1	1	713	25.9	2	K.NVQNINLFVVDEVHLIGGENGPVLEVICSR.M
*	HsFlag-ZnF-HIT2_Ti_	2.8452	0.0953	929.41	929.107	3121	1	726.5	92.9	1	K.PVYHAITK.H
	HsFlag-ZnF-HIT2_Ti_	3.4364	0.2942	1141.89	1142.43	6661.8	1	1298.6	88.9	3	K.KPVIVFVPSR.K
	HsARP6-FLAG_Ti_1	2.7164	0.2849	1776.76	1776.006	9443	4	577.5	46.7	1	R.LTAIDILTTCAADIQR.Q
	HsFLAG-p53-DNA-D	2.088	0.1135	934.36	935.034	5049.7	9	486.6	75	3	R.FLHCTEK.D
	HsFLAG-p53-DNA-D	2.6665	0.2833	1791.71	1792.001	8966.3	2	459.3	50	2	K.QDAVDYLTWTFLYR.R
	HsSrcap_Ti_204.184	4.3585	0.4584	1936.36	1937.14	7963.3	1	1270.5	66.7	7	R.MTQNPNYYNLQGISHR.H
	HsFLAG-p53-DNA-D	5.0855	0.3322	2409.07	2409.612	10887.7	1	2532.3	42.5	1	R.HLSDHLSELVEQTLSDLEQSK.C
	HsFLAG-p53-DNA-D	4.3068	0.2607	2410.24	2409.612	10810.4	1	1709.8	55	1	R.HLSDHLSELVEQTLSDLEQSK.C
	HsARP6-FLAG_Ti_1	2.5799	0.373	2015.98	2016.302	5224.5	1	336.4	44.1	2	R.GLIEIISNAAEYENIPIR.H

	HsFLAG-Lin9_Ti_20	3.8218	0.2643	1265.94	1266.486	6792	2	1434.8	85	4	K.TNLLLQAHLSR.M
	HsARP6-FLAG_Ti_1	5.3565	0.4009	1729.19	1728.943	7800.9	1	2035.4	76.7	3	R.NALLQLTDSQIADVAR.F
	HsFlag-ZnF-HIT2_Ti_	4.8145	0.3945	2146.69	2147.358	9168.9	1	2760.3	75	2	R.FCNRYPNIELSYEVVDK.D
	HsFlag-ZnF-HIT2_Ti_	4.3897	0.2296	1570.66	1569.752	7721.5	1	1572.9	83.3	1	R.YPNIELSYEVVDK.D
	HsFlag-DPCD_Ti_20	2.941	0.27	1354.64	1353.605	8161.2	4	586	54.2	1	R.SGGPVVVLVQLER.E
	HsSrcap_Ti_204.436	3.6337	0.2291	3089.94	3089.602	7912.4	1	621.7	33.9	2	R.SGGPVVVLVQLEREEEVTGPVIAPLFPQK.R
gi|10863927|r	6	18	39.40%	165	18012	7.8	peptidylprolyl isomerase A isoform 1 [Homo sapiens]				
gi|89058333|r	6	18	29.30%	222	24517	7.4	PREDICTED: similar to peptidylprolyl isomerase A isoform 1 [Homo sapiens]				
gi|89058151|r	6	18	29.30%	222	24517	7.4	PREDICTED: similar to peptidylprolyl isomerase A isoform 1 [Homo sapiens]				
gi|56847632|r	6	18	39.40%	165	17998	7.8	peptidylprolyl isomerase A-like [Homo sapiens]				
	HsFLAG-p53-DNA-D	2.9499	0.1615	1055.43	1056.203	8045	2	1014.4	75	2	R.VSFELFADK.V
	HsFlag-VPS71_Ti_1	3.1335	0.1359	1056.34	1056.203	4341	1	902.5	87.5	1	R.VSFELFADK.V
	HsFLAG-p53-DNA-D	2.6769	0.3203	1598.5	1599.811	2545.3	1	252.6	65.4	2	R.IIPGFMCQGGDFTR.H
	HsFlag-VPS71_Ti_1	4.5369	0.4051	1833.43	1833.048	6087.3	1	1085.6	67.9	7	K.SIYGEKFEDENFILK.H
	HsFlag-VPS71_Ti_1	3.9824	0.4562	2791.88	2793.093	7977	1	788.1	40.4	1	K.HTGPGILSMANAGPNTNGSQFFICTAK.T
	HsFLAG-p53-DNA-D	5.0583	0.344	2794.97	2793.093	9340.7	1	1339.6	29.8	5	K.HTGPGILSMANAGPNTNGSQFFICTAK.T
gi|7657351|re	42	236	39.30%	1328	148850	9.2	MYB binding protein 1a [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.0042	0.3855	2171.04	2172.401	7369.1	1	867.8	56.2	13	R.EFLDFFWDIAKPEQETR.L
*	HsFlag-DPCD_Ti_20	6.4704	0.4222	3865.73	3865.348	7493.1	1	1516.2	31.2	7	R.ETARPCYSLALAQLLQSFEDLPLCSILQQIQEK.Y
*	HsFLAG-Lin9_Ti_20	5.3355	0.4318	2051.15	2051.313	8308.2	1	1513.8	65.6	14	K.LLQALAQYQNHLQEQPR.K
*	HsFLAG-UTX1_Ti_2	4.3767	0.2907	2051.83	2051.313	6093.7	1	1366.4	45.3	4	K.LLQALAQYQNHLQEQPR.K
*	HsFLAG-p53-DNA-D	4.4662	0.3122	1302.6	1302.554	6854.5	1	1519.7	81.8	2	R.KALVDILSEVSK.A
*	HsFLAG-Lin9_Ti_20	4.0556	0.3152	1174.01	1174.38	7908.8	1	1857.8	85	2	K.ALVDILSEVSK.A
*	HsFLAG-p53-DNA-D	3.9904	0.2668	1354.43	1354.63	6235.7	2	1013.8	72.7	8	K.ATLQEILPEVLK.A
*	HsFLAG-p53-DNA-D	4.9046	0.4418	2483.78	2484.896	6643.3	1	1022.4	52.4	11	K.ADLNIILSSPEQLELFLLAQQK.V
*	HsFLAG-FLJ20309_	5.6719	0.4221	2485.31	2484.896	10458.1	1	1587.5	35.7	12	K.ADLNIILSSPEQLELFLLAQQK.V
*	HsFLAG-Lin9_Ti_20	5.2884	0.452	1774.54	1775.015	7528.5	1	2532.6	80	7	K.KLVGSVNLFSDENVPR.L
*	HsFLAG-Lin9_Ti_20	3.7385	0.3513	1646.77	1646.841	7184.9	1	1347	71.4	2	K.LVGSVNLFSDENVPR.L
*	HsFLAG-BC014022_	2.9306	0.1856	1224.28	1223.545	4427.9	1	669.8	80	2	R.KLPAIALDLLR.L
*	HsFLAG-Lin9_Ti_20	3.446	0.1961	1095.44	1095.371	6606.3	1	1236.6	88.9	4	K.LPAIALDLLR.L
*	HsFlag-NUFIP_Ti_2	2.8944	0.3142	1201.95	1202.278	5883.2	2	706.5	77.8	1	R.HYGEHVCTAK.L
*	HsFLAG-Lin9_Ti_20	4.1715	0.492	1717.76	1719.039	3717.1	1	681.4	71.4	13	R.FLSPPALQGYVAWLR.A
*	HsFLAG-FLJ20729_	3.5817	0.2676	2283.38	2284.546	10168.7	2	938.1	31.6	1	R.AMFLQPDLDSLVDFSTNNQK.K
*	HsFLAG-p53-DNA-D	5.1606	0.4385	2285	2284.546	4805.5	1	1145.6	65.8	4	R.AMFLQPDLDSLVDFSTNNQK.K
*	HsFlag-DPCD_Ti_20	2.8771	0.1635	1271.2	1271.39	6270.3	1	900.8	70	1	K.AQDSSLHMPER.A
*	HsFLAG-p53-DNA-D	3.4148	0.2859	1129.4	1129.299	7637	1	1468.9	88.9	3	K.KPTSQIPETK.H
*	HsFLAG-Lin9_Ti_20	2.3207	0.1979	1443.44	1443.605	4038.8	1	197.5	50	2	K.HPFSFPLENQAR.E
*	HsFLAG-BC014022_	2.7479	0.1536	1444.4	1443.605	3337.8	2	251.5	50	6	K.HPFSFPLENQAR.E
*	HsFLAG-FLJ20309_	5.554	0.5064	2104.8	2105.395	11138.1	1	2049.8	61.1	53	R.EAVSSAFFSLLQTLSTQFK.Q
*	HsFLAG-Lin9_Ti_20	4.6741	0.2868	2105.17	2105.395	10040.7	1	1222.5	36.1	1	R.EAVSSAFFSLLQTLSTQFK.Q
*	HsFlag-DPCD_Ti_20	4.885	0.4531	1936.6	1936.058	7674.8	1	1492.4	65.6	3	K.SPAESCDLLGDIQTCIR.K
*	HsFLAG-p53-DNA-D	4.1348	0.3158	1511.18	1511.69	7573.5	1	1138.2	70.8	6	R.SVFGHICSHLTPR.A
*	HsFLAG-Lin9_Ti_20	4.0624	0.3814	2285.36	2285.47	6484.9	1	1066.9	55.3	5	R.ALQLILDVLNPETSEDENDR.V

*	HsFLAG-Lin9_Ti_20	3.8548	0.2391	3557.45	3557.807	11317.3	4	550.4	20.8	1	R.ALQLILDVLNPETSEDENDRVVVTDDSDERR.L
*	HsFLAG-FLJ20309_	4.6929	0.3225	1228.52	1228.515	6751.1	1	1714.2	90	6	R.VLDLVEVLVTK.Q
*	HsFLAG-Lin9_Ti_20	4.7664	0.1786	2161.45	2161.59	7371.4	1	1544	43.1	5	K.QPENALVLELLEPLLSIIR.R
*	HsFLAG-Lin9_Ti_20	4.2085	0.29	2161.62	2161.59	9533.6	1	1189.5	55.6	6	K.QPENALVLELLEPLLSIIR.R
*	HsFLAG-p53-DNA-D	3.347	0.2521	1084.21	1084.232	7563.3	2	1146.5	92.9	4	R.IFTHHLCR.A
*	HsFLAG-FLJ20309_	3.0364	0.2777	1052.43	1052.178	6431.6	1	775.8	77.8	5	R.AGALHAQVER.L
*	HsFLAG-FLJ20729_	3.9785	0.3295	2959.9	2960.365	11944.7	1	943.8	28	1	R.LVQQAGRQPDSPTALYHFNASLYLLR.V
*	HsARP6-FLAG_Ti_1	3.59	0.3674	1317.18	1317.525	6553.6	1	1219.2	81.8	3	R.VYSTALSSFLTK.R
*	HsFLAG-p53-DNA-D	2.713	0.2666	1709.8	1710.044	3924	1	769.9	71.4	1	R.NSPLTVPMFLSLFSR.H
*	HsFLAG-Lin9_Ti_20	3.3832	0.206	1111.23	1111.296	6319.1	1	1031.7	87.5	4	R.HQACLLLQK.T
*	HsFLAG-p53-DNA-D	6.5532	0.4141	2068.07	2068.384	9303.9	1	2772.5	76.5	5	K.AQHQQALSSLELLNVLFR.T
*	HsFLAG-Lin9_Ti_20	4.1468	0.3694	3137.4	3137.52	5298.4	2	415.6	25.9	1	K.LTLDLTVLLGVLQGQQQSLQQGAHSTGSSR.L
*	HsFLAG-p53-DNA-D	3.2046	0.0997	1305.36	1305.537	5107.6	1	830.2	77.8	2	R.LHDLYWQAMK.T
*	HsFLAG-FLJ20309_	3.8799	0.3682	2375.12	2374.455	7547.5	1	818.5	45.8	1	K.SEDGTPAEDGTPAATGGSQPPSMGR.K
*	HsFLAG-p53-DNA-D	5.0442	0.424	2092.62	2093.261	6526.7	1	986.7	55	2	K.NQKPSQVNGAPGSPTEPAGQK.Q
*	HsFLAG-p53-DNA-D	2.601	0.1929	987.56	988.129	6492.6	1	551.6	66.7	2	R.SPSLLQSGAK.K
gi|39725938|r	41	173	39.20%	1390	155641	8.5	polymerase (RNA) III (DNA directed) polypeptide A, 155kDa [Homo sapiens]				
*	HsFlag-FLJ20643_Ti	2.5048	0.1195	1138.57	1138.312	3016.7	1	386.4	83.3	1	R.QQAHIQVVSK.N
*	HsFlag-NUFIP_Ti_1	4.9698	0.3903	2353.98	2354.587	9691.8	1	972.9	47.4	3	K.NLYSQDNQHAPLLYGVLDHR.M
*	HsFlag-NUFIP_Ti_1	4.6682	0.3907	2354.08	2354.587	5778.4	1	822.8	39.5	6	K.NLYSQDNQHAPLLYGVLDHR.M
*	HsFlag-NUFIP_Ti_11	2.9496	0.1388	1076.36	1076.284	5610.7	1	814.4	87.5	4	K.RPGLTYLQK.R
*	HsFlag-NUFIP_Ti_11	3.6077	0.3942	1615.44	1615.721	8842.1	1	1368.5	69.2	2	K.NICHHCGAFNGTVK.K
*	HsFlag-NUFIP_Ti_1	4.2795	0.3989	2387.86	2388.682	6704.1	1	1108.2	57.5	3	K.VVDPIVSNFLQSFETAIEHNK.E
*	HsFLAG-p53-DNA-D	4.904	0.4109	1712.8	1713.03	5623.2	1	1142	71.4	15	R.AQENLNPLVVLNLFK.R
*	HsFlag-NUFIP_Ti_11	6.6801	0.4593	2859.94	2860.385	6449.3	1	1725.3	41	13	K.RIPAEDVPLLLMNPEAGKPSDLILTR.L
*	HsFlag-NUFIP_Ti_1	4.7156	0.4315	2860.74	2860.385	7088.6	1	757.3	42	2	K.RIPAEDVPLLLMNPEAGKPSDLILTR.L
*	HsFlag-NUFIP_Ti_1	4.998	0.4281	2703.77	2704.197	4338.7	1	850.3	35.4	2	R.IPAEDVPLLLMNPEAGKPSDLILTR.L
*	HsFlag-NUFIP_Ti_11	3.2238	0.2322	1906.25	1907.314	3988.3	1	732.3	65.6	6	R.LLVPPLCIRPSVVSDLK.S
*	HsFlag-FLJ20643_Ti	2.6083	0.1853	1212.1	1211.286	7441.1	6	691.7	65	1	K.SGTNEDDLTMK.L
*	HsFlag-FLJ20643_Ti	3.6014	0.2329	1278.41	1277.506	4457.2	4	686.6	68.2	8	R.IDEVAVPVHVAK.I
*	HsFlag-FLJ20643_Ti	2.5367	0.0812	848.43	847.993	5894.6	5	766.4	91.7	1	K.ANINFLR.K
*	HsFlag-NUFIP_Ti_1	4.6754	0.4497	2004.75	2005.244	4463.1	1	1039.4	70.6	18	K.LVQNGPEVHPGANFIQQR.H
*	HsFlag-ZnF-HIT2_Ti_	3.9056	0.2795	2005.18	2005.244	6727.2	1	852	41.2	2	K.LVQNGPEVHPGANFIQQR.H
*	HsFlag-NUFIP_Ti_1	3.8371	0.277	1398.75	1398.605	5345.1	1	1265.9	86.4	1	R.HLIDGDVVLFNR.Q
*	HsFlag-NUFIP_Ti_11	3.4082	0.2359	1013.57	1012.258	5719.3	1	941.8	87.5	3	K.LSIMAHLAR.V
*	HsFlag-NUFIP_Ti_1	4.9674	0.3461	3447.23	3446.612	5446.4	1	631	28.6	2	R.FNECVCTPYNADFDGDEMNLHLPQTEEAK.A
*	HsFlag-NUFIP_Ti_11	6.7302	0.473	2363.64	2362.772	6796.4	1	2286	66.7	15	R.NGEPLIAAIQDFLTGAYLLTLK.D
*	HsFlag-FLJ20643_Ti	2.5792	0.1821	1646.16	1645.903	8628.2	1	568.7	50	1	K.ACQIIASILVGKDEK.I
*	HsFlag-NUFIP_Ti_11	2.7108	0.1256	1134.58	1134.451	6010.6	2	898.9	77.8	1	K.VRLPPPTILK.P
*	HsFlag-FLJ20643_Ti	2.5062	0.0948	903.05	902.081	2977	6	466.8	85.7	1	K.PVTLWTGK.Q
*	HsFlag-FLJ20643_Ti	2.7268	0.3875	1033.46	1033.216	2923.6	1	470.7	81.2	1	R.LAPVYLSNR.G
*	HsFLAG-UTX1_Ti_2	3.3262	0.4033	1659.22	1659.923	5750.2	1	690.9	56.2	1	R.GFSIGIGDVTPGQGLLK.A
*	HsFlag-FLJ20643_Ti	3.5131	0.2368	1541.11	1541.664	8876.9	1	1588.9	70.8	2	K.KCDEYIEALNTGK.L

*	HsFlag-NUFIP_Ti_1	4.7152	0.3554	2142.35	2143.408	3750.2	1	723.6	63.9	13	K.LQQQPGCTAEETLEALILK.E
*	HsFlag-FLJ20643_Ti	5.6855	0.3344	2326.73	2325.611	7861.9	1	3031.2	71.4	6	K.GSFINISQMIACVGQQAISGSR.V
*	HsFlag-NUFIP_Ti_11	4.7636	0.3653	2685.08	2686.016	7909.4	1	1792.4	40.2	8	K.GFVANSFYSGLTPTEFFFHTMAGR.E
*	HsFlag-NUFIP_Ti_11	4.017	0.3941	2685.24	2686.016	5629.2	1	433.9	34.8	6	K.GFVANSFYSGLTPTEFFFHTMAGR.E
*	HsFlag-NUFIP_Ti_1	2.768	0.2473	1699.21	1699.821	7844.2	1	749.4	61.5	1	K.SLEDLCSQYDLTVR.S
*	HsFlag-ZnF-HIT2_Ti_	2.5292	0.3527	2032.8	2033.218	8647.8	1	425	43.3	1	K.KSEFLCCQDSFLQEIK.K
*	HsFlag-NUFIP_Ti_1	5.1139	0.505	2732.84	2734.078	7629.6	1	1371.3	46.2	1	R.AQMEPGSAVGALCAQSIGEPGTQMTLK.T
*	HsFlag-NUFIP_Ti_1	2.858	0.1647	1992.99	1991.264	6115	1	655.4	52.8	3	R.VKPGDVAVHGEAVVCVTPR.E
*	HsFLAG-p53-DNA-D	4.3352	0.2732	1962.88	1962.311	8863.6	1	1643.2	66.7	1	K.SSMYYVLQFLKEDLPK.V
*	HsFlag-FLJ20643_Ti	3.3819	0.3722	1198.46	1197.334	5363.8	3	988.8	75	3	R.AVIHIDEQSGK.E
*	HsFLAG-p53-DNA-D	2.8697	0.1729	1454.45	1454.623	8364.1	1	1047.4	66.7	1	R.AVIHIDEQSGKEK.Y
*	HsFlag-ZnF-HIT2_Ti_	2.8302	0.1909	914.14	914.111	4313.4	4	884	87.5	2	R.AVMATHGVK.G
*	HsFlag-NUFIP_Ti_1	4.3142	0.3915	1453.72	1451.782	4776.5	1	1029	81.8	3	R.HVMLLSDLMTYK.G
*	HsFlag-NUFIP_Ti_1	4.5779	0.3313	1584.43	1584.728	6560.4	1	1326.1	73.1	4	K.TADHLFDAAYFGQK.D
*	HsFlag-NUFIP_Ti_11	2.732	0.3105	1912.4	1913.227	4495	1	324.2	46.7	5	K.RPLIFDTNEFHIPLVT.-
gi|4506613|re	5	15	39.10%	128	14787	9.2	ribosomal protein L22 proprotein [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	3.5129	0.4514	3087.24	3085.338	4765.5	1	596.4	42	1	K.FTLDCTHPVEDGIMDAANFEQFLQER.I
*	HsFLAG-p53-DNA-D	5.7698	0.2804	3088.3	3085.338	11794.6	1	1858	34	9	K.FTLDCTHPVEDGIMDAANFEQFLQER.I
	HsFLAG-ARP6_Ti_1	3.7536	0.3109	1244.26	1243.406	6167.6	1	808.9	66.7	1	K.AGNLGGGVVTIER.S
	HsFLAG-TCF3_Ti_1	2.1208	0.1909	1207.61	1208.397	5920.7	3	393.3	60	2	K.ITVTSEVPFSK.R
	HsFlag-Ies6_293_Ti_	3.6215	0.2194	1209.3	1208.397	6864.4	1	1146.2	80	2	K.ITVTSEVPFSK.R
gi|4503545|re	5	12	39.00%	154	16832	5.2	eukaryotic translation initiation factor 5A [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	3.5707	0.2797	1299.24	1299.556	6072.8	1	1606.1	86.4	5	K.VHLVGIDIFTGK.K
	HsFlag-VPS71_Ti_1	3.46	0.3571	1299.64	1299.556	6797.5	1	1199.6	72.7	1	K.VHLVGIDIFTGK.K
*	HsFLAG-p53-DNA-D	4.482	0.3036	2737.31	2738.029	7155.6	1	1345.5	37	2	K.RNDFQLIGIQDGYLSLLQDSGEVR.E
*	HsFLAG-p53-DNA-D	3.9154	0.3424	2582.24	2581.842	9403.7	1	873.2	43.2	2	R.NDFQLIGIQDGYLSLLQDSGEVR.E
	HsFlag-VPS71_Ti_1	5.5635	0.4932	2628.12	2627.973	7298	1	1473.5	52.2	2	K.YDCGEEILITVLSAMTEEAAVAIK.A
gi|6005926|re	10	52	38.90%	475	53501	9.1	U2 (RNU2) small nuclear RNA auxiliary factor 2 isoform a [Homo sapiens]				
gi|60279268|r	10	52	39.30%	471	53121	9.1	U2 (RNU2) small nuclear RNA auxiliary factor 2 isoform b [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.0673	0.1894	1167.3	1167.31	5762.5	3	1054	80	2	R.GAKEEHGGLIR.S
	HsFlag-NUFIP_Ti_1	3.8369	0.3819	2205.52	2206.523	5411.4	1	468.6	50	1	K.YWDVPPPGFEHITPMQYK.A
	HsFlag-NUFIP_Ti_1	3.7039	0.3265	3789.88	3791.474	6077.3	2	538.6	22.3	2	K.AMQAAGQIPATALLPTMTPDGLAVTPTPVPVVGSQMTR.Q
	HsFLAG-ARP6_Ti_1	5.2242	0.4829	2134.2	2134.44	4509.4	1	774.2	55	17	R.LGGLTQAPGNPVLAVQINQDK.N
	HsFlag-NUFIP_Ti_2	5.3266	0.2861	2134.88	2134.44	7986.9	1	1280.9	38.8	4	R.LGGLTQAPGNPVLAVQINQDK.N
	HsFLAG-p53-DNA-D	3.3439	0.1469	1043.48	1044.198	5254.6	2	1039.1	92.9	1	K.NFAFLEFR.S
	HsFLAG-p53-DNA-D	4.9578	0.404	2387.39	2387.667	8045.4	1	1753.2	57.1	3	R.SVDETTQAMAFDGIIFQGQSLK.I
	HsFLAG-p53-DNA-D	4.7449	0.4298	3560.8	3561.994	5208.6	1	894.6	32	2	R.RPHDYQPLPGMSENPSVYVPGVVSTVVPDSAHK.L
	HsFlag-NUFIP_Ti_1	4.6521	0.2964	1808.45	1807.056	4182.6	1	1173.4	80	10	K.LFIGGLPNYLNDDQVK.E
	HsFlag-DPCD_Ti_20	3.9865	0.3184	1910.86	1910.144	5428.4	1	802.7	58.8	10	K.SIEIPRPVDGVEVPGCGK.I
gi|7019485|re	6	24	38.70%	191	21868	5.4	programmed cell death 6 [Homo sapiens]				
	HsFLAG-p53-DNA-D	5.1708	0.2676	3190.38	3190.497	7642.8	2	675.6	26.8	6	K.DRSGVISDTELQQALSNGTWTPFNPVTVR.S
	HsFLAG-Lin9_Ti_20	3.5559	0.3357	2917.73	2919.221	6965.2	1	564.5	36.5	2	R.SGVISDTELQQALSNGTWTPFNPVTVR.S
*	HsFLAG-ARP6_Ti_1	3.4757	0.1871	1340.86	1340.537	7773.7	1	1074.4	75	3	R.SIISMFDRENK.A

*	HsFLAG-ARP6_Ti_1	3.9828	0.2618	1442.17	1442.614	5685.5	1	1485.7	83.3	6	K.AGVNFSEFTGVWK.Y
*	HsARP6-FLAG_Ti_1	3.3131	0.2916	1342.45	1342.497	4717.3	1	964.3	88.9	3	K.YITDWQNVFR.T
*	HsFLAG-ARP6_Ti_1	3.7771	0.3185	1358.35	1357.552	7108.2	3	1118.1	80	4	R.LSDQFHDILIR.K
gi|4507873|re	8	14	38.60%	197	22626	7.1	von Hippel-Lindau binding protein 1 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	5.3766	0.4121	2302.76	2303.681	9215.6	1	2235.2	65.8	2	R.RLHLGIPEAVFVEDVDSFMK.Q
*	HsFLAG-p53-DNA-D	4.7539	0.3527	2145.8	2147.494	3546.7	1	692.3	63.9	1	R.LHLGIPEAVFVEDVDSFMK.Q
*	HsFLAG-p53-DNA-D	5.0464	0.3223	2149.1	2147.494	8197.5	1	1901	43.1	3	R.LHLGIPEAVFVEDVDSFMK.Q
*	HsFLAG-p53-DNA-D	3.5791	0.2402	3401.38	3401.856	3581.1	2	313.2	24.2	1	R.LHLGIPEAVFVEDVDSFMKQPGNETADTVLK.K
*	HsFLAG-p53-DNA-D	2.6087	0.108	1093.54	1094.314	7700.4	2	640.4	68.8	1	K.FMELNLAQK.K
*	HsFLAG-p53-DNA-D	2.5943	0.1169	1256.29	1257.438	8977.8	9	724.9	66.7	1	R.FLLADNLYCK.A
*	HsFLAG-p53-DNA-D	3.827	0.1555	1257.36	1257.438	5357.9	9	1171.6	88.9	1	R.FLLADNLYCK.A
*	HsFLAG-p53-DNA-D	4.818	0.3288	2973.27	2974.226	11285.1	1	1772	32.3	4	K.NLDSLEEDLDFLRDQFTTTEVNMAR.V
gi|34147630|r	13	49	38.50%	455	49875	7.6	Tu translation elongation factor, mitochondrial [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.0477	0.4186	1810.74	1811.01	8695.6	1	786.1	53.1	1	R.DKPHVNVGTIGHVDHGK.T
*	HsFLAG-ARP6_Ti_1	3.9632	0.3165	1493.35	1493.57	8911.1	1	1768.8	81.8	2	K.KYEEIDNAPEER.A
*	HsFLAG-ARP6_Ti_1	4.4988	0.4928	1673.88	1674.854	6357.2	1	827.3	56.7	10	R.GITINAAHVEYSTAAR.H
*	HsFLAG-TIP49b_Ti_	4.4181	0.4307	1771.17	1771.852	10540.7	1	1487.5	67.9	6	R.HYAHTDCPGHADYVK.N
*	HsFLAG-TIP49b_Ti_	2.4134	0.0937	851.48	852.024	3765	2	483.3	83.3	2	R.EHLLLAR.Q
*	HsFLAG-ARP6_Ti_1	5.0134	0.3741	3690.17	3693.152	5094.1	1	547	25.8	6	R.ELLTEFGYKGEETPVIVGSALCALEGRDPELGLK.S
*	HsFLAG-ARP6_Ti_1	4.3123	0.316	1543.48	1543.803	5760	1	1644.8	80.8	5	K.LLDAVDTYIPVPAR.D
*	HsFLAG-TIP49b_Ti_	2.0895	0.1156	1543.59	1543.803	4329.2	2	401.4	50	1	K.LLDAVDTYIPVPAR.D
*	HsFLAG-p53-DNA-D	4.0538	0.1671	2131.46	2130.492	6142.3	1	814.3	55.6	2	R.DLEKPFLLPVEAVYSVPGR.G
*	HsFLAG-ARP6_Ti_1	4.9964	0.329	1644.6	1644.954	3705.2	1	1097.1	82.1	6	K.PFLLPVEAVYSVPGR.G
*	HsFLAG-TIP49b_Ti_	4.1076	0.2675	1373.03	1373.472	8827.2	1	1682.7	81.8	2	K.KGDECELLGHSK.N
*	HsFLAG-ARP6_Ti_1	3.2631	0.304	1263.11	1262.51	6097.9	1	1221.1	85	1	R.TVVTGIEMFHK.S
*	HsFLAG-ARP6_Ti_1	4.5041	0.4242	1909.34	1909.159	6056.8	1	866.4	58.8	5	R.TIGTGLVTNTLAMTEEEK.N
gi|15431301|r	10	35	38.30%	248	29226	10.7	ribosomal protein L7 [Homo sapiens]				
	HsFLAG-TCF3_Ti_1(	2.39	0.1633	1082.56	1083.27	3478.7	5	345	66.7	2	K.EVPAVPETLK.K
	HsFLAG-p53-DNA-D	3.574	0.1246	1321.49	1321.519	5782.4	1	974.7	72.7	2	R.KAGNFYVPAEPK.L
	HsFLAG-p53-DNA-D	3.6901	0.2783	1663.5	1663.957	8822.3	1	1301.4	65.4	4	R.IVEPYIAWGYPNLK.S
	HsFLAG-ARP6_Ti_1	4.5214	0.2638	1327.63	1327.57	4994.4	1	1086.9	81.8	6	K.RIALTDNALIAR.S
	HsFLAG-ARP6_Ti_1	3.7275	0.2982	1171.17	1171.382	8397.7	2	1661.9	90	6	R.IALTDNALIAR.S
	HsFLAG-ARP6_Ti_1	4.5206	0.4447	2153.68	2155.48	8550.3	1	1632.5	64.7	7	K.YGIICMEDLIHEIYTVGK.R
	HsFLAG-TCF3_Ti_1(	3.8286	0.1607	2156.23	2155.48	4540.7	1	656.8	39.7	1	K.YGIICMEDLIHEIYTVGK.R
	HsFLAG-TCF3_Ti_1(	2.5879	0.2406	1265.29	1266.442	5966.8	2	386.8	66.7	1	K.EANNFLWPFK.L
	HsFLAG-ARP6_Ti_1	3.3089	0.2606	1266.21	1266.442	5403.6	1	1000.7	83.3	5	K.EANNFLWPFK.L
	HsFLAG-ARP6_Ti_1	4.0549	0.2269	2117.6	2117.199	6719.3	1	720.7	52.8	1	K.TTHFVEGGDAGNREDQINR.L
gi|33469139|r	53	330	38.20%	1556	176752	9.5	yeast INO80-like protein [Homo sapiens]				
gi|38708321|r	53	330	38.20%	1556	176752	9.5	yeast INO80-like protein [Homo sapiens]				
	HsFLAG-ARP5_Ti_1	4.1374	0.3929	2241.83	2242.457	10725.6	1	1711.5	41.7	2	R.DDGGCTELAKPLYLQYLER.A
	HsFLAG-FLJ20309_	3.6675	0.1655	1195.39	1195.404	5468.1	1	1176.8	93.8	7	K.PLYLQYLER.A
	HsFLAG-FLJ20309_	3.8956	0.2874	3070.18	3070.248	4746	2	261.9	30.4	1	R.NISSDDSEDGLDDSNPLLPQSGDPLIQVK.E
	HsFLAG-FLJ20309_	5.4514	0.4724	2991.3	2992.227	7269	1	1207.9	35.9	3	K.ELQQYQYYSAGLLSTYDPFYEQQR.H

HsFLAG-FLJ20309_	5.5298	0.3751	2991.97	2992.227	7459.3	1	1317.9	50	15	K.ELQQYQYYSAGLLSTYDPFYEQQR.H
HsFLAG-FLJ20309_	2.8132	0.2324	1153.46	1154.268	5469.6	1	704	70	9	K.FSHDAPPPGTK.K
HsFLAG-FLJ20309_	3.3296	0.295	1153.68	1154.268	5233.4	1	1274.7	90	8	K.FSHDAPPPGTK.K
HsFLAG-TIP49a_Ti_	2.5577	0.2261	1180.44	1181.337	4016.5	2	313.6	66.7	6	K.HLSIEQLNAR.R
HsFLAG-ARP5_Ti_1	3.1394	0.0847	1182.67	1181.337	4281.8	1	950.3	88.9	6	K.HLSIEQLNAR.R
HsFLAG-TCF3_Ti_1	2.2211	0.0954	964.53	965.097	3062.4	3	214.9	71.4	1	R.NLFLTNSR.K
HsFLAG-ARP5_Ti_1	2.2768	0.1182	1015.54	1016.213	5912.5	5	390.4	64.3	1	R.KLAHQCMK.E
HsFLAG-ARP5_Ti_1	3.5031	0.3288	1346.12	1346.529	9005.1	1	1329.5	83.3	2	K.KYEKVEKEHR.K
HsFLAG-ARP8_Ti_2	4.7697	0.3562	2085.37	2085.428	6834.5	1	1199	62.5	2	K.LNFLITQTELYAHFMSR.K
HsFLAG-ARP5_Ti_1	3.5926	0.1859	1797.35	1798.027	5524.4	2	797.8	64.3	1	R.KRDMGHDGIQEEILR.K
HsFLAG-ARP5_Ti_1	3.5394	0.3093	1514.46	1513.665	8357.9	1	943.6	66.7	4	R.DMGHDGIQEEILR.K
HsFLAG-TIP49b_Ti_	3.0129	0.3418	1423.92	1424.519	3699.1	1	228.5	54.5	4	K.NAENAYHIHQAR.T
HsFLAG-ARP5_Ti_1	4.2605	0.4156	1424.02	1424.519	7393	1	1167.4	72.7	17	K.NAENAYHIHQAR.T
HsFLAG-TCF3_Ti_1	4.5792	0.4765	1743.63	1743.871	10208.4	1	1633.8	62.5	13	K.SGTGFGESYSLANPSIR.A
HsFlag-FLJ90652_2	3.3884	0.2409	1487.42	1487.652	3924.8	6	415.4	57.7	1	R.AGEDIPQPTIFNGK.L
HsFlag-FLJ90652_2	4.805	0.3546	1521.64	1522.788	7712.3	1	1649.9	80.8	13	K.TVQSIALLAHLAER.E
HsFLAG-ARP8_Ti_2	2.7908	0.2526	1522.25	1522.788	5977.2	2	497.2	57.7	1	K.TVQSIALLAHLAER.E
HsFLAG-TIP49a_Ti_	3.818	0.4227	2971.5	2972.332	4440.5	1	384.3	37.5	1	R.ENIWGPFLIISPASTLNNWHQEFTR.F
HsFlag-FLJ90652_2	2.9903	0.3165	1353.7	1354.511	3712.5	1	547.6	80	2	K.VLPYWGNPHDR.K
HsFLAG-ARP5_Ti_1	2.7789	0.1733	1482.68	1482.685	5044.9	6	365.2	59.1	1	K.VLPYWGNPHDRK.V
HsFlag-FLJ90652_2	4.272	0.3908	1597.2	1595.854	6822.6	1	1566.6	83.3	1	K.WQYMVLDEAQALK.S
HsFlag-FLJ90652_2	2.6233	0.2666	1048.19	1049.079	4779.8	1	334.5	68.8	1	K.DVENELSDK.I
HsFLAG-ARP5_Ti_1	4.0605	0.3029	2557.58	2557.842	9893.2	1	1371.9	35	1	K.DVENELSDKIEILMYCQLTSR.Q
HsFLAG-ARP5_Ti_1	2.8723	0.2476	1429.16	1429.585	5445.3	1	855.2	80	1	R.KVCNHPELFER.Q
HsFlag-FLJ90652_2	3.0491	0.2711	1300.74	1301.411	4864	1	924.7	88.9	6	K.VCNHPELFER.Q
HsFlag-FLJ90652_2	2.7725	0.1669	1473.85	1473.671	3511.6	9	222.9	54.5	1	R.QETWSPFHISLK.P
HsFLAG-TCF3_Ti_1	2.9816	0.224	1406.71	1406.624	5644.2	1	858.3	77.3	3	R.VLSPFAPDYIQR.S
HsFLAG-FLJ20309_	4.1612	0.3286	1461.61	1459.565	6695.5	1	1475.9	81.8	5	K.GINEESCFSFLR.F
HsFlag-FLJ90652_2	6.5722	0.4901	2203.27	2204.651	7279.3	1	2253.8	71.1	4	R.FIDISPAEMANLMLQGLLAR.W
HsFLAG-FLJ20309_	2.8818	0.128	1341.58	1341.382	5869.7	2	711.9	72.7	3	R.SWGAPEGESHQR.Y
HsFLAG-ARP5_Ti_1	6.4722	0.325	2796.2	2795.226	6256.5	1	1188.1	37	5	R.NKDFLLGVNFPLSFPNLCSCPLLK.S
HsFlag-FLJ90652_2	5.2761	0.4612	2552.76	2552.948	6731.6	1	829.7	47.6	30	K.DFLLGVNFPLSFPNLCSCPLLK.S
HsFLAG-ARP8_Ti_2	2.4928	0.1035	1065.13	1065.18	6729.9	1	738.6	75	5	K.SLVFSSHCK.A
HsFLAG-FLJ20309_	4.4438	0.4572	1446.54	1446.563	6552	1	1321.5	75	16	K.AVSGYSDQVVHQR.R
HsFLAG-ARP8_Ti_2	4.2602	0.3536	1862.8	1864.124	4412.5	1	831.8	70	11	R.CLLTELPSFLCVASPR.V
HsFLAG-TIP49a_Ti_	3.6018	0.3314	1511.02	1510.61	2550.3	2	395.4	70.8	1	R.VTAVPLDSYCNDR.S
HsFLAG-TCF3_Ti_1	4.155	0.2933	1942.56	1942.148	4704.3	1	1023	75	7	K.QCLLNGAPELAADWLNR.R
HsFLAG-ARP8_Ti_1	2.0786	0.3196	949.23	950.034	3634	1	257.3	68.8	1	K.ESLITDSGK.L
HsFLAG-FLJ20309_	4.4353	0.2437	1177.52	1177.429	5036.5	1	1547.8	94.4	12	K.LYALDVLLTR.L
HsFLAG-ARP5_Ti_1	3.9939	0.3397	1325.38	1325.55	8453	1	1787.8	80	10	R.NDIFVFLLSTR.A
HsFLAG-FLJ20309_	4.5598	0.3718	1732.44	1733.079	7321.4	1	1439	73.3	17	R.MVISGGNFKPDTLKPK.E
HsFLAG-FLJ20309_	5.0039	0.3179	1632.51	1631.817	6769.4	1	1813	84.6	13	K.EVVSLLLDDEELEK.K
HsFLAG-TCF3_Ti_1	3.166	0.3319	1221.5	1222.402	6821.1	1	591.4	53.8	4	R.KSTAGSAAAMAGAK.A

	HsFLAG-TCF3_Ti_1	2.9596	0.3463	1222.38	1222.402	6547.9	1	809.4	65.4	3 R.KSTAGSAAAMAGAK.A
	HsFlag-FLJ90652_2	2.2022	0.1637	1093.45	1094.228	5845.4	4	353	54.2	1 K.STAGSAAAMAGAK.A
	HsFlag-Ies6_293_Ti_	3.3522	0.2722	1095.28	1094.228	6694.5	1	1096.1	70.8	5 K.STAGSAAAMAGAK.A
	HsFLAG-ARP8_Ti_2	5.2807	0.5347	1850.41	1849.01	9469.7	1	1833.6	57.9	8 K.AGAAAASAAAYAAYGYNVSK.G
	HsFLAG-FLJ20309_	6.8488	0.571	3473.03	3471.889	6925	1	1410.3	30	22 K.GISASSPLQTSLVRPAGLADFGPSSASSPLSSPLSK.G
	HsFLAG-ARP5_Ti_1	4.4911	0.4716	1641.62	1641.883	7947.3	1	1337.4	67.9	12 K.NLHMTSSLAPDSLVR.K
gi|13376810|r	25	95	38.20%	836	93463	8.6	enhancer of polycomb 1 [Homo sapiens]			
*	HsFLAG-TIP49b_Ti_	3.8671	0.2835	1314.54	1314.571	3692.2	1	540.4	72.7	6 R.ALDASKPLPVFR.C
*	HsTIP60_Ti_102.149	2.2503	0.1449	1193.4	1194.33	8774.2	4	620.4	55	1 R.AISAQQVYGEK.R
*	HsTIP60_Ti_104.143	2.8205	0.2468	1350.13	1350.517	7720.8	3	679.4	63.6	1 R.AISAQQVYGEKR.D
*	HsMRGBP-FLAG_Ti_	4.3425	0.2336	3134.16	3133.499	8004	1	864.1	26.9	1 K.RDNMVIPVPEAESNIAYYESIYPGEFK.M
*	HsFLAG-TIP49b_Ti_	5.0459	0.494	3134.42	3133.499	9279.2	1	1297.7	44.2	1 K.RDNMVIPVPEAESNIAYYESIYPGEFK.M
*	HsYL1_Ti_102.3148.	3.4618	0.3167	2977.42	2977.312	6941.7	1	821.5	42	4 R.DNMVIPVPEAESNIAYYESIYPGEFK.M
*	HsFLAG-TIP49b_Ti_	3.5519	0.1152	2296.17	2296.668	9642.2	2	956	35.3	1 K.KMDICPLQFEEMIDRLEK.G
*	HsTIP60_Ti_101.145	3.9549	0.3046	1329.23	1329.453	4334.8	1	797.3	75	4 K.GSGQQPVSLQEAK.L
*	HsTIP60_Ti_106.236	3.2611	0.224	1357.32	1357.59	5116.9	1	1036.1	85	4 K.LLLKEDDELIR.E
*	HsTIP60_Ti_102.181	4.1815	0.4093	1430.05	1429.486	6572.6	1	982.9	70.8	4 R.DGSSTNDPYVAFR.R
*	HsMRGBP-FLAG_Ti_	2.0736	0.118	1018.08	1018.3	6222.3	4	460	68.8	1 R.AVTILEMIK.R
*	HsFLAG-TIP49b_Ti_	3.3117	0.2834	2247.44	2247.505	5942.5	1	418.7	41.7	1 K.RYNLGDYNGEIMSEVMAQR.Q
*	HsFLAG-TIP49b_Ti_	3.8727	0.3383	2373.81	2375.832	4773.3	1	540.3	47.5	7 R.QPMKPTYAIPIIPITNSSQFK.H
*	HsH2AZ-FLAG_293_	5.3531	0.5265	2366.34	2367.707	5040.9	1	918.3	54.3	8 K.VLPSSAAATPQQTSPAALPVFNAK.D
*	HsMRGBP-FLAG_Ti_	4.2108	0.3756	2368.99	2367.707	7185.3	1	1293.3	37	2 K.VLPSSAAATPQQTSPAALPVFNAK.D
*	HsFLAG-TIP49b_Ti_	4.8531	0.3856	2578.23	2578.769	6971.9	1	1088.1	52.4	5 K.AGCQYYAPHLDQTGNWPWTSPK.D
*	HsFLAG-TIP49b_Ti_	3.3727	0.2012	1142.63	1143.369	9005.7	8	919.2	72.2	1 K.DLSQILVNIK.S
*	HsTIP60_Ti_104.291	3.7366	0.2252	1142.68	1143.369	7815	3	1525.8	83.3	10 K.DLSQILVNIK.S
*	HsMRGBP-FLAG_Ti_	4.219	0.4133	1746.55	1746.751	6420.2	1	1419.6	71.4	4 R.TPSLHDSDNDELSCR.K
*	HsMRGBP-FLAG_Ti_	4.7054	0.4721	1874.75	1874.925	8536.2	1	1443.2	66.7	4 R.TPSLHDSDNDELSCRK.L
*	HsFLAG-TIP49b_Ti_	5.9091	0.3649	3052.48	3053.335	10600.8	1	2682.9	37.5	2 K.SSSGSAHFAFTAEQYQQHQQQLALMQK.Q
*	HsMRGBP-FLAG_Ti_	5.8506	0.4806	2474.56	2474.788	7994.8	1	1636.8	56.5	13 K.TLDSASAQFAASALVTSEQLMGFK.M
*	HsMRGBP-FLAG_Ti_	4.2404	0.3802	1911.69	1911.209	9070.9	1	1233.1	58.3	4 R.LTVPSSVATVNSIAPINAR.H
*	HsH2AZ-FLAG_293_	3.3865	0.2041	1133.96	1133.256	7720.9	1	1261.7	80	4 K.LAAAANCQVSK.V
*	HsTIP60_Ti_102.142	3.1052	0.2337	1217.33	1217.321	6282.6	1	1695	86.4	2 K.VPSSSSVDSVPR.E
gi|13904870|r	7	184	37.70%	204	22876	9.7	ribosomal protein S5 [Homo sapiens]			
*	HsFlag-NUFIP_Ti_1	5.0929	0.4385	2322.76	2324.549	8044.2	1	1326.2	55.3	139 K.WSTDDVQINDISLQDYIAVK.E
*	HsFlag-NUFIP_Ti_1	2.4105	0.1623	900.59	901.013	5426.2	2	331.6	71.4	2 K.YLPHSAGR.Y
*	HsFlag-NUFIP_Ti_1	3.5391	0.3258	1178.14	1178.428	8616.1	1	1327.5	88.9	5 R.LTNSMMMHGR.N
*	HsFLAG-ARP8_Ti_2	2.6712	0.1626	1139.62	1141.316	6693.6	2	687.8	77.8	1 R.RQAVDVSPLR.R
*	HsFlag-NUFIP_Ti_11	5.0773	0.419	1658.81	1658.91	7087	1	1472.5	76.9	9 R.RVNQAIWLLCTGAR.E
*	HsFlag-NUFIP_Ti_1	5.2076	0.3615	1502.42	1502.723	7463.1	1	1803.7	83.3	12 R.VNQAIWLLCTGAR.E
*	HsFlag-NUFIP_Ti_1	5.1702	0.3795	1632.52	1632.818	9139.2	1	2297.1	75	16 K.TIAECLADELINAAK.G
gi|54112117|r	31	126	37.30%	1304	145830	7.1	splicing factor 3b, subunit 1 isoform 1 [Homo sapiens]			
*	HsARP6-FLAG_Ti_1	2.7648	0.1878	1226.97	1226.375	6592.2	1	1180.1	75	1 K.VVNGAAASQPPSK.R
*	HsARP6-FLAG_Ti_1	3.0865	0.2831	1517.83	1516.607	8607.8	1	784	57.7	1 R.WDQTADQTPGATPK.K

*	HsFlag-VPS71_Ti_1	4.9735	0.4614	2010.13	2011.202	8427	1	1672.6	64.7	1	K.KLSSWDQAETPGHTPSLR.W
*	HsFlag-NUFIP_Ti_2	2.7184	0.2416	1883.42	1883.027	8796.8	1	599.5	46.9	2	K.LSSWDQAETPGHTPSLR.W
*	HsFlag-NUFIP_Ti_1	4.4317	0.4299	1831.93	1833.013	7250.7	1	2058.1	73.5	7	K.IWDPTPSHTPAGAATPGR.G
*	HsFLAG-p53-DNA-D	2.5287	0.2575	1733.7	1734.782	4962.6	4	273.1	50	2	R.GDTPGHATPGHGGATSSAR.K
*	HsFLAG-p53-DNA-D	3.3365	0.4056	1467.89	1468.525	5543.2	1	565.2	65.4	1	R.DTPGHGSGWAETPR.T
*	HsFlag-VPS71_Ti_1	3.7346	0.3424	1746.42	1746.828	7579.8	1	1018.6	55.9	1	R.TDRGGDSIGETPTPGASK.R
*	HsFLAG-p53-DNA-D	5.4149	0.4531	2302.46	2303.552	9804.2	1	1569.1	54.8	4	K.SRWDETPASQMGGSTPVLTPGK.T
*	HsFlag-DPCD_Ti_20	2.9145	0.2089	2061.8	2060.286	9366.5	1	631.4	47.4	1	R.WDETPASQMGGSTPVLTPGK.T
*	HsFLAG-FLJ20729_	4.053	0.4015	2111.62	2112.319	10234.2	1	981.3	50	3	R.NRPLSDEELDAMFPEGYK.V
*	HsFlag-VPS71_Ti_1	3.0296	0.2991	2262.33	2262.56	9379.8	1	406.9	35	1	K.LTATPTPLGGMTGFHMQTEDR.T
*	HsFlag-VPS71_Ti_1	3.9897	0.2005	2639.01	2638.893	7430.3	3	591.1	40.9	3	K.SVNDQPSGNLPFLKPDDIQYFDK.L
*	HsFlag-VPS71_Ti_1	5.2549	0.2786	1804.36	1802.973	5545.5	1	1345.9	76.7	8	K.LLVDVDESTLSPEEQK.E
*	HsFlag-NUFIP_Ti_11	5.6081	0.3452	3043.63	3044.496	9426.9	1	1343.5	30.8	3	K.AREFGAGPLFNQILPLLMSPTLEDQER.H
*	HsFLAG-p53-DNA-D	3.9249	0.3191	2816.19	2817.229	5292.7	1	448.8	37.5	3	R.EFGAGPLFNQILPLLMSPTLEDQER.H
*	HsFLAG-p53-DNA-D	5.5995	0.2944	2035.97	2035.388	5545.2	1	1600.2	78.1	19	K.ILVVIEPLLIDEDYYAR.V
*	HsFLAG-FLJ20309_	4.2509	0.2843	1915.04	1915.37	5127.2	1	989.5	61.1	19	R.AFAVVASALGIPSLLPFLK.A
*	HsARP6-FLAG_Ti_1	4.9002	0.4203	1915.24	1915.37	5951.6	1	1154.3	41.7	2	R.AFAVVASALGIPSLLPFLK.A
*	HsFLAG-Lin9_Ti_20	4.5486	0.3134	2047.54	2047.519	7556.5	1	1923.7	70.6	1	K.IVQQIAILMGCAILPHLR.S
*	HsFlag-VPS71_Ti_1	5.8598	0.4476	1837.78	1838.068	8393.6	1	2225.2	76.7	7	R.SLVEIIEHGLVDEQQK.V
*	HsARP6-FLAG_Ti_1	3.7942	0.2935	3248.67	3248.787	7104.8	1	721.8	24.2	1	R.TISALAIAALAEAATPYGIESFDSVLKPLWK.G
*	HsFLAG-p53-DNA-D	4.547	0.3992	2237.43	2238.563	4847.2	1	947.1	63.9	5	K.AIGYLIPLMDAEYANYYTR.E
*	HsFlag-VPS71_Ti_1	3.3181	0.2145	1603.65	1603.871	3721.7	1	982.4	83.3	4	K.PYLPQICGTVLWR.L
*	HsFLAG-FLJ20729_	4.5978	0.2435	3163.78	3164.727	5980.5	1	685.6	29.5	1	K.LMGHLGVVLYEYLGEEYPEVLGSILGALK.A
*	HsFLAG-ARP6_Ti_1	3.211	0.1882	1081.85	1082.349	7738.9	1	1600.9	88.9	3	K.AIVNVIGMHK.M
*	HsFlag-VPS71_Ti_1	3.6966	0.1027	1278.49	1278.541	3708.8	2	913.4	88.9	1	R.ICFELLELLK.A
*	HsFLAG-ARP6_Ti_1	3.1908	0.2769	1341.33	1341.553	5964.8	1	890.2	68.2	2	R.RATVNTFGYIAK.A
*	HsFlag-NUFIP_Ti_1	5.6894	0.3705	1689.56	1689.996	10203.7	1	2428.4	73.3	17	K.AIGPHDVLATLLNNLK.V
*	HsFLAG-FLJ20729_	3.5281	0.4328	1997.66	1999.286	6050.2	1	824.4	59.4	1	K.DYIYAVTPLLEDALMDR.D
*	HsFLAG-Lin9_Ti_20	3.2109	0.3288	2194.07	2195.483	10138.8	1	553.2	41.7	1	K.IYNSIYIGSQDALIAHYPR.I
gi|HsSRCAP	123	961	37.00%	3170	337678	5.8	current presumptive full-length human SRCAP [Homo sapiens]				
	HsFlag-VPS71_Ti_1	2.561	0.2774	1085.37	1084.174	4658.7	7	482.2	66.7	1	K.SHAEIAEQAK.H
	HsYL1_Ti_106.1976.	5.6175	0.457	2050.85	2050.192	6598.1	1	2092.3	76.5	11	K.SHAEIAEQAKHEAEIETR.I
	HsFlag-VPS71_Ti_1	5.7387	0.4556	2672.06	2672.854	7846	1	1836.7	60	9	K.GHWDYLCEEMQWLSADFAQER.R
	HsFlag-VPS71_Ti_1	4.1515	0.2924	2673.82	2672.854	6051.4	1	660.2	31.2	3	K.GHWDYLCEEMQWLSADFAQER.R
	HsH2AZ-FLAG_293_	5.3539	0.4085	1701.79	1699.944	6503.9	1	1889.6	78.6	10	K.ALDLHLDFIVGQTEK.Y
	HsH2AZ-FLAG_293_	5.6765	0.3709	1880.66	1882.078	7943.6	1	1937.3	75	17	K.YSDLLSQSLNQPLTSSK.A
	HsH2AZ-FLAG_293_	4.7889	0.4789	2029.33	2029.137	4745	1	784.7	54.8	11	K.AGSSPCLGSSSAASSPPPPASR.L
	HsH2AZ-FLAG_293_	6.0534	0.4174	4481.32	4483.361	4999.4	1	996.9	29.1	5	E
	HsSrcap_Ti_202.340	3.2729	0.1679	1298.8	1298.479	3825.2	5	543.9	75	14	R.EGELPLEELLR.S
	HsFlag-VPS71_Ti_1	2.0372	0.134	1299.7	1298.479	2415.9	8	154.5	60	2	R.EGELPLEELLR.S
	HsYL1-FLAG_Ti_20	5.3459	0.4086	2900.62	2901.156	6375.6	1	1132.3	34.6	6	R.DGPEEGAEEEPPQVLEIKPPPSAVTQR.N
	HsYL1-FLAG_Ti_20	3.1465	0.0819	2901.68	2901.156	5341.9	2	377.6	34.6	1	R.DGPEEGAEEEPPQVLEIKPPPSAVTQR.N
	HsYL1-FLAG_Ti_20	5.7219	0.4571	2338.15	2339.431	7143.7	1	1397.8	56.5	12	R.DEEQSEADAGSGPPTPGPTTLGPK.K

HsH2AZ-FLAG_293_	5.7209	0.3265	1685.38	1685.915	6526.6	1	2643	83.3	18	K.KEITDIAAAAESLQPK.G
HsH2AZ-FLAG_293_	4.2573	0.117	1686.22	1685.915	7070.2	1	2371	51.7	2	K.KEITDIAAAAESLQPK.G
HsH2AZ-FLAG_293_	5.1173	0.1921	1557.23	1557.741	5532.6	1	1620.6	78.6	17	K.EITDIAAAAESLQPK.G
HsFLAG-TIP49a_Ti_	3.596	0.2963	1557.41	1557.741	3532	1	555.4	71.4	10	K.EITDIAAAAESLQPK.G
HsH2AZ-FLAG_293_	2.1068	0.2388	1081.27	1082.242	7689.8	4	513.2	66.7	1	K.GYTLATTQVK.T
HsH2AZ-FLAG_293_	2.8829	0.2279	1082.23	1082.242	5166.6	1	836.1	83.3	4	K.GYTLATTQVK.T
HsFlag-VPS71_Ti_1	4.8006	0.4047	2025.9	2026.314	4265.1	1	1320.1	76.7	12	R.EYQHIGLDWLVTMYEK.K
HsFlag-VPS71_Ti_1	4.1045	0.1388	2028.27	2026.314	5581.3	2	1048.3	48.3	2	R.EYQHIGLDWLVTMYEK.K
HsFLAG-TIP49b_Ti_	3.8366	0.3906	1458.54	1459.744	6234.4	1	768.8	61.5	5	K.KLNGILADEMGLGK.T
HsFLAG-TIP49b_Ti_	5.6703	0.3117	1459	1459.744	7242.6	1	2031	84.6	11	K.KLNGILADEMGLGK.T
HsH2AZ-FLAG_293_	5.0063	0.439	1700.25	1698.967	5635.8	1	1299.3	71.4	34	K.TIQTISLLAHLACEK.G
HsFlag-VPS71_Ti_1	2.8294	0.1959	981.26	981.108	5106	1	822.5	100	1	K.RWCPSFK.I
HsH2AZ-FLAG_293_	2.2104	0.1518	1056.32	1057.235	7899.5	8	558.1	62.5	2	K.ILTYYGAQK.E
HsYL1_Ti_104.1423.	2.8489	0.1776	1344.63	1342.538	5387.5	1	838.9	75	1	K.ILTYYGAQKER.K
HsFLAG-TIP49b_Ti_	3.4783	0.3347	1437.39	1437.604	8184.3	1	992.6	68.2	1	K.PNAFHVCITSYK.L
HsFlag-VPS71_Ti_1	3.3616	0.3664	1226.56	1227.409	6017.2	1	1166.6	88.9	16	K.LVLQDHQAFR.R
HsFLAG-TIP49b_Ti_	1.9468	0.1013	1226.57	1227.409	4527.2	8	251.5	55.6	3	K.LVLQDHQAFR.R
HsYL1_Ti_102.1919.	4.0643	0.1561	1319.69	1320.528	6869.6	2	1228.7	80	14	R.YLILDEAQNIK.N
HsH2AZ-FLAG_293_	3.9574	0.2078	1320.12	1320.528	5846.2	2	1699.9	90	15	R.YLILDEAQNIK.N
HsH2AZ-FLAG_293_	3.7127	0.2475	1393.04	1393.545	5397	1	1179.3	90	29	R.WQSLLNFNSQR.R
HsYL1_Ti_102.3188.	5.4738	0.4734	2629	2629.901	6896.4	1	1136.8	50	49	K.EWFSNPLTGMIEGSQEYNEGLVK.R
HsFlag-VPS71_Ti_1	4.7562	0.3791	2631.23	2629.901	8616.9	1	1350.4	35.2	2	K.EWFSNPLTGMIEGSQEYNEGLVK.R
HsYL1_Ti_106.1854.	2.0021	0.0822	944.62	945.109	4414.1	2	364.1	75	1	K.KYEHVIR.C
HsH2AZ-FLAG_293_	2.5665	0.2329	945.36	945.109	4375.8	2	736.5	91.7	1	K.KYEHVIR.C
HsFlag-VPS71_Ti_1	2.3506	0.3791	1593.51	1594.743	2410.2	1	105.7	50	1	R.CLYDDFMAQTTTK.E
HsH2AZ-FLAG_293_	4.5654	0.4831	1594.67	1594.743	6195.3	1	1835.2	87.5	9	R.CLYDDFMAQTTTK.E
HsH2AZ-FLAG_293_	5.4697	0.3981	2263.35	2264.636	3717.5	1	1149.8	67.5	24	R.PVTSPFITPGICFSTASLVLR.A
HsFlag-VPS71_Ti_1	5.0732	0.4421	2265.27	2264.636	6759.2	1	1316.4	40	8	R.PVTSPFITPGICFSTASLVLR.A
HsFLAG-TIP49b_Ti_	2.2874	0.2259	1036.37	1037.164	3744.4	3	321.3	62.5	3	R.ATDVHPLQR.I
HsFLAG-ARP6_Ti_1	3.3128	0.2472	1037.36	1037.164	3729.8	2	785.5	87.5	8	R.ATDVHPLQR.I
HsFLAG-TIP49b_Ti_	3.1482	0.1889	1592.1	1592.854	3576.1	1	492.9	69.2	1	R.IDMGRFDLIGLEGR.V
HsH2AZ-FLAG_293_	3.1687	0.1672	1020.25	1020.173	4155.1	4	829.6	87.5	5	R.FDLIGLEGR.V
HsH2AZ-FLAG_293_	3.952	0.2758	1454.44	1454.626	4205.5	1	1057	77.3	13	R.VSRYEADTFLPR.H
HsFlag-VPS71_Ti_1	3.5125	0.2261	1455.48	1454.626	8258.8	3	1220.5	47.7	1	R.VSRYEADTFLPR.H
HsFlag-VPS71_Ti_1	2.3929	0.1922	1111.61	1112.227	3642.2	3	391.9	75	1	R.YEADTFLPR.H
HsH2AZ-FLAG_293_	3.6929	0.332	1112.65	1112.227	4653.4	2	988.4	93.8	8	R.YEADTFLPR.H
HsH2AZ-FLAG_293_	2.8901	0.2487	1700.17	1701.019	2922.5	1	390.6	60	2	R.VLLEVATAPDPPPRPK.P
HsH2AZ-FLAG_293_	4.0388	0.3007	2025.1	2025.442	4936.4	3	683.5	40.3	3	R.VLLEVATAPDPPPRPKPVK.M
HsH2AZ-FLAG_293_	1.9708	0.084	812.36	813.046	3593.6	5	447.2	75	2	R.MLQPVPK.Q
HsFLAG-ARP6_Ti_2	1.8492	0.0952	997.5	998.17	4149.9	5	252.1	75	1	R.TVVVVNNPR.A
HsVPS71-FLAG_Ti_	2.3572	0.1092	1350.81	1351.586	4172.4	7	290.8	50	2	R.LSPAPPPGSSSLLK.P
HsFLAG-TIP49a_Ti_	2.6062	0.1391	1144.46	1144.375	4537.3	1	383.9	72.2	2	R.LILSPDMQAR.L
HsFLAG-TIP49b_Ti_	5.0998	0.1539	2607.76	2607.97	7643.6	1	1167	48.1	10	R.LPSGEVVSIGQLASLAQRPVANAGGSK.P

HsFlag-VPS71_Ti_1(	6.0224	0.2725	2608.78	2607.97	5541.8	1	962.3	32.7	12	R.LPSGEVVSIGQLASLAQRPVANAGGSK.P
HsH2AZ-FLAG_293_	6.2265	0.1553	3733.77	3735.278	6663.7	1	885.6	26.4	3	R.LPSGEVVSIGQLASLAQRPVANAGGSKPLTFQIQGNK.L
HsFLAG-TIP49a_Ti_	3.0643	0.198	1145.48	1146.332	4823.4	2	434.2	66.7	3	K.PLTFQIQGNK.L
HsFLAG-TIP49a_Ti_	3.7088	0.2691	1146.52	1146.332	5022.6	1	748.1	77.8	7	K.PLTFQIQGNK.L
HsH2AZ-FLAG_293_	2.9223	0.1624	959.24	959.134	5458.3	2	962.5	87.5	2	K.LTLTGAQVR.Q
HsFlag-VPS71_Ti_1(	3.8077	0.3133	1726.26	1727.09	2989.6	1	408	60	6	R.PLQMPPTMVNNTGVVK.I
HsSrcap_Ti_203.177	3.5013	0.3981	1583.67	1584.81	4943.5	1	712.2	69.2	6	R.LPVSKDEPDTLTLR.S
HsFLAG-TIP49b_Ti_	4.5561	0.3786	1583.97	1584.81	6906.6	1	1429.1	76.9	27	R.LPVSKDEPDTLTLR.S
HsH2AZ-FLAG_293_	4.0447	0.2823	1584.52	1584.81	4519.8	2	696.1	44.2	4	R.LPVSKDEPDTLTLR.S
HsYL1-FLAG_Ti_206	2.8279	0.179	945.47	945.112	5010.2	2	818.5	92.9	2	R.RQPPPPPR.S
HsFLAG-TIP49b_Ti_	3.5172	0.2124	1327.34	1328.461	8925.6	2	919.8	65	14	R.SPFYLDSLEEK.R
HsFlag-VPS71_Ti_1(	3.547	0.3155	1328.44	1328.461	5598.5	1	1185.5	80	17	R.SPFYLDSLEEK.R
HsH2AZ-FLAG_293_	3.526	0.337	1483.76	1484.649	7348.7	1	1063	77.3	1	R.SPFYLDSLEEKR.K
HsH2AZ-FLAG_293_	5.7689	0.476	3853.46	3853.376	6112.4	1	876	28.6	19	R.IFQLSEAHGALAPVYGTEVLDFCTLPQPVASPIGPR.S
HsH2AZ-FLAG_293_	4.4647	0.3893	2042.97	2043.205	8338.6	1	1330.3	41.2	6	R.SPGPSHPTFWTYTEAAHR.A
HsFLAG-TIP49b_Ti_	3.8212	0.4231	2045.72	2043.205	5309.2	1	579.5	55.9	7	R.SPGPSHPTFWTYTEAAHR.A
HsSrcap_Ti_202.233	3.471	0.1128	1215.6	1216.377	3835.9	7	438.9	77.8	4	R.LDQLSEIIER.F
HsH2AZ-FLAG_293_	4.2018	0.0982	1216.38	1216.377	6405.9	1	1452.2	94.4	7	R.LDQLSEIIER.F
HsFlag-VPS71_Ti_1(	5.1857	0.3581	1775.72	1774.974	7308	1	1894.1	78.6	18	R.QAAFQEQLASELWPR.A
HsH2AZ-FLAG_293_	4.8083	0.3004	1775.85	1774.974	6528.3	1	1875.7	53.6	3	R.QAAFQEQLASELWPR.A
HsFlag-VPS71_Ti_1(	2.1839	0.2382	996.49	997.102	5154.6	2	489.7	71.4	2	R.LIQYDCGK.L
HsH2AZ-FLAG_293_	3.4198	0.1753	1027.39	1027.296	4544.8	1	950.3	93.8	15	K.LQTLAVLLR.Q
HsScrap_Ti_103.234	3.2054	0.2633	1110.68	1109.372	5683.1	1	1098.9	93.8	2	R.VLIFTQMTR.M
HsFlag-VPS71_Ti_1(	3.0901	0.2743	1313.89	1313.552	6675.3	1	809.1	77.8	1	K.RIFCFILSTR.S
HsFLAG-TIP49a_Ti_	2.0409	0.1108	1156.38	1157.364	5054.3	2	413.5	75	1	R.IFCFILSTR.S
HsH2AZ-FLAG_293_	3.7138	0.2508	1157.28	1157.364	5783.3	1	1422	93.8	21	R.IFCFILSTR.S
HsFlag-VPS71_Ti_1(	5.1023	0.3423	2124.86	2123.449	7600.3	1	1812.9	69.4	5	K.RMLGDMAIEGGNFTTAYFK.Q
HsFLAG-TIP49a_Ti_	6.1078	0.4235	1967.62	1967.262	4835.2	1	1452.5	73.5	6	R.MLGDMAIEGGNFTTAYFK.Q
HsVPS71-FLAG_Ti_	3.4614	0.3293	3152.76	3152.361	3562.3	1	270.4	33.9	4	R.ELFDMPLEEPSSSSVPSAPEEEEETVASK.Q
HsFLAG-TIP49b_Ti_	2.4198	0.1126	1368.4	1369.53	2235.8	1	169.6	75	1	K.QTHILEQALCR.A
HsFLAG-TIP49b_Ti_	2.6946	0.1643	1369.07	1369.53	6513.4	7	579.8	70	1	K.QTHILEQALCR.A
HsYL1-FLAG_Ti_206	5.7286	0.4972	3838.63	3839.95	6508.2	1	806.8	25	9	K.AEQVAELAEFNENDGFPAGEGEEAGRPGAEDEEMSR.A
HsH2AZ-FLAG_293_	4.7395	0.2131	1910.8	1911.163	6510.5	1	1675.5	51.6	5	R.AEQEIAALVEQLTPIER.Y
HsFlag-VPS71_Ti_1(	4.5835	0.1698	1911.93	1911.163	4578.5	1	929.8	65.6	4	R.AEQEIAALVEQLTPIER.Y
HsYL1-FLAG_Ti_203	2.6096	0.1046	1281.78	1280.42	8171.8	1	1199.5	80	1	K.FLEASLEEVSR.E
HsH2AZ-FLAG_293_	5.427	0.252	1779.6	1779.985	6844.6	1	2591.5	89.3	27	K.FLEASLEEVSREELK.Q
HsH2AZ-FLAG_293_	2.7294	0.1422	1131.04	1131.188	4185.5	1	674.4	94.4	2	K.QAEEQVEAAR.K
HsH2AZ-FLAG_293_	7.3506	0.4836	3847.36	3846.937	10449.1	1	2448.5	31.4	13	K.DLDQAKEEVFRLPQEEEEGPGAGDESSCGTGGGTHR.R
HsFLAG-TIP49a_Ti_	6.7335	0.438	3176.49	3176.216	9335.2	1	1463.9	31	3	K.EEVFRLPQEEEEGPGAGDESSCGTGGGTHR.R
HsH2AZ-FLAG_293_	5.2233	0.3802	1918.69	1919.064	7170.1	1	2438.2	54.4	16	R.AETQGANHTPVISAHQTR.S
HsSrcap_Ti_205.149	4.8344	0.4506	1918.89	1919.064	5635.8	1	1008.6	58.8	23	R.AETQGANHTPVISAHQTR.S
HsH2AZ-FLAG_293_	4.0393	0.2913	1623.37	1622.943	6141.7	1	1336	75	12	K.DLLPVAVEILPVSEK.N
HsFLAG-TIP49b_Ti_	4.0524	0.2877	3991.69	3991.315	4599.2	1	460.6	23.1	5	.R

	HsFlag-VPS71_Ti_1(	2.5566	0.1701	891.36	890.969	5077.5	6	895.3	92.9	1	R.TSADVEIR.G
	HsYL1-FLAG_Ti_20(	3.254	0.2884	1337	1334.478	4870	1	640.4	65.4	8	R.GQGTGRPGQPPGPK.V
	HsFLAG-ARP6_Ti_2	1.945	0.1342	916.48	917.09	7651.4	6	752	78.6	2	R.LVTVVEEK.E
	HsH2AZ-FLAG_293_	2.8844	0.2121	917.15	917.09	2513.2	2	518.1	92.9	2	R.LVTVVEEK.E
	HsScrap_Ti_102.188	4.6303	0.4417	2114.84	2115.305	4055.8	1	919.8	56.8	19	R.GAASTLVPGVSETSASPGSPSVR.S
	HsYL1-FLAG_Ti_20(	4.5521	0.3236	3438.46	3436.784	6520.9	1	712.8	25.8	1	R.SMSGPESSPPIGGPCEAAPSSSLPTPPQQPFIAR.R
	HsSrcap_Ti_203.262	6.1277	0.4553	2671.35	2672.01	7951.5	1	2648.8	61.1	15	R.HIELGVTGGGSPENGDGALLAITPPAVK.R
	HsFlag-VPS71_Ti_1(	2.1684	0.34	1103.48	1104.202	5483.4	5	399.1	55	3	R.GVDEAPSSTLK.G
	HsH2AZ-FLAG_293_	2.7176	0.1568	1104.28	1104.202	3657.3	6	594.2	75	1	R.GVDEAPSSTLK.G
	HsYL1_Ti_103.1574.	5.3792	0.4394	2102.25	2101.238	3960.6	1	695.3	60	18	K.ARDLPIPGTISSAGDGNSESR.T
	HsH2AZ-FLAG_293_	5.0941	0.2758	2102.66	2101.238	7415.3	1	1749.1	42.5	4	K.ARDLPIPGTISSAGDGNSESR.T
	HsYL1_Ti_102.1759.	4.9499	0.3528	1875.05	1873.971	5555.9	1	721.2	61.1	8	R.DLPIPGTISSAGDGNSESR.T
	HsFlag-VPS71_Ti_1(	3.6027	0.1689	2386.67	2387.618	7316.9	1	601.4	40.5	3	R.PSQLPVLDRDSTSVLESCGLGR.R
	HsH2AZ-FLAG_293_	4.6056	0.265	2388.1	2387.618	4094.5	1	828.7	41.7	7	R.PSQLPVLDRDSTSVLESCGLGR.R
	HsYL1_Ti_101.1960.	4.1061	0.3249	1383.11	1381.449	5604.8	1	919.9	70.8	3	R.DSTSVLESCGLGR.R
	HsYL1_Ti_104.1455.	3.0463	0.2427	1075.66	1075.271	6111.2	1	1220.6	87.5	4	R.LRLEAEGMR.G
	HsFlag-VPS71_Ti_1(	3.7486	0.3223	1538.26	1536.812	5326.6	1	901.5	73.1	23	R.LRPGSLVPPLETEK.L
	HsFlag-VPS71_Ti_1(	2.9791	0.291	1237.66	1238.432	2852.4	3	287.4	65.4	2	K.RAGAPVGGSPGLAK.R
	HsH2AZ-FLAG_293_	3.806	0.3005	1238.52	1238.432	6272	1	940.5	69.2	6	K.RAGAPVGGSPGLAK.R
	HsH2AZ-FLAG_293_	2.4172	0.3561	1081.32	1082.245	5007.1	1	513.8	58.3	4	R.AGAPVGGSPGLAK.R
	HsFlag-VPS71_Ti_1(	3.003	0.3169	1082.48	1082.245	3782.4	2	575.2	70.8	2	R.AGAPVGGSPGLAK.R
	HsFlag-VPS71_Ti_1(	3.5469	0.288	1190.4	1189.271	6551.4	1	1496.8	90	4	R.LVGTTNQGDQR.I
	HsH2AZ-FLAG_293_	3.4518	0.3871	1433.56	1434.595	2997.6	1	431.3	67.9	16	R.SSAPPSLAGPAVSHR.G
	HsSrcap_Ti_205.163	2.1125	0.2718	1433.61	1434.595	5988	1	353.7	46.4	1	R.SSAPPSLAGPAVSHR.G
gi|4506679|re	7	75	37.00%	165	18898	10.2	ribosomal protein S10 [Homo sapiens]				
	HsFLAG-ARP8_Ti_2	3.6829	0.0914	1109.69	1110.382	4283.8	1	909.8	87.5	5	R.IAIYELLFK.E
*	HsFlag-NUFIP_Ti_1(	2.1028	0.2022	809.52	809.897	2610.2	9	302.1	83.3	3	K.HPELADK.N
*	HsFlag-NUFIP_Ti_11	5.6023	0.4669	2003.85	2004.255	7665.1	1	2992.9	89.3	22	R.HFYWYLTNEGIQYLR.D
*	HsFlag-NUFIP_Ti_11	5.2927	0.3262	2004.24	2004.255	9248.6	1	2533.4	57.1	13	R.HFYWYLTNEGIQYLR.D
*	HsFlag-NUFIP_Ti_1(	2.7159	0.0873	1734.8	1735.036	3007	7	374.9	57.1	3	R.DYLHLPPEIVPATLR.R
	HsFlag-NUFIP_Ti_1(	3.7736	0.2264	1570.77	1570.702	5692.1	1	1108.6	51.8	2	K.KAEAGAGSATEFQFR.G
	HsFlag-NUFIP_Ti_1(	4.4652	0.3688	1573.09	1570.702	7596.9	1	1655.3	75	27	K.KAEAGAGSATEFQFR.G
gi|5031653|re	6	24	36.90%	225	26131	5.6	breast carcinoma amplified sequence 2 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.9038	0.4373	2370.88	2371.623	4169.9	1	406.2	50	3	K.NYLSYLTAPDYSAFETDIMR.N
*	HsFlag-NUFIP_Ti_2(	4.1134	0.3311	1333.35	1333.487	6508.3	1	1478.3	86.4	8	K.RYELPAPSSGQK.N
*	HsFlag-NUFIP_Ti_2(	4.0189	0.416	1825.7	1826.08	8868.6	1	1035.9	57.1	2	K.VYNENLVHMIEHAQK.E
*	HsFlag-NUFIP_Ti_2(	2.6567	0.1116	1210.41	1210.338	5114.2	1	623.6	81.2	1	K.HIQDLNWQR.K
*	HsFlag-NUFIP_Ti_2(	4.819	0.3912	1678.57	1678.944	7132.4	1	1444.5	73.1	3	K.LREMESNWVSLVSK.N
*	HsFlag-NUFIP_Ti_2(	4.3089	0.1691	1590.88	1591.845	7863.2	1	1775.7	79.2	7	R.TIVQLENEIYQIK.Q
gi|41406064|r	52	139	36.80%	1976	228997	5.5	myosin, heavy polypeptide 10, non-muscle [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	3.9426	0.3192	1650.86	1649.844	5190.6	1	927.2	71.4	1	R.AVIYNPATQADWTAK.K
*	HsFLAG-BC014022_	3.0212	0.1678	1128.14	1128.36	6564.5	1	1101.3	87.5	3	K.KLVWIPSER.H
*	HsFLAG-Lin9_Ti_20	2.5175	0.2233	1373.96	1374.496	7814.3	5	569.5	63.6	1	R.HGFEAASIKEER.G

	HsFLAG-ARP6_Ti_1	4.3483	0.3981	2286.24	2287.556	7047.8	1	714	47.4	1	K.VEDMAELTCLNEASVLHNLK.D
*	HsFLAG-ARP6_Ti_1	3.0244	0.4114	1755.14	1756.026	4579.7	1	593.8	65.4	2	K.NLPIYSENIIEMYR.G
	HsFLAG-Lin9_Ti_20:	3.8076	0.3868	2125.48	2126.205	8110.7	1	708	44.7	1	R.EDQSILCTGESGAGKTENTK.K
*	HsFLAG-BC014022_	4.3103	0.4181	1454.17	1453.684	7405.9	1	1123	70.8	8	K.VIQYLAHVASSHK.G
*	HsFLAG-Lin9_Ti_20:	4.3101	0.3539	1743.57	1744.001	6147.2	1	1311.4	73.3	3	R.QLLQANPILESFGNAK.T
	HsFLAG-ARP6_Ti_1	4.8327	0.3425	2373.85	2373.708	5896	1	1097.7	55	5	R.INFDVTGYIVGANIETYLLEK.S
*	HsFLAG-ARP6_Ti_1	2.7996	0.2079	1961.61	1962.258	8629.4	1	615.9	46.9	1	R.TFHIFYQLLSGAGEHLK.S
*	HsFLAG-ARP6_Ti_1	4.1063	0.3475	1441.39	1441.583	7057.9	1	1384.8	77.3	3	K.SDLLLEGFNNYR.F
*	HsFLAG-Lin9_Ti_20:	3.2736	0.2531	1677.56	1677.897	4004.9	1	579.2	64.3	3	R.FLSNGYIPIPGQQDK.D
*	HsFLAG-ARP6_Ti_1	4.3862	0.478	1524.96	1525.788	6448.5	1	1695.5	80.8	3	K.VVSSVLQFGNISFK.K
*	HsFLAG-Lin9_Ti_20!	3.3398	0.2523	1653.58	1653.962	7007.1	1	814.5	60.7	1	K.VVSSVLQFGNISFKK.E
*	HsFLAG-ARP6_Ti_1	4.0471	0.3311	1722.79	1722.039	6276.4	1	1270.4	73.1	1	K.LCHLLGMNVMEFTR.A
	HsFLAG-ARP6_Ti_1	3.9279	0.1225	2468.62	2468.789	8469.2	1	1635.8	41.7	1	K.LQQLFNHTMFILEQEEYQR.E
	HsFLAG-ARP6_Ti_1	3.8076	0.3428	1296.43	1295.447	6649.5	1	1344	85	2	K.ADFCIIHYAGK.V
*	HsFLAG-ARP6_Ti_1	4.044	0.4691	2140.09	2141.32	5292.3	1	430.2	47.2	1	K.NMDPLNDNVATLLHQSSDR.F
*	HsFLAG-ARP6_Ti_1	6.4213	0.5642	2088.72	2089.368	5680	1	1957.3	73.7	4	R.IVGLDQVTGMTETAFGSAYK.T
	HsFLAG-BC014022_	4.6953	0.3416	1578.18	1575.852	3947.8	1	735	69.2	4	R.AGKLDPHLVLDQLR.C
	HsFLAG-Lin9_Ti_20:	2.6215	0.2311	1319.1	1319.547	3341.6	1	429.6	75	2	K.LDPHLVLDQLR.C
	HsFLAG-ARP6_Ti_1	2.9294	0.2075	1543.17	1543.806	4525.3	2	644.1	70.8	1	R.QRYEILTPNAIPK.G
	HsFLAG-ARP6_Ti_1	4.1988	0.3798	1224.38	1224.359	6572.6	1	1434.4	85	2	R.AGVLAHLEEER.D
*	HsFLAG-ARP6_Ti_1	3.3407	0.3363	1595.79	1596.876	9028.9	1	1151.4	66.7	1	K.ITDIIIFFQAVCR.G
*	HsFLAG-ARP6_Ti_1	3.9547	0.2514	2439.2	2436.696	10565.7	1	1050	45	1	K.NILAEQLQAETELFAEAEEMR.A
*	HsFLAG-Lin9_Ti_20:	3.2123	0.2489	2244.21	2242.379	7930.6	1	516	47.2	1	K.MQAHIQDLEEQLDEEEGAR.Q
*	HsFLAG-ARP6_Ti_1	3.835	0.1914	2871.37	2872.159	11321	3	1030.9	29.2	2	K.RKLDGETTDLQDQIAELQAQIDELK.L
*	HsFLAG-ARP6_Ti_1	5.1937	0.2602	2587.79	2587.797	7555.5	1	1263.5	52.3	2	K.LDGETTDLQDQIAELQAQIDELK.L
*	HsFLAG-Lin9_Ti_20:	3.785	0.2098	1244.1	1244.39	7408	4	1366.4	85	1	K.KEEELQGALAR.G
*	HsFLAG-Lin9_Ti_20:	4.7329	0.3101	2006.92	2008.146	9418	1	2180.7	68.8	4	R.ELQAQIAELQEDFESEK.A
*	HsFLAG-ARP6_Ti_1	4.0222	0.3099	3219.3	3219.484	10670.3	1	985	27.8	1	K.RDLSEELEALKTELEDTLDTTAAQQELR.T
*	HsFLAG-p53-DNA-D	5.3287	0.3432	3062.66	3063.296	10086	1	1338.7	29.8	4	R.DLSEELEALKTELEDTLDTTAAQQELR.T
*	HsFLAG-Lin9_Ti_20:	5.9491	0.4741	1797.88	1797.96	8541.5	1	2892.6	83.3	5	R.HATALEELSEQLEQAK.R
*	HsFLAG-BC014022_	3.6913	0.2754	1379.82	1380.587	8478.3	2	1337.4	72.7	2	K.KLDAQVQELHAK.V
*	HsFLAG-Lin9_Ti_20:	5.0078	0.4456	1945.67	1946.119	6027	1	1194.6	68.8	10	K.LQNELDNVSTLLEEAEK.K
*	HsFLAG-ARP6_Ti_1	6.0352	0.3984	2404.22	2405.535	7870.1	1	2183.5	65	5	K.DAASLESQLQDTQELLQEETR.Q
*	HsFLAG-Lin9_Ti_20:	3.3261	0.2845	1761.29	1762.908	7517.2	1	1221.9	70	1	K.KVDDDLGTIESLEEAK.K
*	HsFLAG-Lin9_Ti_20:	3.3395	0.318	1938.13	1939.089	9211.8	1	864.2	56.7	2	R.LQQELDDLTVDLDHQR.Q
	HsFLAG-Lin9_Ti_20:	3.416	0.1163	1220.85	1221.396	6427.8	2	1186.2	83.3	2	K.KFDQLLAEEK.S
*	HsFLAG-Lin9_Ti_20:	4.1596	0.3535	1663.95	1664.81	6757.6	1	1069.2	69.2	1	R.ALEEALEAKEEFER.Q
	HsFLAG-ARP6_Ti_1	6.8581	0.5173	1962.21	1963.059	10191.7	1	3429.4	81.2	12	R.TQLEELEDELQATEDAK.L
*	HsFLAG-Lin9_Ti_20:	3.2932	0.2766	1360.99	1361.448	7778.8	4	886.1	75	2	R.ELEAELEDERK.Q
*	HsFLAG-Lin9_Ti_20:	6.16	0.4314	2046.29	2046.239	9509.9	1	3084.7	51.5	2	K.SLEAEILQLQEELASSER.A
*	HsFLAG-ARP6_Ti_1	6.0676	0.4075	2046.49	2046.239	9273.3	1	2679.6	73.5	10	K.SLEAEILQLQEELASSER.A
*	HsFLAG-Lin9_Ti_20:	3.2909	0.1892	2201.03	2201.268	7709.1	1	567.9	42.1	1	R.HAEQERDELADEITNSASGK.S
*	HsFLAG-ARP6_Ti_1	4.3947	0.3592	1450.23	1450.499	9411.6	1	2736.4	84.6	1	R.DELADEITNSASGK.S

*	HsFLAG-ARP6_Ti_1	6.0887	0.4211	2532.68	2533.724	9758.6	1	2143.5	60	2	R.IAQLEEELEEEQSNMELLNDR.F
*	HsFLAG-Lin9_Ti_20	4.5886	0.4247	1744.87	1745.927	9394.3	1	2027.2	70	2	K.TTLQVDTLNAELAAER.S
*	HsFLAG-Lin9_Ti_20	4.7334	0.2667	1514.74	1515.66	7114.6	1	1699.1	83.3	3	K.IGQLEEQLEQEAK.E
*	HsFLAG-Lin9_Ti_20	4.7337	0.358	1461.43	1461.528	10554	1	1837.3	81.8	2	K.RQLEEAEEEATR.A
*	HsFLAG-Lin9_Ti_20	3.627	0.249	1151.19	1151.268	5752.2	1	1053.3	85	2	R.RGGPISFSSSR.S
*	HsFLAG-p53-DNA-D	1.9842	0.2334	1431.36	1432.441	3368.9	9	270.6	54.2	1	K.TSDVNETQPPQSE.-
gi|40255020|r	10	58	36.80%	201	22755	8.3	hypothetical protein LOC64769 [Homo sapiens]				
*	HsFLAG-TIP49b_Ti_	4.8557	0.3712	1671.94	1671.894	6755.1	1	1472.5	80.8	4	K.RKQELAETLANLER.Q
*	HsH2AZ-FLAG_293_	3.6184	0.2958	1515.54	1515.707	9412.2	1	1412.8	70.8	3	R.KQELAETLANLER.Q
*	HsTIP60_Ti_104.24	2.706	0.1263	1387.21	1387.533	5774.3	1	544.9	63.6	1	K.QELAETLANLER.Q
*	HsMRGBP-FLAG_Ti	4.3686	0.4776	2511.92	2512.796	7611.9	1	1058.4	50	2	R.QIYAFEGSYLEDTQMYGNIIR.G
*	HsYL1-FLAG_Ti_20	4.1218	0.3338	2146.3	2146.403	9101.5	1	2309.1	44	1	K.SSVTSAAAVSALAGVQDQLIEK.R
*	HsYL1-FLAG_Ti_20	5.9833	0.4261	2146.9	2146.403	4876.9	1	1156	61.9	16	K.SSVTSAAAVSALAGVQDQLIEK.R
*	HsH2AZ-FLAG_293_	4.2363	0.3357	2302.03	2302.59	6413.9	1	1067.3	37.5	4	K.SSVTSAAAVSALAGVQDQLIEKR.E
*	HsMRGBP-FLAG_Ti	4.6823	0.3595	2302.43	2302.59	6503.7	1	836.1	47.7	15	K.SSVTSAAAVSALAGVQDQLIEKR.E
*	HsYL1-FLAG_Ti_20	3.621	0.3542	1469.62	1468.483	10562.8	1	859.6	53.6	9	K.AASSTSSGSHHSSHK.K
*	HsTIP60_Ti_106.09	3.2996	0.4256	1595.86	1596.657	6418.8	1	783.5	60	3	K.AASSTSSGSHHSSHKK.R
gi|4506607|re	7	17	36.70%	188	21634	11.7	ribosomal protein L18 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.2053	0.1673	1407.21	1407.613	5262.8	1	1017.6	77.3	2	R.RTNSTFNQVVLK.R
*	HsFLAG-FLJ20309_	2.6636	0.2272	1140.82	1141.316	5324.5	1	635.1	72.2	1	R.TNRPPLSLSR.M
*	HsFlag-Ies6_293_Ti_	4.836	0.4021	1346.62	1346.524	7234.9	1	1840.5	83.3	3	K.TAVVVGTITDDVR.V
*	HsFLAG-FLJ20309_	4.4246	0.1195	1461.6	1461.698	8142.2	1	1617.1	79.2	6	K.ILTFDQLALDSPK.G
*	HsFLAG-TCF3_Ti_1	2.9162	0.1015	1461.67	1461.698	6466.5	4	355.1	50	1	K.ILTFDQLALDSPK.G
*	HsFLAG-ARP6_Ti_1	3.7768	0.2986	1119.12	1117.257	8790.9	1	1759.4	90	3	K.GCGTVLLSGPR.K
*	HsFLAG-Lin9_Ti_20	2.7133	0.1435	1032.12	1033.132	6983.9	1	949.3	88.9	1	K.APGTPHSHTK.P
gi|4506681|re	6	34	36.70%	158	18431	10.3	ribosomal protein S11 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.3853	0.2297	973.43	973.161	5435.9	1	1058	93.8	10	K.RVLLGETGK.E
*	HsFLAG-ARP6_Ti_1	2.1439	0.2253	1138.5	1139.248	3628.9	2	208.1	61.1	1	K.EAIEGTYIDK.K
*	HsFLAG-ARP6_Ti_1	3.1371	0.2949	1151.41	1151.274	6792.1	2	802.7	77.8	1	K.CPFTGNVSIR.G
*	HsFlag-NUFIP_Ti_1	2.1152	0.138	1348.61	1348.529	6023.1	5	291.4	55	1	K.NMSVHLSPCFR.D
*	HsFLAG-ARP6_Ti_1	3.3529	0.2882	1350.28	1348.529	4594.2	4	545.8	65	9	K.NMSVHLSPCFR.D
*	HsFLAG-ARP6_Ti_1	5.0299	0.4291	1985.83	1987.227	6568.8	1	1384.7	67.6	12	R.DVQIGDIVTVGECRPLSK.T
gi|5031749|re	5	10	36.70%	90	9393	10	high-mobility group nucleosomal binding domain 2 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	2.0862	0.1578	1359.67	1360.64	6044.8	7	587.8	58.3	2	R.LSAKPAPPKPEPK.P
	HsFLAG-Lin9_Ti_20	3.1572	0.1875	1360.25	1360.64	3808.5	4	485.5	66.7	3	R.LSAKPAPPKPEPK.P
	HsFLAG-Lin9_Ti_20	3.7783	0.1514	1585.59	1585.93	6472.7	2	735.1	42.9	1	R.LSAKPAPPKPEPKPK.K
	HsFLAG-Lin9_Ti_20	3.1823	0.0991	1585.62	1585.93	5668.6	4	538.8	57.1	2	R.LSAKPAPPKPEPKPK.K
	HsFLAG-p53-DNA-D	3.9044	0.3669	1887.95	1887.915	9636.1	1	1065.4	52.9	2	K.EGNNPAENGDAKTDQAQK.A
gi|6005942|re	20	56	36.60%	806	89322	5.3	valosin-containing protein [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.8559	0.2201	1541.7	1541.751	5611.5	1	981.7	73.1	1	R.LGDVISIQPCPDVK.Y
*	HsFlag-VPS71_Ti_1	5.3748	0.4204	2585.99	2586.988	8793.4	1	1984	59.1	4	R.IHVLPIDDTVEGITGNLFEVYLK.P
*	HsFlag-VPS71_Ti_1	5.2497	0.2853	2588.32	2586.988	5017.5	1	856.3	34.1	2	R.IHVLPIDDTVEGITGNLFEVYLK.P
*	HsFlag-VPS71_Ti_1	2.8683	0.1141	1425.82	1425.673	10395.6	2	861.5	65	2	K.PYFLEAYRPIR.K

*	HsFlag-VPS71_Ti_1	3.052	0.0974	948.39	948.153	3912	1	715.5	92.9	2	R.KGDIFLVR.G
*	HsFLAG-ARP6_Ti_1	3.0035	0.3143	2186.41	2187.158	8745.1	1	697.6	44.4	1	R.EDEEESLNEVGYDDIGGCR.K
*	HsFlag-VPS71_Ti_1	3.2925	0.363	1681.13	1681.049	6564.5	1	664.7	65.4	1	K.EMVELPLRHPALFK.A
*	HsFlag-VPS71_Ti_1	4.0566	0.3297	2256.68	2257.609	9768.1	1	779.9	42.5	6	R.AVANETGAFFFLINGPEIMSK.L
*	HsFLAG-FLJ20729_	4.6306	0.3798	1811.44	1812.116	9363.6	1	1864.1	68.8	10	K.NAPAIIFIDELDAIAPK.R
*	HsFlag-VPS71_Ti_1	4.7958	0.3987	1431.65	1431.774	7311.1	1	1832	83.3	3	R.IVSQLLTLMDGLK.Q
*	HsFlag-VPS71_Ti_1	7.246	0.4402	3674.09	3674.97	10580.9	1	2305	30.9	2	K.LADDVDLEQVANETHGHVGADLAALCSEAALQAIR.K
*	HsFLAG-Lin9_Ti_20	2.7293	0.1948	1329.43	1330.486	5086.3	1	799.7	81.8	1	R.WALSQSNPSALR.E
*	HsFLAG-Lin9_Ti_20	3.4224	0.1924	1826.8	1825.028	8102.9	1	801.1	57.1	1	R.ELQELVQYPVEHPDK.F
*	HsFlag-VPS71_Ti_1	2.189	0.1863	1251.55	1252.422	5381.2	1	584.9	59.1	1	K.GVLFYGPPGCGK.T
*	HsFlag-VPS71_Ti_1	3.3058	0.2935	1252.49	1252.422	5512	1	920.9	72.7	2	K.GVLFYGPPGCGK.T
*	HsFlag-VPS71_Ti_1	3.3746	0.1657	1928.07	1925.155	6584.1	1	881.9	59.4	9	R.QAAPCVLFFDELDSIAK.A
*	HsFlag-VPS71_Ti_1	3.3763	0.1046	1682.59	1680.972	7870.9	1	817.7	57.1	1	R.VINQILTEMDGMSTK.K
*	HsFLAG-ARP6_Ti_1	4.4536	0.3234	2520.25	2519.953	5746.4	3	699.3	34.1	2	K.NVFIIGATNRPDIIDPAILRPGR.L
*	HsFlag-VPS71_Ti_1	4.2465	0.17	1558.74	1557.827	5429.2	1	1040.2	75	2	R.LDQLIYIPLPDEK.S
*	HsFlag-VPS71_Ti_1	4.9968	0.4292	1630.74	1630.859	7609.2	1	2201.3	87.5	3	R.KYEMFAQTLQQSR.G
gi|24307971|	16	176	36.60%	464	54003	6.8	serine/threonine kinase 38 like [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.4213	0.3807	2120.67	2120.37	7595.8	1	1417.3	65.6	15	K.LTLENFYSNLILQHEER.E
*	HsARP6-FLAG_Ti_1	4.5275	0.1919	2121.98	2120.37	6423.9	1	1059.1	43.8	7	K.LTLENFYSNLILQHEER.E
*	HsFlag-FLJ20643_Ti	4.3448	0.4565	1821.53	1821.006	8330.2	1	1670	70	1	K.KLEVAMEEEGLADEEK.K
*	HsH2AZ-FLAG_293_	3.336	0.239	1137.16	1137.275	4736.3	2	1083.5	88.9	8	R.LGLDDFESLK.V
	HsFLAG-ARP6_Ti_1	2.2059	0.115	1065.34	1066.216	6161.4	5	554.4	71.4	2	K.MFYSFQDK.R
*	HsFlag-DPCD_Ti_20	4.5199	0.1745	3492.31	3491.879	7564.2	1	1314.7	30.2	2	K.DTLTEEETQFYISETVLAIDAIHQLGFIHR.D
*	HsFlag-NUFIP_Ti_1	2.8822	0.2283	1357.1	1355.574	3371.3	1	518.5	72.7	2	R.DIKPDNLLLDAK.G
	HsFlag-FLJ90652_2	2.8592	0.2419	1210.54	1211.367	4516.1	1	485.6	65	28	K.LSDFGLCTGLK.K
	HsFlag-FLJ90652_2	4.2329	0.2928	1211.36	1211.367	6417.2	1	1697.6	90	38	K.LSDFGLCTGLK.K
	HsFLAG-ARP6_Ti_1	3.4297	0.2592	1339.36	1339.541	6565.3	1	1017.5	77.3	7	K.LSDFGLCTGLKK.A
*	HsFlag-NUFIP_Ti_2	5.3234	0.4887	2079.51	2079.251	3718.1	1	833.6	67.6	28	R.NLTHNPPSDFSFQNMNSK.R
*	HsFlag-NUFIP_Ti_2	5.5779	0.3926	2080.21	2079.251	11209.4	1	2417.6	45.6	4	R.NLTHNPPSDFSFQNMNSK.R
*	HsFLAG-p53-DNA-D	6.2661	0.3891	2753.72	2754.034	10842.6	1	1787.5	35.9	2	R.IGNSGVEEIKGHPFFEGVDWEHIR.E
*	HsFlag-NUFIP_Ti_2	3.6412	0.33	1727.44	1726.891	6480.8	1	960.4	69.2	5	K.GHPFFEGVDWEHIR.E
*	HsFlag-VPS71_Ti_1	3.4614	0.241	1238.23	1237.485	4884.9	1	981.8	85	25	R.ERPAAIPIEIK.S
*	HsFLAG-p53-DNA-D	3.6643	0.284	1565.45	1564.781	6165.5	1	1061.2	77.3	2	K.SKDWVFLNYTYK.R
gi|4501881|re	20	443	36.60%	377	42051	5.4	alpha 1 actin precursor [Homo sapiens]				
gi|4885049|re	20	443	36.60%	377	42019	5.4	cardiac muscle alpha actin proprotein [Homo sapiens]				
	HsFLAG-ARP6_Ti_2	3.3564	0.3342	977.23	977.021	5082.6	1	1225.5	88.9	17	K.AGFAGDDAPR.A
	HsFlag-VPS71_Ti_1	2.159	0.1032	977.47	977.021	5226.9	1	385.5	61.1	2	K.AGFAGDDAPR.A
	HsFLAG-ARP5_Ti_1	3.43	0.2899	1199.05	1199.442	6548.6	1	831.6	80	27	R.AVFPSIVGRPR.H
	HsFLAG-TIP49a_Ti_	3.2318	0.3146	1171.37	1172.406	4944.3	1	760.2	75	54	R.HQGVMVGMGQK.D
	HsFLAG-p53-DNA-D	3.5553	0.3623	1172.01	1172.406	5155.7	1	1022.8	85	49	R.HQGVMVGMGQK.D
	HsFLAG-ARP8_Ti_2	3.7228	0.4	1198.34	1199.216	4824	1	494.9	65	7	K.DSYVGDEAQSK.R
	HsFlag-VPS71_Ti_1	3.4611	0.3002	1199.21	1199.216	3911.9	1	959.2	85	11	K.DSYVGDEAQSK.R
	HsFLAG-p53-DNA-D	2.8615	0.2497	1355.19	1355.404	5881	1	646.6	63.6	2	K.DSYVGDEAQSKR.G

	HsFlag-DPCD_Ti_20	4.6355	0.2069	1961.41	1962.184	8644.2	3	1097.1	41.7	17	K.YPIEHGIITNWDDMEK.I
	HsFlag-DPCD_Ti_20	4.7092	0.1653	1962.55	1962.184	10286.5	1	1307.4	60	38	K.YPIEHGIITNWDDMEK.I
	HsFLAG-TIP49b_Ti_	3.4873	0.339	1515.54	1516.702	6235.6	1	470.4	65	12	K.IWHHTFYNELR.V
	HsFLAG-p53-DNA-D	3.5256	0.379	1516.47	1516.702	6570.8	1	921.4	75	44	K.IWHHTFYNELR.V
	HsFLAG-ARP6_Ti_1	3.5437	0.1582	1517.38	1516.702	6065.3	1	1106.2	57.5	2	K.IWHHTFYNELR.V
	Hs293Flag-Ies2_Ti_1	4.6147	0.0998	1954.42	1957.234	6565	2	1200.2	67.6	6	R.VAPEEHPTLLTEAPLNPK.A
	HsFLAG-p53-DNA-D	2.7022	0.1896	998.54	999.167	6873.8	9	806.7	78.6	9	R.DLTDYLMK.I
	HsFLAG-Lin9_Ti_20	3.6505	0.1696	1791.77	1791.955	7019.8	1	1188.6	45	2	K.SYELPDGQVITIGNER.F
	HsSrcap_Ti_202.259	5.2016	0.2868	1791.82	1791.955	5255.9	1	1548	80	115	K.SYELPDGQVITIGNER.F
	HsFLAG-ARP6_Ti_1	2.8881	0.328	1161.46	1162.387	4673.7	1	620.1	75	20	K.EITALAPSTMK.I
	HsFLAG-ARP6_Ti_1	2.895	0.2843	1161.87	1162.387	4881.7	1	872.9	80	8	K.EITALAPSTMK.I
	HsFLAG-TIP49b_Ti_	2.6775	0.1641	1628.44	1629.77	9935.8	8	643.5	50	1	K.QEYDEAGPSIVHRK.C
gi|4504345|re	4	17	36.60%	142	15258	8.7	alpha 2 globin [Homo sapiens]				
gi|4504347|re	4	17	36.60%	142	15258	8.7	alpha 1 globin [Homo sapiens]				
	HsFLAG-RPB5MP_2	4.1333	0.4734	1530.34	1530.637	5355.7	1	1404	78.6	3	K.VGAHAGEYGAEALER.M
	HsFLAG-RPB5MP_2	3.968	0.3797	1834.32	1835.029	7138.8	1	1115.2	63.3	8	K.TYFPHFDLSHGSAQVK.G
	HsFLAG-RPB5MP_2	2.6805	0.1615	1088.25	1088.295	3953.4	5	447.7	68.8	1	K.LRVDPVNFK.L
	HsFLAG-RPB5MP_2	4.1087	0.3579	1254.28	1253.481	5322.2	1	1248.2	86.4	5	K.FLASVSTVLTSK.Y
gi|4502027|re	18	49	36.50%	609	69367	6.3	albumin precursor [Homo sapiens]				
*	HsFLAG-p53-DNA-D	2.2866	0.108	951.42	952.009	5369.7	2	550.5	78.6	1	K.DLGEENFK.A
*	HsFLAG-p53-DNA-D	4.1739	0.3392	2491.93	2491.858	7425.5	1	711.7	47.5	2	K.ALVLIAFAQYLQQCPFEDHVK.L
*	HsFLAG-p53-DNA-D	2.8193	0.1344	1149.48	1150.317	11156.4	2	873.4	72.2	1	K.LVNEVTEFAK.T
*	HsFLAG-p53-DNA-D	4.4701	0.3332	2652.67	2651.96	9164.9	1	1112.7	35.7	1	R.LVRPEVDVMCTAFHDNEETFLK.K
*	HsFLAG-p53-DNA-D	5.5552	0.3265	2779.57	2780.134	9104	1	1777.1	37.5	1	R.LVRPEVDVMCTAFHDNEETFLKK.Y
	HsFLAG-p53-DNA-D	3.3501	0.1636	1056.45	1056.25	3640.6	1	649.3	92.9	1	K.KYLYEIAR.R
*	HsFLAG-RPB5MP_2	2.5513	0.3038	1443.87	1444.504	6238.4	1	810.5	68.2	2	K.YICENQDSISSK.L
*	HsFLAG-p53-DNA-D	4.1298	0.1924	1547.56	1547.764	10672.6	1	1917	81.8	1	K.LKECCEKPLLEK.S
*	HsFLAG-p53-DNA-D	4.2011	0.1072	2976.58	2976.204	5959.9	1	793.1	31.7	1	K.SHCIAEVENDEMPADLPSLAADFVESK.D
*	HsFLAG-p53-DNA-D	4.4127	0.3954	2045.87	2046.371	4353	1	691.4	59.4	3	K.VFDEFKPLVEEPQNLIK.Q
*	HsFLAG-p53-DNA-D	3.3509	0.2244	1657.94	1658.771	7827.9	1	1021.5	70.8	1	K.QNCELFEQLGEYK.F
	Hs293Flag-Ies2_Ti_1	3.6586	0.4103	1640.53	1640.921	3826.5	1	566.3	67.9	7	K.KVPQVSTPTLVEVSR.N
	HsFLAG-TCF3_Ti_1	2.9267	0.38	1511.68	1512.746	3858.4	1	219.1	53.8	1	K.VPQVSTPTLVEVSR.N
	HsFlag-FLJ90652_2	3.7941	0.3724	1511.77	1512.746	6997.5	1	1553.3	80.8	15	K.VPQVSTPTLVEVSR.N
*	HsFLAG-p53-DNA-D	6.2389	0.4051	2675.43	2676.035	9179.1	1	1804.5	39.3	2	K.RMPCAEDYLSVVLNQLCVLHEK.T
	HsFlag-FLJ90652_2	3.6243	0.2736	1139.23	1139.183	7079.6	1	1285.6	100	2	K.CCTESLVNR.R
*	HsFLAG-p53-DNA-D	3.8687	0.3148	1911.44	1912.116	5660.3	2	545.3	53.3	3	R.RPCFSALEVDETYVPK.E
*	HsFLAG-p53-DNA-D	3.2071	0.1699	1129.35	1129.385	5632.2	2	996.2	83.3	4	K.KQTALVELVK.H
gi|38327552|r	11	23	36.50%	466	52164	5.5	Ras-GTPase-activating protein SH3-domain-binding protein [Homo sapiens]				
gi|5031703|re	11	23	36.50%	466	52164	5.5	Ras-GTPase-activating protein SH3-domain-binding protein [Homo sapiens]				
	HsFlag-VPS71_Ti_1	3.7811	0.3278	1864.83	1864.129	7190.3	1	1155.1	71.4	1	R.QYYTLLNQAPDMLHR.F
	HsFlag-VPS71_Ti_1	4.784	0.4359	2364.87	2365.521	5352.2	1	617.4	50	1	K.NSSYVHGGLDSNGKPADAVYGQK.E
	HsFlag-VPS71_Ti_1	2.9214	0.304	1466.55	1467.606	4173.9	1	183.7	50	1	K.VMSQNFTNCHTK.I
	HsFlag-VPS71_Ti_1	3.5588	0.31	1468.58	1467.606	9017.6	1	976.1	68.2	2	K.VMSQNFTNCHTK.I

	HsFlag-VPS71_Ti_1	4.0838	0.145	2988.97	2987.363	6830.4	1	815.7	31.5	1	R.HVDAHATLNDGVVVQVMGLLSNNNQALR.R
	HsFLAG-ARP6_Ti_1	2.5926	0.2903	1739.39	1740.027	6968.3	3	431.3	46.7	1	R.FMQTFVLAPEGSVANK.F
	HsARP6-FLAG_Ti_1	2.8718	0.356	1211.54	1211.365	6198.6	1	1288.2	93.8	3	K.FYVHNDIFR.Y
	HsFlag-VPS71_Ti_1	3.3408	0.3758	1886.62	1886.026	6798.1	1	776.8	55.9	1	K.SSSPAPADIAQTVQEDLR.T
	HsFLAG-p53-DNA-D	2.6581	0.3011	1879.53	1880.241	3819.9	2	241.6	44.4	1	K.NLPPSGAVPVTGIPPHVVK.V
	HsFlag-VPS71_Ti_1	4.5597	0.2543	1575.64	1574.733	9011.7	1	2004.9	83.3	2	K.DFFQSYGNVVELR.I
	HsFLAG-ARP6_Ti_1	5.2479	0.5061	1939.73	1939.175	7610	1	1903.9	71.9	9	K.LPNFGFVVFDDSEPVQK.V
gi|14211889|r	4	67	36.40%	99	11250	4.9	dpy-30-like protein [Homo sapiens]				
	HsFLAG-p53-DNA-D	5.0352	0.4131	2126.12	2126.588	4290.1	1	849.1	65.8	31	R.AYLDQTVVPILLQGLAVLAK.E
	HsFLAG-p53-DNA-D	6.5927	0.3972	2126.25	2126.588	8924.3	1	2870.1	50	17	R.AYLDQTVVPILLQGLAVLAK.E
*	HsSrcap_Ti_205.498	4.3554	0.3513	1887.65	1888.217	6843.3	1	867.3	60	13	K.ERPPNPIEFLASYLLK.N
*	HsFLAG-BC014022_	5.0225	0.2688	1887.97	1888.217	7217.7	1	1753.3	50	6	K.ERPPNPIEFLASYLLK.N
gi|4826659|re	8	16	36.00%	272	30629	6	F-actin capping protein beta subunit [Homo sapiens]				
*	HsFlag-FLJ90652_2	2.5844	0.0848	1107.95	1109.314	7854	1	861	81.2	1	R.RLPPQQIEK.N
*	HsFLAG-FLJ20729_	4.0844	0.245	2784.98	2785.127	3465.9	1	388.7	41.7	5	K.NLSDLIDLVPSLCEDLLSSVDQPLK.I
*	HsFlag-FLJ90652_2	4.1554	0.3287	2785.97	2785.127	6050.7	1	938.6	33.3	1	K.NLSDLIDLVPSLCEDLLSSVDQPLK.I
*	HsFLAG-ARP6_Ti_1	3.9403	0.3153	2219.89	2219.433	6925.9	1	1080.2	38.2	2	R.SPWSNKYDPPLEDGAMPSAR.L
*	HsFlag-FLJ90652_2	3.2683	0.3706	2221.62	2219.433	3908.1	1	389.5	47.4	1	R.SPWSNKYDPPLEDGAMPSAR.L
*	HsFlag-FLJ90652_2	4.8923	0.3784	1697.43	1697.845	8202.5	1	2177.1	80.8	2	R.KLEVEANNAFDQYR.D
*	HsFlag-FLJ90652_2	4.313	0.2417	1686.3	1686.828	7819.8	1	1722.2	73.1	2	K.GCWDSIHVVEVQEK.S
*	HsFlag-DPCD_Ti_20	3.7528	0.2956	1771.09	1771.847	7246.6	1	1061.5	60	2	K.DETVSDCSPHIANIGR.L
gi|14210536|r	13	213	35.90%	446	49857	4.9	tubulin, beta 6 [Homo sapiens]				
gi|89047323|r	13	213	39.70%	403	45043	4.9	PREDICTED: similar to tubulin, beta 6 [Homo sapiens]				
	HsSrcap_Ti_206.299	3.8732	0.2209	2828.36	2828.119	7315.4	1	679.9	38	2	R.SGPFGQLFRPDNFIFGQTGAGNNWAK.G
	HsFLAG-ARP6_Ti_1	3.7586	0.1316	2830.72	2828.119	9114.5	4	803.9	27	1	R.SGPFGQLFRPDNFIFGQTGAGNNWAK.G
	HsFLAG-ARP6_Ti_1	4.2407	0.3299	1352.9	1352.65	7307.1	1	1886.4	90.9	4	R.IMNTFSVMPSPK.V
	HsFLAG-ARP6_Ti_1	6.4706	0.4855	4594.76	4595.903	4988.3	1	541.4	23.7	83	K.VSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFR.T
	HsYL1_Ti_103.3223.	3.7161	0.3356	2636.29	2636.98	6938.8	1	781.3	41.7	1	K.LTTPTYGDLNHLVSATMSGVTTSLR.F
	HsFLAG-ARP6_Ti_1	2.1817	0.2119	1130.19	1131.277	3484.6	1	331.1	72.2	1	R.FPGQLNADLR.K
	HsFLAG-ARP6_Ti_1	3.1035	0.1934	1133.31	1131.277	4537.1	1	968.3	94.4	20	R.FPGQLNADLR.K
	HsFLAG-ARP6_Ti_1	2.7216	0.2275	1259.45	1259.451	6377.3	1	1130.1	85	3	R.FPGQLNADLRK.L
	Hs293Flag-Ies2_Ti_1	4.1115	0.2404	1271.88	1272.594	7432.2	1	1437.4	85	9	R.KLAVNMVPFPR.L
	HsFLAG-Lin9_Ti_20	3.7432	0.2947	1144.31	1144.42	4934.2	1	1119.4	94.4	37	K.LAVNMVPFPR.L
	HsFLAG-ARP6_Ti_1	3.784	0.2563	1621.62	1621.94	4747.2	1	1118	76.9	9	R.LHFFMPGFAPLTSR.G
	HsFLAG-ARP6_Ti_1	3.1514	0.3044	1065.99	1066.201	5998.7	1	1325.1	87.5	4	R.NMMAACDPR.H
	HsFLAG-ARP6_Ti_1	4.0978	0.3327	1699.12	1697.888	5299.1	1	715	61.5	39	K.NSSYFVEWIPNNVK.V
gi|57242777|r	3	33	35.90%	103	11967	5.9	c-myc binding protein [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.6668	0.3961	2275.58	2276.635	5343.9	1	623.8	50	23	K.VLVALYEEPEKPNSALDFLK.H
*	HsFlag-VPS71_Ti_1	4.7962	0.4065	2276.57	2276.635	5246.8	1	1034.4	42.1	7	K.VLVALYEEPEKPNSALDFLK.H
*	HsFlag-FLJ90652_2	3.7172	0.2362	1898.98	1898.129	9306.6	1	1129.1	59.4	3	K.HHLGAATPENPEIELLR.L
gi|14110414|r	11	47	35.60%	306	32835	8.2	heterogeneous nuclear ribonucleoprotein D isoform c [Homo sapiens]				
gi|14110420|r	11	47	30.70%	355	38434	7.8	heterogeneous nuclear ribonucleoprotein D isoform a [Homo sapiens]				
	HsFlag-NUFIP_Ti_2	2.9	0.3341	1543.82	1543.636	9211.5	1	945	66.7	1	R.HSEAATAQREEWK.M

	HsFLAG-p53-DNA-D	4.0049	0.2653	1484.79	1484.753	7556.2	1	1639.3	83.3	4	K.MFIGGLSWDTTKK.D
	HsFLAG-FLJ20729_	3.3271	0.2535	1921.24	1921.167	5550.5	1	614.8	56.2	2	K.FGEVVDCTLKLDPITGR.S
	HsFLAG-p53-DNA-D	2.9122	0.228	914.45	915.123	2938.3	3	645.5	85.7	3	R.GFGFVLFK.E
	HsFLAG-p53-DNA-D	2.0301	0.1206	915.7	915.123	8175.2	7	803	78.6	1	R.GFGFVLFK.E
	HsFLAG-ARP6_Ti_1	4.9611	0.3419	1616.79	1617.839	6888.4	1	2402.6	82.1	4	K.KIFVGGLSPDTPEEK.I
	HsFLAG-ARP6_Ti_1	4.4488	0.3532	2162.16	2162.375	8648.3	1	1345.8	58.3	9	R.EYFGGFGEVESIELPMDNK.T
	HsFlag-VPS71_Ti_1	4.5374	0.389	1731.77	1731.952	5880.2	1	1013.7	69.2	19	R.GFCFITFKEEEPVK.K
	HsFLAG-p53-DNA-D	3.4851	0.3362	1859.68	1860.126	9002.8	1	905.8	57.1	2	R.GFCFITFKEEEPVKK.I
	HsFLAG-p53-DNA-D	3.0144	0.2175	1046.48	1046.214	6101.3	1	1208.2	93.8	1	K.KYHNVGLSK.C
	HsFlag-VPS71_Ti_1	2.1614	0.2732	917.54	918.04	5262.8	1	502.1	71.4	1	K.YHNVGLSK.C
gi|4502549|re	4	13	35.60%	149	16838	4.2	calmodulin 2 [Homo sapiens]				
gi|5901912|re	4	13	35.60%	149	16838	4.2	calmodulin 1 (phosphorylase kinase, delta) [Homo sapiens]				
gi|58218968|r	4	13	35.60%	149	16838	4.2	calmodulin 3 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	2.3901	0.2026	956.46	957.071	3057.2	8	202.6	64.3	1	K.EAFSLFDK.D
	HsFLAG-ARP6_Ti_1	3.7735	0.2768	1353.32	1353.444	5115.6	1	1108	85	2	K.MKDTDSEEEIR.E
	HsFLAG-ARP6_Ti_1	3.3886	0.3511	1265.89	1266.353	5573.8	1	1070.7	77.3	4	K.DGNGYISAAELR.H
	HsFLAG-ARP6_Ti_1	5.205	0.4853	2492.34	2491.704	5641.9	1	1040.1	54.8	6	R.EADIDGDGQVNYEEFVQMMTAK.-
gi|89030033|r	15	95	35.50%	442	47563	9.2	PREDICTED: hypothetical protein LOC84726 isoform 3 [Homo sapiens]				
gi|89030649|r	15	95	35.50%	442	47418	9.1	PREDICTED: similar to HLA-B associated transcript 2 isoform 12 [Homo sapiens]				
	HsFLAG-KIAA0515_	2.391	0.2466	1073.61	1074.219	6657.1	1	636.5	75	7	K.YSTLSLFDK.Y
	HsFLAG-KIAA0515_	3.0827	0.1453	840.29	839.97	3998.2	1	991.8	100	1	R.HGLQSLGK.V
	HsFLAG-KIAA0515_	2.466	0.0825	1164.3	1165.436	5127.9	9	530.4	65	2	R.MPPPANLPSLK.S
	HsFLAG-KIAA0515_	3.6077	0.1581	1168.37	1166.363	6498.3	2	1325.2	85	1	K.GNDPNIVIVPK.D
	HsFLAG-KIAA0515_	2.7943	0.2972	1836.44	1837.04	3485.8	2	311.8	47.1	1	K.SATASQPPESLPQPGLQK.S
	HsFLAG-KIAA0515_	4.3695	0.245	2598.44	2598.83	4752.8	1	785	47.9	7	K.SVSNLQKPTQSISQENTNSVPGGPK.S
	HsFLAG-KIAA0515_	5.3966	0.2823	2598.52	2598.83	6457.6	1	1407.9	38.5	2	K.SVSNLQKPTQSISQENTNSVPGGPK.S
	HsFLAG-KIAA0515_	4.8296	0.3679	1841.54	1841.973	5817.7	1	1305.1	67.6	4	K.PTQSISQENTNSVPGGPK.S
	HsFLAG-KIAA0515_	4.3862	0.2627	1843.34	1841.973	7585.6	2	1078	41.2	1	K.PTQSISQENTNSVPGGPK.S
	HsFLAG-KIAA0515_	2.4348	0.0813	903.46	904.013	4020.5	8	315.1	71.4	1	K.SWAQLNGK.P
	HsFLAG-KIAA0515_	3.2516	0.2889	1896.38	1896.15	4673.3	1	582.9	56.2	1	R.GSSRLLSFSPEEFPTLK.A
	HsFLAG-KIAA0515_	3.7032	0.0989	1509.55	1508.755	4468.6	1	796.7	70.8	9	R.LLSFSPEEFPTLK.A
	HsFLAG-KIAA0515_	2.9535	0.2142	1431.48	1431.632	4961	1	663.7	61.5	1	K.GVLDLSYGPGPSLR.P
	HsFLAG-KIAA0515_	5.6894	0.4755	1857.7	1858.059	7413.6	1	2156.5	76.5	56	R.HIISATSLSTSPTELGSR.N
	HsFLAG-KIAA0515_	2.7436	0.2778	1729.02	1729.675	3017.7	1	377.2	55.9	1	R.NSSTGDGAPSSACTSDSK.D
gi|4503475|re	19	170	35.20%	463	50470	9	eukaryotic translation elongation factor 1 alpha 2 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	4.6953	0.3853	1589.5	1589.835	9070.4	1	1844.8	71.4	16	K.THINIVVIGHVDSGK.S
	HsSrcap_Ti_206.252	2.9506	0.4242	1589.65	1589.835	7888.4	1	828.8	60.7	1	K.THINIVVIGHVDSGK.S
	HsTIP60_Ti_105.137	1.9632	0.1372	1120.39	1121.279	6519.3	3	584.4	66.7	1	K.STTTGHLIYK.C
	HsFLAG-p53-DNA-D	3.1463	0.3628	1121.3	1121.279	8751.6	1	1234	77.8	21	K.STTTGHLIYK.C
	HsFLAG-ARP5_Ti_1	2.541	0.1763	1611.43	1611.851	9393	1	594.7	53.8	1	R.TIEKFEKEAAEMGK.G
*	HsFLAG-p53-DNA-D	3.8789	0.2921	1419.38	1419.623	6386.6	1	1309.1	77.3	4	K.YYITIIDAPGHR.D
	HsSrcap_Ti_204.512	3.2119	0.2572	2910.96	2911.263	8701.9	2	388.9	28.6	2	K.NMITGTSQADCAVLIVAAGVGEFEAGISK.N
	HsFlag-VPS71_Ti_1	4.5563	0.1844	2913.87	2911.263	6269.6	1	1050.3	33	12	K.NMITGTSQADCAVLIVAAGVGEFEAGISK.N

	HsFlag-VPS71_Ti_1	3.8784	0.3946	1314.66	1315.555	4878	1	770	72.7	24	R.EHALLAYTLGVK.Q
	HsFLAG-p53-DNA-D	3.6805	0.3101	1315.6	1315.555	7027.5	1	1495	86.4	27	R.EHALLAYTLGVK.Q
*	HsFLAG-Lin9_Ti_20	4.0359	0.2129	2595.03	2595.91	6969.8	1	909.6	45.8	2	K.EGNASGVSLLEALDTILPPTRPTDK.P
*	HsFLAG-Lin9_Ti_20	4.0239	0.2288	2597.46	2595.91	5395.1	1	808.6	33.3	1	K.EGNASGVSLLEALDTILPPTRPTDK.P
*	HsFLAG-p53-DNA-D	4.777	0.3723	3920.26	3919.511	9115.3	1	772.1	21.4	2	K.EGNASGVSLLEALDTILPPTRPTDKPLRLPLQDVYK.I
	HsFlag-NUFIP_Ti_2	3.5749	0.2319	1342.49	1342.624	6073.4	1	787.6	70	33	K.PLRLPLQDVYK.I
	HsFLAG-ARP6_Ti_1	4.3757	0.2664	1343.52	1342.624	7402.5	1	1687.2	57.5	5	K.PLRLPLQDVYK.I
	HsFlag-DPCD_Ti_20	1.8412	0.2195	1025.34	1026.224	4853.1	6	236.2	60	1	K.IGGIGTVPVGR.V
	HsFLAG-ARP6_Ti_1	3.7953	0.3438	1026.89	1026.224	5194.3	2	970.8	85	12	K.IGGIGTVPVGR.V
*	HsFLAG-p53-DNA-D	3.9705	0.3563	2571.2	2573.066	6558.7	1	577	41.3	2	R.VETGILRPGMVVTFAPVNITTEVK.S
*	HsFLAG-p53-DNA-D	4.8242	0.3307	2572.29	2573.066	5365	1	891.3	35.9	3	R.VETGILRPGMVVTFAPVNITTEVK.S
gi|7657649|re	6	21	35.20%	352	39595	5.2	tropomodulin 3 (ubiquitous) [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.5511	0.3254	1933.35	1934.061	5678.6	1	1436.3	71.9	4	K.DLDEDELLGNLSETELK.Q
*	HsFLAG-Lin9_Ti_20	3.9116	0.3378	2328.69	2327.596	7285.1	1	615.7	45	3	K.QLETVLDDLDPENALLPAGFR.Q
*	HsFlag-DPCD_Ti_20	4.4552	0.2714	3886.24	3887.311	8622.2	1	737.2	21.4	3	K.VSLDPELEEALTSASDTELCDLAAILGMHNLITNTK.F
*	HsFlag-DPCD_Ti_20	3.9809	0.4774	2139.74	2139.41	4990.5	1	642.2	58.3	7	K.ILPVFDEPPNPTNVEESLK.R
*	HsFLAG-Lin9_Ti_20	3.0941	0.2567	2315.56	2316.703	9976.4	1	645.4	40.5	1	K.SLNVESNFITGVGILALIDALR.D
*	HsFLAG-Lin9_Ti_20	4.4261	0.315	3330.23	3330.803	5527.3	1	466.5	24.2	3	K.SLNVESNFITGVGILALIDALRDNETLAELK.I
gi|34098946|r	7	23	35.20%	324	35924	9.9	nuclease sensitive element binding protein 1 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.925	0.3759	1745.19	1745.93	6667.6	1	1504.7	75	2	R.NDTKEDVFVHQTAIK.K
	HsFlag-NUFIP_Ti_1	3.8133	0.4608	1797.85	1796.882	6497.5	1	815	59.4	9	R.SVGDGETVEFDVVEGEK.G
*	HsFlag-NUFIP_Ti_1	2.9823	0.2566	1696.4	1696.858	5404.5	1	889.3	55.6	1	K.GAEAANVTGPGGVPVQGSK.Y
*	HsFLAG-ARP6_Ti_1	4.8538	0.3332	1690.43	1689.692	9873.1	1	2526.5	84.6	4	R.NYQQNYQNSESGEK.N
*	HsFlag-NUFIP_Ti_11	2.7615	0.089	1131.47	1130.353	5577.9	4	643.1	78.6	2	R.RFPPYYMR.R
*	HsFlag-NUFIP_Ti_1	5.4859	0.3595	3225.31	3225.48	6978	1	606.3	27.6	4	R.RPQYSNPPVQGEVMEGADNQGAGEQGRPVR.Q
*	HsFlag-NUFIP_Ti_11	2.7599	0.1694	1266.36	1266.399	8339.5	1	797.3	70	1	R.RPENPKPQDGK.E
gi|4504897|re	9	53	35.00%	529	57862	5.4	karyopherin alpha 2 [Homo sapiens]				
gi|89042174|r	9	53	35.00%	529	57862	5.4	PREDICTED: similar to Importin alpha-2 subunit (Karyopherin alpha-2 subunit) (SRP1-alpha) (RAG cohort pro				
gi|89042170|r	9	53	35.00%	529	57862	5.4	PREDICTED: similar to Importin alpha-2 subunit (Karyopherin alpha-2 subunit) (SRP1-alpha) (RAG cohort pro				
	HsTIP60_Ti_103.178	4.4208	0.4248	1877.59	1877.962	5080.1	1	951.1	68.8	2	R.NVSSFPDDATSPLQENR.N
	HsTIP60_Ti_105.224	3.7573	0.289	1690.43	1689.822	6639	1	1166.4	67.9	4	R.NNQGTVNWSVDDIVK.G
	HsTIP60_Ti_103.166	5.2124	0.3719	1901.53	1902.031	8038.3	1	1564.7	64.7	5	K.GINSSNVENQLQATQAAR.K
	HsTIP60_Ti_105.320	4.3819	0.3954	2844.32	2844.027	7978.5	1	996.2	42	5	R.TDCSPIQFESAWALTNIASGTSEQTK.A
	HsFLAG-TIP49a_Ti_	3.8466	0.1175	2666.91	2667.102	3563.5	1	436	45.8	2	K.YGAVDPLLALLAVPDMSSLACGYLR.N
	HsFLAG-Lin9_Ti_20	4.2375	0.4047	1944.29	1944.282	4852.7	1	891.2	67.6	17	K.NPAPPIDAVEQILPTLVR.L
	HsTIP60_Ti_106.275	4.3794	0.2575	1551.73	1550.882	4436.8	1	789.3	71.4	10	K.LLGASELPIVTPALR.A
	HsMRGBP-FLAG_Ti_	3.504	0.2646	3357.5	3354.825	6654	1	880.3	28.1	1	R.AIGNIVTGTDEQTQVVIDAGALAVFPSLLTNPK.T
	HsFLAG-Lin9_Ti_20	5.9461	0.4729	1972.6	1972.376	7737	1	2053.7	70.6	7	K.IILVILDAISNIFQAAEK.L
gi|4506455|re	6	23	35.00%	331	38890	5	reticulocalbin 1 precursor [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.8536	0.423	2137.36	2137.308	6595.3	1	1116.1	61.1	4	K.IVDRIDNDGDGFVTTEELK.T
*	HsFLAG-ARP6_Ti_1	2.8865	0.2233	1125.9	1126.301	5457.7	1	1262.9	87.5	2	K.RYIFDNVAK.V
*	HsFLAG-ARP6_Ti_1	5.0923	0.4155	1517.49	1516.729	7555	1	2185.9	87.5	13	K.EIVVLETLEDIDK.N
*	HsFLAG-ARP6_Ti_1	4.4495	0.2751	3700.42	3699.854	7021.3	1	847.6	28.2	1	K.NGDGFVDQDEYIADMFSHEENGPEPDWVLSER.E

*	HsFLAG-ARP6_Ti_1	4.1403	0.3757	1951.33	1951.108	4861	1	858.4	66.7	2	R.HWILPQDYDHAQAEAR.H
*	HsFLAG-ARP6_Ti_1	4.0196	0.3072	3130.48	3132.469	9427.5	1	858.7	26.9	1	K.LTKEEILENWNMFVGSQATNYGEDLTK.N
gi|4827040|re	37	182	34.80%	955	108694	10.2	thyroid hormone receptor associated protein 3 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	5.7077	0.3907	3142.77	3142.19	8119.2	1	1098.1	30.2	2	K.DSRPSQAAGDNQGDEVKEQTFSGGTSQDTK.A
*	HsFLAG-ARP6_Ti_2	4.4129	0.3566	2056.52	2056.153	3282.6	1	538.5	52.6	11	K.ASESSKPWPDATYGTGSASR.A
*	HsFLAG-FLJ20309_	3.4917	0.2551	1017.38	1017.127	4826.1	2	959.7	83.3	3	R.ASAVSELSPR.E
*	HsFLAG-p53-DNA-D	2.4044	0.2619	984.57	985.172	3984.3	1	264.7	75	1	K.SPLQSVVVR.R
*	HsFLAG-Lin9_Ti_20	3.2727	0.1249	984.9	985.172	6572.2	1	1293.4	93.8	7	K.SPLQSVVVR.R
*	HsFLAG-Lin9_Ti_20	3.6196	0.3879	2606.62	2607.704	8319.2	1	668.2	38.5	3	K.SPPSTGSTYGSSQKEESAASGGAAYTK.R
*	HsFLAG-ARP6_Ti_2	4.2426	0.4799	2607.73	2607.704	3868.7	1	531.3	31.7	4	K.SPPSTGSTYGSSQKEESAASGGAAYTK.R
*	HsFLAG-ARP6_Ti_2	2.0039	0.3213	1140.25	1141.18	5310.7	1	576.7	68.2	1	K.GSFSDTGLGDGK.M
*	HsFLAG-FLJ20309_	4.0033	0.3724	1141.41	1141.18	7367.9	1	1534.2	81.8	4	K.GSFSDTGLGDGK.M
*	HsFlag-NUFIP_Ti_2	4.952	0.3403	1739.55	1739.869	9394.7	1	1617.2	69.2	2	K.MADFHKEEMDDQDK.D
*	HsFLAG-ARP5_Ti_1	4.7811	0.2721	2182.7	2182.385	9914.9	1	1207.2	38.2	2	K.MADFHKEEMDDQDKDKAK.G
*	HsFLAG-Lin9_Ti_20	2.8062	0.3796	1488.55	1489.714	3706.5	2	282.2	50	1	K.SGKWEGLVYAPPGK.E
*	HsFLAG-UTX1_Ti_2	4.6593	0.458	1490.61	1489.714	5269.6	1	1266.4	76.9	26	K.SGKWEGLVYAPPGK.E
*	HsFLAG-ARP5_Ti_1	4.2377	0.3162	1746.48	1747.004	7971.9	1	1491.6	66.7	4	K.SGKWEGLVYAPPGKEK.Q
*	HsFLAG-ARP6_Ti_1	4.0262	0.3182	1217.19	1217.41	6846.8	1	1693.7	90	3	K.WEGLVYAPPGK.E
*	HsFLAG-p53-DNA-D	3.7508	0.3065	1474.35	1474.7	6328.9	1	968.5	75	2	K.WEGLVYAPPGKEK.Q
*	HsFLAG-ARP6_Ti_2	4.4022	0.3749	1623.27	1623.714	7996.6	1	1886.9	79.2	1	R.KTEELEEESFPER.S
*	HsFLAG-ARP6_Ti_2	4.1405	0.2839	1496.32	1495.54	8476.2	1	2117.7	86.4	3	K.TEELEEESFPER.S
*	HsFLAG-ARP6_Ti_1	3.4279	0.2473	2150.75	2151.356	4024.7	2	249.7	41.7	1	R.MDSFDEDLARPSGLLAQER.K
*	HsFlag-NUFIP_Ti_1	4.4901	0.3874	2151.5	2151.356	5492.5	1	898.4	40.3	7	R.MDSFDEDLARPSGLLAQER.K
*	HsFlag-NUFIP_Ti_1	2.0818	0.1789	940.62	941.075	4483.9	1	389.5	71.4	3	R.DLVHSNKK.E
*	HsFlag-NUFIP_Ti_1	4.4055	0.3462	1530.38	1530.683	8327.7	1	1812.5	83.3	27	R.SIFQHIQSAQSQR.S
*	HsFLAG-ARP6_Ti_1	5.6429	0.4341	2042.61	2043.376	6735.6	1	1551.5	48.5	6	R.SPSELFAQHIVTIVHHVK.E
*	HsFLAG-Lin9_Ti_20	4.9997	0.4175	2042.79	2043.376	11587.6	1	2569.5	67.6	9	R.SPSELFAQHIVTIVHHVK.E
*	HsFLAG-p53-DNA-D	3.4303	0.4267	1625.64	1625.759	7899.2	1	1056.3	69.2	3	K.EHHFGSSGMTLHER.F
*	HsFLAG-p53-DNA-D	3.1038	0.1697	1192.47	1192.36	6138.1	2	839.9	77.8	3	R.RIDISPSTFR.K
*	HsFLAG-p53-DNA-D	2.6801	0.1451	1037.26	1038.166	5186.9	2	557.6	75	4	K.HGLAHDEMK.S
*	HsFLAG-p53-DNA-D	3.2209	0.2765	1038.38	1038.166	7787	7	1089	81.2	4	K.HGLAHDEMK.S
*	HsFLAG-Lin9_Ti_20	1.977	0.1257	1120.52	1121.235	3512.8	9	268.6	56.2	1	K.YKDDPVDLR.L
*	HsFLAG-ARP6_Ti_2	3.1557	0.196	1121.32	1121.235	4141.2	1	985.6	87.5	5	K.YKDDPVDLR.L
*	HsFLAG-FLJ20309_	4.9369	0.3666	2379.9	2381.379	10466.6	1	1334.7	55.3	8	K.AEEYTEETEEREESTTGFDK.S
*	HsFLAG-ARP5_Ti_1	3.2024	0.2366	1694.53	1693.767	4711.8	1	571.5	66.7	2	R.NREEEWDPEYTPK.S
	HsFLAG-ARP6_Ti_2	2.869	0.2573	1424.11	1423.475	4503.7	1	739.1	80	3	R.EEEWDPEYTPK.S
*	HsFLAG-p53-DNA-D	4.0666	0.4017	1812.32	1812.89	5931.1	1	726.5	64.3	1	K.KYYLHDDREGEGSDK.W
*	HsFLAG-FLJ20309_	4.3182	0.4121	1683.95	1684.716	10314	1	1644	73.1	12	K.YYLHDDREGEGSDK.W
*	HsFLAG-Lin9_Ti_20	3.8396	0.3902	2386.58	2387.343	8888	2	621.1	40	2	K.FSGEEGEIEDDESGTENREEK.D
*	HsFLAG-p53-DNA-D	1.9225	0.146	917.11	917.948	4635	2	466.9	71.4	1	K.DNIQPTTE.-
gi|4758012|re	39	139	34.70%	1675	191613	5.7	clathrin heavy chain 1 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	6.0129	0.3073	3146.86	3147.53	6086.6	1	1614.1	38	8	R.FQEHLQLQNLGINPANIGFSTLTMESDK.F
*	HsFLAG-ARP6_Ti_1	4.0465	0.3157	2197.14	2196.483	9099.1	1	1135.1	50	2	K.VGEQAQVVIIDMNDPSNPIR.R

*	HsFLAG-p53-DNA-D	4.6307	0.3887	1559.59	1558.793	6246.5	1	1147.6	71.4	10	R.RPISADSAIMNPASK.V
*	HsFLAG-TCF3_Ti_1	3.8461	0.3809	2336.83	2339.802	7252.3	1	773	31.8	3	R.RPISADSAIMNPASKVIALKAGK.T
*	HsFLAG-ARP6_Ti_1	3.9721	0.3411	1519.22	1519.667	5599.5	1	765.5	70.8	3	R.HSSLAGCQIINYR.T
*	HsARP6-FLAG_Ti_1	3.8184	0.3038	1501.51	1500.741	7599.1	1	1274.7	75	2	K.WLLLTGISAQQNR.V
*	HsFLAG-ARP6_Ti_1	4.2196	0.3316	1718.38	1717.922	6070.9	1	1155.3	70	5	K.VSQPIEGHAASFAQFK.M
*	HsFLAG-Lin9_Ti_20	4.7809	0.3474	1945.49	1946.257	5856.3	1	845.1	58.8	7	K.LHIIEVGTPPTGNQPFPK.K
*	HsFLAG-ARP6_Ti_1	2.6337	0.3343	1073.17	1072.293	4861.8	1	639.9	81.2	1	K.HDVVFLITK.Y
*	HsFLAG-ARP6_Ti_1	4.0643	0.471	2353.55	2354.668	4790.3	1	603.2	47.7	1	R.ISGETIFVTAPHEATAGIIGVNR.K
*	HsARP6-FLAG_Ti_1	3.9534	0.3105	2354.83	2354.668	6792.3	1	870.3	33	2	R.ISGETIFVTAPHEATAGIIGVNR.K
*	HsFLAG-p53-DNA-D	5.6841	0.3692	1759.48	1759.959	6688.5	1	1754.6	76.7	2	R.KFNALFAQGNYSEAAK.V
*	HsFLAG-ARP6_Ti_1	5.2277	0.3601	1633.03	1631.785	5991.5	1	1925.9	85.7	3	K.FNALFAQGNYSEAAK.V
*	HsFlag-NUFIP_Ti_1	2.7847	0.244	3188.36	3189.638	5705.5	1	233.6	28.6	1	R.FQSVPAQPGQTSPLLQYFGILLDQGQLNK.Y
*	HsFLAG-Lin9_Ti_20	6.4557	0.3875	3190.03	3189.638	9891.3	1	1249.8	31.2	4	R.FQSVPAQPGQTSPLLQYFGILLDQGQLNK.Y
*	HsFLAG-ARP6_Ti_1	3.3856	0.2625	1848.57	1849.063	5525.3	3	311.5	50	3	K.YESLELCRPVLQQGR.K
	HsFLAG-ARP6_Ti_1	3.4464	0.3159	1609.61	1608.924	5551.2	1	1130.8	75	2	K.KVGYTPDWIFLLR.N
	HsFLAG-UTX1_Ti_2	3.5603	0.3113	1481.6	1480.75	3638.8	1	704.1	81.8	3	K.VGYTPDWIFLLR.N
*	HsFlag-FLJ90652_2	3.1672	0.3313	1368.43	1369.48	5189.8	1	707.6	72.7	3	K.NNRPSEGPLQTR.L
*	HsFLAG-ARP8_Ti_2	4.1739	0.3329	3133.45	3130.625	10789.5	1	1071.1	28.8	1	R.LLEMNLMHAPQVADAILGNQMFTHYDR.A
	HsFlag-VPS71_Ti_1	3.1346	0.3219	1069.55	1070.2	5953.7	1	723.3	75	6	R.AHIAQLCEK.A
	HsFlag-VPS71_Ti_1	2.8183	0.1175	1070.33	1070.2	4666.1	5	680.9	75	1	R.AHIAQLCEK.A
*	HsFLAG-ARP6_Ti_1	4.0257	0.338	1466.78	1465.646	5603.7	1	1079.2	77.3	1	R.ALEHFTDLYDIK.R
*	HsFlag-VPS71_Ti_1	3.172	0.2431	2198.86	2200.453	8541.2	1	684.4	50	2	K.YHEQLSTQSLIELFESFK.S
*	HsFLAG-ARP6_Ti_1	3.5927	0.2102	2043.4	2042.344	8120.5	1	760.4	47.2	1	R.LPVVIGGLLDVDCSEDVIK.N
*	HsFlag-VPS71_Ti_1	4.6244	0.3884	1777.62	1777.898	6876.2	1	1590.5	76.7	2	R.IHEGCEEPATHNALAK.I
*	HsFlag-DPCD_Ti_20	4.5079	0.3488	2153.68	2154.314	6109.3	1	1025.7	61.8	5	R.GQCDLELINVCNENSLFK.S
*	HsFLAG-ARP6_Ti_1	3.6894	0.4418	1875.81	1876.076	10010.6	1	1600.9	63.3	3	K.DPELWGSVLLESNPYR.R
*	HsFLAG-ARP6_Ti_1	4.6427	0.3389	2882.11	2883.225	9002.2	1	1794.5	36	2	R.RPLIDQVVQTALSETQDPEEVSVTVK.A
	HsFlag-VPS71_Ti_1	4.0616	0.248	1950.64	1948.282	3686.6	1	775.8	68.8	11	K.AFMTADLPNELIELLEK.I
	HsFlag-VPS71_Ti_1	2.9052	0.1604	1418.56	1416.577	7873.4	1	1145.6	72.7	2	K.IVLDNSVFSEHR.N
	HsFLAG-ARP6_Ti_1	4.5161	0.2736	1354.38	1354.676	8474.1	1	1871	86.4	13	R.NLQNLLILTAIK.A
*	HsFlag-VPS71_Ti_1	6.0626	0.3722	2370.75	2369.683	8073.9	1	2018.4	43.8	4	R.KFDVNTSAVQVLIEHIGNLDR.A
*	HsFLAG-ARP6_Ti_1	3.2339	0.3312	1297.41	1297.456	6664.8	1	1236.2	85	2	K.LLYNNVSNFGR.L
*	HsFlag-VPS71_Ti_1	4.623	0.3908	1971.79	1972.208	5677.8	1	1368.2	63.9	7	R.LASTLVHLGEYQAAVDGAR.K
*	HsFLAG-ARP6_Ti_1	3.5709	0.1269	3130.67	3131.496	11146	1	949.8	28	1	R.LAQMCGLHIVVHADELEELINYYQDR.G
*	HsFLAG-ARP6_Ti_1	4.4561	0.4169	2355.1	2356.551	7977.9	1	1092.6	52.6	3	K.SVNESLNNLFITEEDYQALR.T
*	HsFLAG-ARP6_Ti_1	4.9078	0.3743	1944.2	1944.065	8069.4	1	2307.6	75	5	R.TSIDAYDNFDNISLAQR.L
*	HsFLAG-UTX1_Ti_2	3.8562	0.2917	2121.7	2122.336	7707.7	1	1353.7	59.4	2	K.DTELAEELLQWFLQEEK.R
gi|5031699|re	11	30	34.70%	427	47355	7.5	flotillin 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.6026	0.2262	1217.3	1216.464	8443.2	1	1739	90	2	R.ISLNTLTLNVK.S
*	HsFLAG-ARP6_Ti_1	4.1158	0.3613	1407.62	1406.668	3312.4	1	724.1	80.8	3	R.HGVPISVTGIAQVK.I
*	HsFLAG-ARP6_Ti_1	4.9615	0.4198	2020.72	2019.222	6004.4	1	1275.5	47.1	5	K.TEAEIAHIALETLEGHQR.A
*	HsFLAG-ARP6_Ti_1	4.5111	0.5334	1983.39	1984.315	7208	1	1270	58.3	9	K.VASSDLVNMGISVVSYTLK.D
*	HsFLAG-ARP6_Ti_1	4.1036	0.3231	1470.26	1470.625	7687	1	1934.4	83.3	1	R.AQQVAVQEQEIAR.R

*	HsFLAG-ARP6_Ti_1	4.3679	0.3464	1379.37	1379.577	6213.1	1	1409.3	79.2	2	R.MRGEAEAFAIGAR.A
*	HsFLAG-ARP6_Ti_1	2.9455	0.302	2338.89	2340.697	10816.8	1	566.4	39.5	1	K.KAEAFQLYQEAAQLDMLLEK.L
*	HsFLAG-ARP6_Ti_1	3.5473	0.2547	2339.96	2340.697	10239.8	1	1267.4	34.2	1	K.KAEAFQLYQEAAQLDMLLEK.L
*	HsFLAG-ARP6_Ti_1	4.6753	0.4925	1753.91	1754.978	6879.8	1	1501.7	68.8	2	K.LPQVAEEISGPLTSANK.I
*	HsFLAG-ARP6_Ti_1	4.0222	0.222	1216.59	1216.42	6169.7	1	1645	90	1	K.VTGEVLDILTR.L
*	HsFLAG-ARP6_Ti_1	3.4345	0.2344	1283.41	1283.47	6249.3	1	743.8	68.2	3	R.LTGVSISQVNHK.P
gi|4885379|re	17	223	34.70%	219	21865	11	H1 histone family, member 4 [Homo sapiens]				
	HsFLAG-TCF3_Ti_1	3.2643	0.3269	1326.71	1327.564	6954.3	2	515.5	50	5	R.KASGPPVSELITK.A
	HsFLAG-TCF3_Ti_1	4.9006	0.3748	1327.44	1327.564	7126.5	1	2047.7	87.5	16	R.KASGPPVSELITK.A
	HsFLAG-ARP6_Ti_1	4.397	0.2266	1328.74	1327.564	4535.9	1	1145.4	56.2	1	R.KASGPPVSELITK.A
	HsFlag-NUFIP_Ti_1	3.3729	0.2564	1198.14	1199.39	5929.5	1	866.6	77.3	68	K.ASGPPVSELITK.A
	HsFLAG-FLJ20309_	3.0382	0.2718	1198.52	1199.39	8477.2	3	646.4	59.1	6	K.ASGPPVSELITK.A
	HsFLAG-Lin9_Ti_20	3.0617	0.1302	847.04	846.015	3664.5	3	944	93.8	10	R.SGVSLAALK.K
	HsFLAG-p53-DNA-D	3.6663	0.1223	973.78	974.189	5265.2	3	1165.6	94.4	20	R.SGVSLAALKK.A
	HsFLAG-p53-DNA-D	3.6718	0.3489	1235.52	1236.411	6430.2	1	1295.6	77.3	2	K.KALAAAGYDVEK.N
	HsFLAG-p53-DNA-D	4.871	0.4075	1236.42	1236.411	8171.8	1	2418	90.9	3	K.KALAAAGYDVEK.N
	HsFLAG-p53-DNA-D	4.9255	0.4111	1707.39	1707.884	8048	1	1885.7	70	3	K.KALAAAGYDVEKNNSR.I
	HsFlag-FLJ20643_Ti	3.4651	0.3974	1107.57	1108.236	9933.9	1	1436.6	75	24	K.ALAAAGYDVEK.N
	HsFLAG-ARP6_Ti_2	3.7074	0.3214	1108.09	1108.236	4889.2	1	1195.4	85	40	K.ALAAAGYDVEK.N
	HsFLAG-ARP6_Ti_1	4.1777	0.3647	1579.17	1579.71	7228.5	1	1615.9	75	4	K.ALAAAGYDVEKNNSR.I
	HsVPS71-FLAG_Ti_	3.6461	0.2615	1540.18	1539.729	5699.1	1	976.7	66.7	2	K.GTLVQTKGTGASGSFK.L
	HsFLAG-ARP6_Ti_1	3.3753	0.2545	1167.29	1167.307	7149.1	1	1246.2	77.3	2	K.GTGASGSFKLNK.K
	HsFLAG-p53-DNA-D	2.2696	0.0973	987.61	987.144	3002.7	6	378.2	66.7	1	K.KAASGEAKPK.A
*	HsFLAG-p53-DNA-D	3.1523	0.0897	784.57	784.934	3943.9	1	678.9	81.2	16	K.KPAAAAGAK.K
gi|51036603|r	2	2	34.70%	72	8006	9	G-protein gamma-12 subunit [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.0581	0.2012	1147.26	1147.233	7964.1	2	1138.6	80	1	K.TASTNNIAQAR.R
*	HsFLAG-ARP6_Ti_1	2.6231	0.1742	1640.87	1640.731	4447.1	4	407.8	53.8	1	K.ASADLMSYCEEHAR.S
gi|4506661|re	12	64	34.60%	266	29996	10.6	ribosomal protein L7a [Homo sapiens]				
	HsFLAG-TCF3_Ti_1	2.3847	0.2042	979.61	980.239	5836.4	1	651.2	66.7	3	K.KVAPAPAVVK.K
	HsFLAG-ARP6_Ti_1	2.7499	0.2699	980.34	980.239	3621.3	1	694.6	83.3	3	K.KVAPAPAVVK.K
	HsFLAG-p53-DNA-D	2.4982	0.2511	851.54	852.065	3578.9	1	460.9	68.8	11	K.VAPAPAVVK.K
	HsFlag-Ies6_293_Ti_	1.9708	0.1172	945.5	946.134	4193.3	9	486	78.6	1	K.VVNPLFEK.R
	HsFlag-Ies6_293_Ti_	3.5635	0.2422	1217.12	1217.367	4843.6	1	1149.1	85	4	K.NFGIGQDIQPK.R
	HsFLAG-TCF3_Ti_1	2.7097	0.2127	1569.68	1570.789	5391.8	3	303.7	46.2	2	K.VPPAINQFTQALDR.Q
	HsFLAG-UTX1_Ti_2	3.9383	0.3688	1571.6	1570.789	5595.3	1	1298.2	80.8	23	K.VPPAINQFTQALDR.Q
	HsFLAG-TCF3_Ti_1	4.1887	0.2465	1346.52	1346.524	6235.8	1	848.1	70.8	7	R.AGVNTVTTLVENK.K
	HsFLAG-ARP6_Ti_1	3.7392	0.1839	1475.6	1474.698	5372.9	1	786.3	69.2	4	R.AGVNTVTTLVENKK.A
*	HsFLAG-TCF3_Ti_1	4.416	0.2206	2689.01	2689.18	6101.8	1	762.3	45.7	2	K.AQLVVIAHDVDPIELVVFLPALCR.K
	HsFLAG-ARP6_Ti_1	2.8566	0.3316	1221.4	1221.407	4864	1	627.1	80	2	R.RHWGGNVLGPK.S
	HsFLAG-TCF3_Ti_1	3.0447	0.2716	1064.47	1065.22	5436.9	1	717.3	77.8	2	R.HWGGNVLGPK.S
gi|14916501|r	4	27	34.60%	130	15069	10.9	ribosomal protein S24 isoform a [Homo sapiens]				
gi|4506703|re	4	27	33.80%	133	15423	10.8	ribosomal protein S24 isoform c [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.5025	0.312	1238.07	1237.503	5411	8	666.3	80	2	K.QMVIDVLHPGK.A

	HsFLAG-TCF3_Ti_1	3.6934	0.3935	1399.62	1399.632	4657.3	1	870.2	81.8	22	K.TTPDVIFVFGFR.T
	HsFLAG-TIP49b_Ti_	1.8817	0.121	703.23	703.776	3961.3	2	438.3	83.3	1	R.THFGGGK.T
	HsFLAG-TCF3_Ti_1	3.0533	0.3235	1683.35	1682.885	6028	1	575.6	53.6	2	K.TTGFGMIYDSLDYAK.K
gi|4758302|re	6	75	34.60%	104	12259	5.9	enhancer of rudimentary homolog [Homo sapiens]				
*	HsFLAG-ARP6_Ti_2	6.1107	0.5545	2056.2	2056.137	5563.5	1	1562.8	78.1	41	R.TYADYESVNECMEGVCK.M
*	HsFLAG-ARP6_Ti_1	2.6939	0.172	950.11	950.097	3741.3	7	609.9	91.7	2	K.MYEEHLK.R
*	HsFLAG-ARP5_Ti_1	1.8455	0.098	1105.47	1106.285	5346.2	4	400.8	64.3	1	K.MYEEHLKR.M
*	HsFLAG-ARP5_Ti_1	2.8906	0.1695	1107.12	1106.285	6682.9	6	706.9	78.6	3	K.MYEEHLKR.M
*	HsFLAG-p53-DNA-D	2.4415	0.252	1328.46	1329.409	5649.9	1	517.8	65	8	R.ADTQTYQPYNK.D
*	HsFLAG-ARP6_Ti_2	3.7224	0.2571	1329.43	1329.409	5641.8	1	1007.9	80	20	R.ADTQTYQPYNK.D
gi|4507645|re	6	10	34.50%	249	26669	6.9	triosephosphate isomerase 1 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.6427	0.3131	1543.38	1543.804	8726.8	1	2389	82.1	1	R.KQSLGELIGTLNAAK.V
*	HsH2AZ-FLAG_293_	3.8349	0.3863	1415.41	1415.63	5688.4	1	1740.9	92.3	1	K.QSLGELIGTLNAAK.V
*	HsH2AZ-FLAG_293_	4.3017	0.3778	2192.54	2193.427	3917.3	1	375.9	44.7	5	K.VPADTEVVCAPPTAYIDFAR.Q
	HsFLAG-RPB5MP_2	2.7392	0.2182	1137.84	1138.275	5705.1	1	1105.3	88.9	1	K.IAVAAQNCYK.V
	HsFLAG-RPB5MP_2	4.1735	0.364	1235.4	1235.296	6808.1	1	1590.9	86.4	1	K.SNVSDAVAQSTR.I
*	HsFLAG-Lin9_Ti_20	3.8439	0.2589	3031.8	3031.433	2685.8	1	269.7	27.7	1	K.ELASQPDVDGFLVGGASLKPEFVDIINAK.Q
gi|39930523|r	8	42	34.40%	381	41037	5	hypothetical protein LOC144097 [Homo sapiens]				
*	HsFLAG-FLJ20729_	4.2551	0.3534	2121.49	2122.262	4886.2	1	671.8	38.2	1	K.TPPPRPSPLEAGSDGCEEPK.Q
*	HsFlag-NUFIP_Ti_1	2.7395	0.1665	2121.56	2122.262	7431.5	4	370	36.8	1	K.TPPPRPSPLEAGSDGCEEPK.Q
*	HsFLAG-FLJ20729_	4.4819	0.4088	2069.61	2069.282	7014.5	1	990.9	58.8	2	R.SHILEQHPHTLDLSPSEK.S
*	HsFlag-FLJ90652_2	4.9139	0.3511	2001.89	2001.247	7970.9	1	2501.9	73.5	16	K.SNILEAWSEGVALLQDVR.A
*	HsFlag-DPCD_Ti_20	3.1036	0.3114	2068.34	2068.39	4566.3	2	288.4	44.4	1	R.MPAEIVVLLDSEDNPSLPK.R
*	HsFlag-NUFIP_Ti_1	4.1901	0.4337	1859.52	1860.164	6226.3	1	867.6	58.8	18	R.GLRPLELPAVPATEPGNK.K
*	HsFlag-FLJ90652_2	2.9046	0.1253	1198.65	1199.309	4557.8	2	799.1	80	1	K.DREVAEGGLPR.A
*	HsFLAG-Lin9_Ti_20	4.0942	0.3086	2776.35	2777.017	8117.2	1	977.1	31.7	2	K.RVGAGDTSDWPTVLSESSTTVAGKPEK.G
gi|4503841|re	16	75	34.20%	609	69843	6.6	ATP-dependent DNA helicase II, 70 kDa subunit [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	5.5653	0.4578	2501.19	2502.428	8914.1	1	1465.5	54.8	3	K.TEGDEEAEEEQEENLEASGDYK.Y
*	HsFLAG-p53-DNA-D	3.5972	0.39	2027.62	2027.325	9525.6	1	978.9	52.9	1	K.IISSDRDLLAVVFYGTEK.D
*	HsFlag-VPS71_Ti_1	5.7104	0.2506	1574.74	1574.774	8744.4	1	2593.5	80.8	9	K.NIYVLQELDNPGAK.R
*	HsFLAG-ARP6_Ti_1	3.1173	0.1768	1162.52	1162.374	4531.5	1	822.9	87.5	2	K.RILELDQFK.G
	HsFlag-VPS71_Ti_1	4.2385	0.3186	1405.63	1403.679	5011.9	1	1302.6	86.4	3	R.DTGIFLDLMHLK.K
*	HsFlag-VPS71_Ti_1	3.8727	0.2843	1653.67	1652.842	5532.2	1	805.1	63.3	3	R.TFNTSTGGLLLPSDTK.R
*	HsFLAG-p53-DNA-D	3.4677	0.4079	1808.84	1809.029	5546	1	588.2	53.1	2	R.TFNTSTGGLLLPSDTKR.S
	HsFLAG-p53-DNA-D	2.8285	0.3096	2035.26	2035.554	4898.7	2	342.9	44.1	1	R.FDDPGLMLMGFKPLVLLK.K
*	HsFlag-VPS71_Ti_1	4.0793	0.3511	2501.7	2501.798	4448.9	1	580.6	52.5	3	R.RNIPPYFVALVPQEEELDDQK.I
	HsARP6-FLAG_Ti_1	4.4795	0.4061	2132.56	2133.495	4576.3	1	1127.4	66.7	32	K.IQVTPPGFQLVFLPFADDK.R
	HsFLAG-p53-DNA-D	3.0905	0.2592	2288.17	2289.682	5492.4	1	441.5	47.4	1	K.IQVTPPGFQLVFLPFADDKR.K
	HsFLAG-p53-DNA-D	4.001	0.3032	1704.26	1704.839	5518.5	1	826.3	65.4	6	R.SDSFENPVLQQHFR.N
	HsFLAG-FLJ20729_	4.2945	0.2217	2423.84	2424.812	9501.5	8	1365.2	34.5	1	R.NLEALALDLMEPEQAVDLTLPK.V
	HsFLAG-p53-DNA-D	5.1543	0.2645	2424.95	2424.812	7109.7	1	923.4	50	4	R.NLEALALDLMEPEQAVDLTLPK.V
	HsFLAG-Lin9_Ti_20	3.311	0.2879	1215.51	1215.268	6838.7	5	756	70	2	K.RKHDNEGSGSK.R
	HsFLAG-p53-DNA-D	3.1948	0.1408	1173.21	1173.395	6459.7	1	1000	83.3	2	K.KQELLEALTK.H

gi|5729850|re	7	24	34.20%	354	40532	5.7	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.6666	0.3103	1789.45	1790.156	10750.8	1	1446.4	63.3	4	K.VVVYSNTIQSIIAIIR.A
*	HsFLAG-ARP6_Ti_1	4.9672	0.4619	2079.36	2080.172	8248	1	1889.6	71.9	2	R.EYQLNDSASYYLNDLDR.I
*	HsFLAG-ARP6_Ti_1	4.0968	0.3085	1762.53	1762.96	4858	1	653.7	67.9	1	R.ISQSNYIPTQQDVLR.T
	HsFLAG-ARP6_Ti_1	3.3505	0.2431	1381.35	1381.571	5505.5	1	661.5	68.2	5	K.TTGIVETHFTFK.D
*	HsFLAG-ARP6_Ti_1	5.5585	0.4319	3959.82	3962.207	10219	1	1164.1	25.8	4	K.RSPLTICYPEYTGSNTYEEAAAYIQCQFEDLNR.R
	HsFLAG-ARP6_Ti_1	3.3771	0.3264	1587.44	1587.692	7621.9	1	909.3	66.7	2	K.EIYTHFTCATDTK.N
	HsFLAG-ARP6_Ti_1	3.2254	0.2473	1708.53	1708.995	6149.4	1	791.4	57.1	6	K.NVQFVFDAVTDVIIK.N
gi|35493987|r	4	6	34.20%	158	18007	8.7	ubiquitin-conjugating enzyme E2I [Homo sapiens]				
gi|4507785|re	4	6	34.20%	158	18007	8.7	ubiquitin-conjugating enzyme E2I [Homo sapiens]				
gi|35494003|r	4	6	34.20%	158	18007	8.7	ubiquitin-conjugating enzyme E2I [Homo sapiens]				
gi|35493996|r	4	6	34.20%	158	18007	8.7	ubiquitin-conjugating enzyme E2I [Homo sapiens]				
	HsFlag-VPS71_Ti_1	2.3337	0.3761	1314.71	1315.514	4386.8	1	553.5	63.6	1	K.DHPFGFVAVPTK.N
	HsFlag-NUFIP_Ti_2	3.5102	0.4287	1315.33	1315.514	3968.1	1	682	77.3	3	K.DHPFGFVAVPTK.N
	HsFlag-VPS71_Ti_1	3.1085	0.2654	1219.86	1220.414	5939.4	1	701.5	70	1	K.KGTPWEGGLFK.L
	HsFLAG-Lin9_Ti_20	4.9069	0.3505	3619.64	3618.004	10218.2	1	1312.4	27.5	1	K.QILLGIQELLNEPNIQDPAQAEAYTIYCQNR.V
gi|22094079|r	4	11	34.20%	155	17607	5.7	thyroid hormone receptor interactor 3 isoform 2 [Homo sapiens]				
	HsFlag-NUFIP_Ti_2	3.9584	0.3587	1468.07	1468.629	6231.5	1	1611.2	86.4	2	K.CSTVVCVICLEK.P
	HsFlag-NUFIP_Ti_2	3.7965	0.3509	1692.91	1693.92	7042.4	1	986.5	65.4	6	K.CSTVVCVICLEKPK.Y
*	HsFlag-NUFIP_Ti_2	3.522	0.2038	1392.22	1390.551	7112.5	7	787.1	72.7	2	R.QLMVNLDQGEDK.A
*	HsFlag-NUFIP_Ti_2	3.9156	0.3149	3163.51	3164.396	7779.8	1	742.7	26.9	1	R.AYMQEPLFVEFADCCLGIVEPSQNEES.-
gi|11067747|r	20	60	33.80%	802	92251	8.2	CDC5-like [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.3883	0.3674	1838.77	1839.021	9042.2	1	1461.2	64.3	6	R.TAAQCLEHYEFLLDK.A
*	HsFlag-NUFIP_Ti_2	3.6626	0.3656	1566.56	1566.795	5214.7	1	657.8	65.4	1	R.KLKPGEIDPNPETK.P
*	HsFlag-NUFIP_Ti_2	2.8622	0.2283	1439.32	1438.621	5219.1	1	595.8	66.7	2	K.LKPGEIDPNPETK.P
*	HsFlag-NUFIP_Ti_2	4.5344	0.3841	2429.27	2430.664	7774.3	1	1773.8	41.2	2	K.PARPDPIDMDEDELEMLSEAR.A
*	HsFlag-NUFIP_Ti_2	3.5245	0.2431	1539.27	1538.7	4632.2	1	741	70.8	2	K.RGVDYNAEIPFEK.K
*	HsFlag-NUFIP_Ti_2	4.4685	0.2935	2551.43	2551.728	9529.3	1	1734	38.1	3	K.KPALGFYDTSEENYQALDADFR.K
*	HsFlag-NUFIP_Ti_2	5.4652	0.4271	2678.54	2679.902	12032.8	1	2125	37.5	4	K.KPALGFYDTSEENYQALDADFRK.L
*	HsFlag-NUFIP_Ti_2	3.4635	0.0886	1344.64	1343.483	5800.2	2	1053.6	80	2	K.LRQQDLDGELR.S
*	HsFLAG-FLJ20729_	4.9053	0.297	2010.58	2010.205	7851.7	1	1008.5	55.6	6	K.ESDLPSAILQTSGVSEFTK.K
*	HsFlag-NUFIP_Ti_2	3.0095	0.3714	1948.6	1950.283	4229.8	1	416.5	55.9	5	K.LVLPAPQISDAELQEVVK.V
*	HsFlag-NUFIP_Ti_2	4.9823	0.4879	2011.64	2013.174	10170.1	1	1500.8	55.6	5	K.GGLNTPLHESDFSGVTPQR.Q
*	HsFlag-NUFIP_Ti_2	3.8832	0.2296	2013.02	2013.174	7417.9	1	1153	38.9	2	K.GGLNTPLHESDFSGVTPQR.Q
*	HsFLAG-Lin9_Ti_20	3.9056	0.4258	1688.27	1687.936	7166.8	1	833.7	60.7	2	R.QVVQTPNTVLSTPFR.T
*	HsFlag-NUFIP_Ti_2	2.6341	0.2901	1514.5	1512.706	4588.5	1	456.6	57.1	1	R.SGTTPKPVINSTPGR.T
*	HsFlag-NUFIP_Ti_2	3.4292	0.2114	979.22	979.251	3491.5	1	984.4	94.4	4	R.LGLLGLPAPK.N
*	HsFlag-NUFIP_Ti_2	2.0341	0.19	979.45	979.251	7638.4	7	531.3	61.1	1	R.LGLLGLPAPK.N
*	HsFlag-NUFIP_Ti_2	4.1838	0.4065	1811.41	1811.854	7509.4	1	1678.2	70	4	R.EIDDTYIEDAADVDAR.K
*	HsFLAG-p53-DNA-D	4.5493	0.2936	3086.16	3085.528	7464.2	1	938.2	31.7	3	K.DLPRPSEVNETILRPLNVEPPLTDLQK.S
*	HsFlag-NUFIP_Ti_2	3.5962	0.2423	2553.91	2551.731	4974.7	2	480.8	31	1	K.TVGFGTNNSEHITYLEHNPYEK.F
*	HsFlag-NUFIP_Ti_2	4.4249	0.2672	1489.51	1488.739	8060.7	1	1729.2	79.2	4	K.AQDVLVQEMEVVK.Q
gi|17986258|r	5	27	33.80%	151	16930	4.7	smooth muscle and non-muscle myosin alkali light chain isoform 1 [Homo sapiens]				

gi|17986264|r	5	27	32.50%	157	17557	4.6	smooth muscle and non-muscle myosin alkali light chain isoform 3 [Homo sapiens]				
gi|17986262|r	5	27	44.00%	116	12939	4.9	smooth muscle and non-muscle myosin alkali light chain isoform 4 [Homo sapiens]				
gi|17986260|r	5	27	44.00%	116	12970	4.7	smooth muscle and non-muscle myosin alkali light chain isoform 2 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.778	0.2425	1355.69	1355.534	5029.6	1	804.1	75	3	R.ALGQNPTNAEVLK.V
	HsFlag-VPS71_Ti_1(	4.9027	0.3715	1889.66	1889.263	4533.5	1	946.2	63.3	7	K.VLDFEHFLPMLQTVAK.N
	HsFLAG-ARP6_Ti_1	4.198	0.4159	1545.82	1545.602	8109.8	1	2061.7	87.5	6	K.DQGTYEDYVEGLR.V
	HsFlag-VPS71_Ti_1(	2.9399	0.2406	995.55	996.195	4331.1	2	733.6	75	7	R.HVLVTLGEK.M
	HsFLAG-Lin9_Ti_20	3.6874	0.262	995.98	996.195	3256.9	2	778.9	93.8	4	R.HVLVTLGEK.M
gi|50659095|r	24	102	33.70%	783	87344	9.3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21 [Homo sapiens]				
*	HsFLAG-FLJ20729_	3.9818	0.3468	1650.83	1651.764	7728.2	1	1620.5	80.8	1	K.TEEIAEEEETVFPK.A
*	HsFLAG-ARP5_Ti_1	2.6904	0.338	1560.09	1560.763	6691.4	1	576.1	57.7	1	K.KKAEPSEVDMNSPK.S
*	HsFlag-VPS71_Ti_1(	2.692	0.2745	1432.49	1432.588	5566.3	1	781.3	70.8	1	K.KAEPSEVDMNSPK.S
*	HsFLAG-p53-DNA-D	4.2709	0.1579	1500.42	1500.649	7373.7	2	984.4	70.8	1	K.KKEEPSQNDISPK.T
*	HsFLAG-Lin9_Ti_20	4.0318	0.2285	1712.76	1712.808	6160.6	1	1656.4	78.6	5	K.NEEPSEEEIDAPKPK.K
	HsFLAG-FLJ20729_	3.5926	0.2982	1670.26	1669.828	4527.4	1	895.6	71.4	9	K.EGAFSNFPISEETIK.L
*	HsFLAG-p53-DNA-D	3.6244	0.3108	1221.39	1221.485	4852.7	1	738.9	75	2	R.GVTFLFPIQAK.T
*	HsFLAG-Lin9_Ti_20	2.6023	0.305	1075.45	1076.2	7475.5	2	524.5	62.5	2	K.TFHHVYSGK.D
*	HsFLAG-Lin9_Ti_20	3.506	0.2472	1266.31	1266.523	5194.1	1	1086	85	7	K.TFSFAIPLIEK.L
*	HsFLAG-Lin9_Ti_20	4.2433	0.3646	1378.3	1378.661	9261.5	1	1102.4	66.7	1	R.GRAPQVLVLAPTR.E
*	HsFlag-VPS71_Ti_1(	2.7815	0.3071	1164.7	1165.421	4717.6	1	312.2	65	1	R.APQVLVLAPTR.E
*	HsFlag-DPCD_Ti_20	4.0825	0.2708	1164.9	1165.421	7089.6	1	1318.8	80	9	R.APQVLVLAPTR.E
*	HsFLAG-Lin9_Ti_20	5.3263	0.4541	2137.62	2138.353	7366.6	1	1399.4	63.9	4	K.KLSVACFYGGTPYGGQFER.M
*	HsFLAG-FLJ20729_	3.6936	0.4019	2009.24	2010.179	7120.5	1	803.9	52.9	8	K.LSVACFYGGTPYGGQFER.M
	HsFLAG-Lin9_Ti_20	2.5579	0.1996	1212.13	1212.392	8600.2	7	674.6	63.6	1	R.NGIDILVGTPGR.I
*	HsFLAG-FLJ20729_	3.3099	0.2993	1382.01	1382.56	8223.3	1	915.5	72.7	2	K.DHIQNGKLDLTK.L
*	HsFLAG-Lin9_Ti_20	4.1908	0.3902	2777.79	2778.016	8574.2	1	1418.3	50	1	K.DSEDNPQTLLFSATCPHWVFNVAK.K
*	HsFlag-DPCD_Ti_20	4.7327	0.3394	2778.16	2778.016	5453.4	1	861.4	33.7	4	K.DSEDNPQTLLFSATCPHWVFNVAK.K
*	HsFLAG-Lin9_Ti_20	3.0287	0.2957	1381.33	1381.569	9765.6	1	1331	72.7	1	K.STYEQVDLIGKK.T
*	HsFLAG-UTX1_Ti_2	3.4931	0.2986	1526.09	1525.788	2825.1	1	403.9	73.1	6	R.LLDSVPPTAISHFK.Q
*	HsFlag-DPCD_Ti_20	6.4566	0.3938	2108.9	2109.347	8765.1	1	3420.7	50	9	K.GAVEALAAALAHISGATSVDQR.S
*	HsFlag-VPS71_Ti_1(	5.972	0.5571	2109.73	2109.347	6683.1	1	2034	66.7	12	K.GAVEALAAALAHISGATSVDQR.S
*	HsFLAG-Lin9_Ti_20	4.2981	0.4114	1993.63	1994.215	4005.5	1	541.9	52.9	9	K.LGVCFDVPTASVTEIQEK.W
*	HsFLAG-Lin9_Ti_20	4.3601	0.3125	1840.34	1841.031	8663.8	1	1240.7	63.3	5	R.WQLSVATEQPELEGPR.E
gi|46195723|r	14	87	33.70%	490	54774	10.1	ribosomal L1 domain containing 1 [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1(	2.4946	0.1389	1127.59	1128.28	6240.8	2	512.8	66.7	3	K.AVDALLTHCK.S
*	HsFLAG-ARP6_Ti_1	3.5376	0.2457	1128.34	1128.28	7215.7	2	1180.4	83.3	7	K.AVDALLTHCK.S
*	HsFLAG-ARP6_Ti_1	3.679	0.2924	1330.47	1331.596	6972.7	1	1343.9	86.4	2	K.TVSQIISLQTLK.K
*	HsFlag-NUFIP_Ti_1(	4.6571	0.4098	1532.46	1532.736	7892.2	1	1356	75	4	R.LLSSFDFFLTDAR.I
*	HsFLAG-ARP6_Ti_1	3.4369	0.1629	1025.81	1025.283	7147.6	3	1048.2	87.5	7	R.RLLPSLIGR.H
*	HsFlag-NUFIP_Ti_1(	2.509	0.2563	1184.47	1184.465	2699.6	3	431.3	80	1	K.KVPVSVNLLSK.N
*	HsFLAG-ARP6_Ti_1	2.9022	0.2612	1056.26	1056.291	4374.2	2	747.5	77.8	1	K.VPVSVNLLSK.N
*	HsFlag-NUFIP_Ti_1(	4.0686	0.3697	1634.23	1633.805	6198.1	1	1004.3	71.4	3	R.EINDCIGGTVLNISK.S
*	HsFlag-NUFIP_Ti_11	5.2563	0.4521	2203.17	2202.62	11681.3	1	1270.3	52.6	25	R.IGHVGMQIEHIIENIVAVTK.G

*	HsFLAG-ARP6_Ti_1	2.6893	0.106	1116.3	1116.302	6802.5	3	848.9	81.2	2	K.LPEKWESVK.L
*	HsFlag-NUFIP_Ti_1	5.3313	0.4546	2072.49	2071.294	7441.4	1	1533.9	63.9	23	K.SAALPIFSSFVSNWDEATK.R
*	HsFLAG-ARP6_Ti_1	4.9976	0.3445	2021.16	2021.186	6400.4	1	966.7	55.3	4	K.TASVLSKDDVAPESGDTTVK.K
*	HsFlag-NUFIP_Ti_1	3.3754	0.3558	1840.55	1841.025	4591.8	1	581.1	53.1	4	K.ATNESEDEIPQLVPIGK.K
*	HsFLAG-p53-DNA-D	1.8942	0.1051	1041.32	1042.221	3117.3	2	184.2	61.1	1	R.KALPASETPK.A
gi|16753227|r	11	65	33.70%	288	32728	10.6	ribosomal protein L6 [Homo sapiens]				
gi|67189747|r	11	65	33.70%	288	32728	10.6	ribosomal protein L6 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.2765	0.3518	1284.41	1285.527	5043.8	1	541.4	62.5	6	K.VLATVTKPVGGDK.N
	HsMRGBP-FLAG_Ti_	3.5938	0.2853	1285.55	1285.527	5390.4	1	667	66.7	19	K.VLATVTKPVGGDK.N
	HsFLAG-ARP6_Ti_1	4.249	0.44	1526.92	1526.86	4827	1	651.2	64.3	10	R.ASITPGTILIILTGR.H
	HsFLAG-TCF3_Ti_1	5.21	0.4479	1765.84	1765.15	7982.2	1	1285.9	65.6	7	K.QLASGLLLVTGPLVLNR.V
	HsFLAG-TCF3_Ti_1	1.9579	0.1203	866.54	867.033	6606.4	1	673	78.6	2	K.FVIATSTK.I
	HsFLAG-TCF3_Ti_1	2.0581	0.2744	994.37	995.123	4964.4	1	452.5	71.4	1	K.HLTDAYFK.K
	HsFLAG-TCF3_Ti_1	3.1567	0.291	995.35	995.123	5083.4	1	970.1	92.9	4	K.HLTDAYFK.K
	HsFlag-Ies6_293_Ti_	3.1622	0.352	1333.56	1333.397	6713.5	1	1139	80	1	R.HQEGEIFDTEK.E
	HsFLAG-ARP6_Ti_1	3.0241	0.0922	1196.4	1196.302	5949.6	1	845.8	81.2	3	K.EKYEITEQR.K
	HsFLAG-ARP6_Ti_1	4.1922	0.381	1448.91	1447.677	8202.7	1	1294.9	75	11	R.SVFALTNGIYPHK.L
	HsFLAG-TCF3_Ti_1	2.6685	0.1755	1806.39	1807.145	8782.8	7	368.3	43.3	1	R.SVFALTNGIYPHKLVF.-
gi|7661958|re	31	219	33.60%	920	106122	10	BCL2-associated transcription factor 1 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	4.2612	0.3994	2608.33	2609.676	5946.2	1	803	50	1	K.SQEEPKDTFEHDPSESIDEFNK.S
	HsFLAG-FLJ20309_	4.4768	0.3065	2609.29	2609.676	5563.1	1	1164.5	40.5	3	K.SQEEPKDTFEHDPSESIDEFNK.S
	HsFLAG-Lin9_Ti_20	3.3212	0.393	1909.47	1910.945	5751.3	1	598.7	60	1	K.DTFEHDPSESIDEFNK.S
	HsFLAG-ARP6_Ti_1	5.1513	0.412	2081.01	2082.191	4345.3	1	1197.2	65.8	14	K.SSATSGDIWPGLSAYDNSPR.S
	HsFLAG-ARP6_Ti_1	5.7567	0.5084	3149.59	3150.41	5943.5	1	989.4	33.3	5	R.SPHSPSPIATPPSQSSSCSDAPMLSTVHSAK.N
	HsFLAG-Lin9_Ti_20	3.2888	0.3921	1841.82	1842.925	8446.2	1	920.3	60	1	K.NTPSQHSHSIQHSPER.S
	HsFLAG-ARP6_Ti_1	2.5523	0.1984	967.27	968.101	4600.9	6	828.2	87.5	1	K.TIAPQNAPR.D
	HsH2AZ-FLAG_293_	2.8249	0.2658	1502.15	1502.534	2926	1	542.6	73.1	2	R.SSFYPDGGDQETAK.T
	HsFLAG-Lin9_Ti_20	5.2958	0.3655	2246.57	2246.308	7267	1	1898.4	69.4	4	K.GRAEGEWEDQEALDYFSDK.E
	HsFLAG-Lin9_Ti_20	5.0374	0.3337	2032.96	2033.069	9320.5	1	2207.5	71.9	1	R.AEGEWEDQEALDYFSDK.E
	HsFLAG-FLJ20309_	5.5489	0.5305	1922.24	1922.824	6865.1	1	1753.4	73.3	20	K.FNDSEGDDTEETEDYR.Q
*	HsFLAG-p53-DNA-D	4.7777	0.3353	1708.24	1708.952	9846.3	1	1611.4	64.3	3	K.LKETGYVVERPSTTK.D
	HsARP6-FLAG_Ti_1	4.0025	0.399	1467.31	1467.619	6423.2	1	915.3	75	17	K.ETGYVVERPSTTK.D
	HsFLAG-p53-DNA-D	4.3204	0.369	1573.66	1573.832	9737	1	1775.8	75	1	K.LKDLFDYSPPLHK.N
	HsFLAG-Lin9_Ti_20	3.5931	0.26	1332.32	1332.499	7653.8	1	1005.4	70	12	K.DLFDYSPPLHK.N
	HsFlag-DPCD_Ti_20	3.8989	0.261	1370.22	1370.566	8028.2	1	1481.2	81.8	15	K.MIASDSHRPEVK.L
	HsFLAG-ARP6_Ti_1	4.047	0.3734	1812.47	1813.079	5550.3	2	533.8	56.2	24	K.MAPVPLDDSNRPASLTK.D
	HsARP6-FLAG_Ti_1	3.247	0.2366	1439.34	1439.698	6648.9	1	1365.4	83.3	9	K.DRLLASTLVHSVK.K
	HsFlag-NUFIP_Ti_11	4.0313	0.1564	1439.98	1439.698	6001.1	1	1627.3	58.3	4	K.DRLLASTLVHSVK.K
	HsFLAG-UTX1_Ti_2	2.5908	0.1827	1169.61	1168.422	4573.5	8	374.5	60	8	R.LLASTLVHSVK.K
	HsFLAG-FLJ20309_	3.8371	0.2884	1169.73	1168.422	6485.1	1	1340.1	85	32	R.LLASTLVHSVK.K
	HsFLAG-Lin9_Ti_20	3.9334	0.3292	1296.14	1296.596	8716.5	1	1516.9	77.3	2	R.LLASTLVHSVKK.E
	HsFLAG-p53-DNA-D	3.9366	0.2838	1484.42	1484.739	9225.3	1	1148.9	66.7	4	R.SIFDHIKLPQASK.S
	HsFLAG-FLJ20729_	4.3567	0.3409	2048.13	2049.337	9388	1	952.6	50	5	K.STSESFIQHIVSLVHHVK.E

	HsFLAG-BC014022_	4.3344	0.463	2049.27	2049.337	4916.2	1	977.5	45.6	6	K.STSESFIQHIVSLVHHVK.E
*	HsFLAG-ARP6_Ti_2	2.9345	0.2083	993.29	993.123	5521	1	1044.5	87.5	2	K.SAAMTLNER.F
*	HsFLAG-p53-DNA-D	3.4994	0.3769	1804.69	1804.954	4238.6	1	580.4	65.4	2	K.RPKEEEWDPEYTPK.S
	HsFLAG-ARP6_Ti_2	2.869	0.2573	1424.11	1423.475	4503.7	1	739.1	80	3	K.EEEWDPEYTPK.S
*	HsFLAG-p53-DNA-D	3.0895	0.1037	2143.73	2144.307	9303.3	1	622.9	46.9	1	K.KYFLHDDRDDGVDYWAK.R
*	HsFLAG-ARP5_Ti_1	4.3283	0.3842	2015.29	2016.133	7258.6	1	935.9	60	7	K.YFLHDDRDDGVDYWAK.R
	HsFLAG-ARP6_Ti_2	4.9742	0.2722	2358.56	2359.391	6939.8	1	1704.2	63.2	9	K.YQGDGIVEDEEETMENNEEK.K
gi|21614544|r	3	4	33.30%	93	10834	7	S100 calcium-binding protein A8 [Homo sapiens]				
*	HsFLAG-RPB5MP_2	3.7614	0.3114	1272.9	1273.475	5506.7	1	933.7	80	1	K.ALNSIIDVYHK.Y
*	HsFLAG-RPB5MP_2	2.7361	0.3326	964.12	964.071	5188.2	1	810.7	85.7	1	K.GNFHAVYR.D
*	HsFLAG-RPB5MP_2	2.833	0.2527	1550.55	1550.761	7247.9	1	859	68.2	2	K.KLLETECPQYIR.K
gi|4758086|re	4	11	33.20%	193	20567	8.6	cysteine and glycine-rich protein 1 [Homo sapiens]				
*	HsSrcap_Ti_204.209	4.5908	0.4102	2045.37	2046.166	9583.2	1	855.3	53.1	4	K.TVYFAEEVQCEGNSFHK.S
*	HsSrcap_Ti_201.076	4.1274	0.4051	1475.4	1475.555	7512.8	1	1273.7	71.4	2	K.GYGYGQGAGTLSTDK.G
*	HsSrcap_Ti_206.185	4.06	0.4164	1843.46	1843.954	6886.4	1	964.4	62.5	2	K.HEEAPGHRPTTNPNASK.F
*	HsSrcap_Ti_202.230	4.1239	0.4268	1434.81	1434.551	7278.6	1	1123.4	67.9	3	K.GFGFGQGAGALVHSE.-
gi|4758504|re	4	9	33.00%	261	26923	7.8	hydroxyacyl-Coenzyme A dehydrogenase, type II isoform 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	5.338	0.3935	2195.53	2196.466	6254.5	1	1038.9	52.3	2	R.LVGQGASAVLLDLPNSGGEAQAK.K
*	HsFLAG-ARP6_Ti_1	3.8679	0.4339	1850.06	1851.033	6723.4	1	956.4	59.4	1	K.KLGNNCVFAPADVTSEK.D
*	HsFlag-NUFIP_Ti_10	4.4187	0.326	2086.32	2086.538	5214.2	1	1017.4	60.5	3	R.VMTIAPGLFGTPLLTSLPEK.V
*	HsSrcap_Ti_203.509	4.4184	0.284	2880.06	2880.273	9363.5	1	1087.4	30	3	R.LGDPAEYAHLVQAIIENPFLNGEVIR.L
gi|4506645|re	3	10	32.90%	70	8218	10.1	ribosomal protein L38 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.9994	0.2956	1576.43	1576.877	7888.6	1	2031.2	87.5	6	R.KIEEIKDFLLTAR.R
*	HsFLAG-ARP6_Ti_1	2.6435	0.1236	1228.54	1229.459	9020.1	4	874.2	72.2	2	R.YLYTLVITDK.E
*	HsFLAG-ARP6_Ti_1	2.7021	0.2023	1229.62	1229.459	5439.9	1	956.9	88.9	2	R.YLYTLVITDK.E
gi|51988900|r	32	77	32.80%	1186	133307	5.3	XPG-complementing protein [Homo sapiens]				
*	HsSrcap_Ti_205.501	5.0755	0.4137	1698.43	1698.059	7149.2	1	1650.1	75	1	K.ILAVDISIWLNQALK.G
*	HsSrcap_Ti_205.336	4.854	0.2223	1702.04	1702.05	8021.1	1	1935.9	51.8	2	R.IRPIFVFDGDAPLLK.K
*	HsSrcap_Ti_205.335	4.1484	0.3665	1702.41	1702.05	5658	1	986.8	67.9	2	R.IRPIFVFDGDAPLLK.K
*	HsSrcap_Ti_203.178	3.528	0.1723	1385.81	1385.563	8025.9	1	1657.1	81.8	2	K.RDEALPSLTQVR.R
*	HsSrcap_Ti_206.219	2.8224	0.1909	1522.6	1523.691	5027.2	1	559.3	63.6	1	K.NYLNQHIEHVQK.E
*	HsSrcap_Ti_206.219	4.5852	0.2618	1523.4	1523.691	10614.2	1	2244.6	86.4	2	K.NYLNQHIEHVQK.E
*	HsSrcap_Ti_205.111	1.9443	0.0911	1336.48	1337.456	4261	1	246	60	1	K.EMNQQHSGHIR.R
*	HsSrcap_Ti_206.187	2.9119	0.2798	1337.63	1337.456	6516.3	1	610.9	70	2	K.EMNQQHSGHIR.R
*	HsSrcap_Ti_204.185	3.4399	0.1765	1660.73	1660.911	5781.8	2	776.7	73.1	2	R.RVVSEDTSHYILIK.G
*	HsScrap_Ti_103.198	2.6077	0.2878	1505.32	1504.723	7779.8	1	1060.2	70.8	1	R.VVSEDTSHYILIK.G
*	HsScrap_Ti_102.164	2.6283	0.3362	1535.32	1536.633	5385.9	1	515.5	50	2	K.TVAEVDSESLPSSSK.M
*	HsSrcap_Ti_201.075	4.634	0.4634	1535.95	1536.633	6865	1	1854.7	78.6	4	K.TVAEVDSESLPSSSK.M
*	HsSrcap_Ti_203.229	4.4889	0.3637	3586.77	3587.836	8356	1	851.3	23.5	3	K.GIPFTATLASSSVNSAEEHVASTNEGREPTDSVPK.E
*	HsSrcap_Ti_202.285	3.9336	0.4246	2450.63	2449.796	7388.9	1	1660.9	59.5	2	K.EQMSLVHVGTEAFPISDESMIK.D
*	HsSrcap_Ti_203.185	2.8078	0.2477	1257.21	1255.46	4446.1	1	668.2	80	3	K.DRLPLESAVVR.H
*	HsSrcap_Ti_201.068	2.695	0.3356	1592.34	1592.709	5280	1	432.1	53.6	1	R.ELTPASPTCTNSVSK.N
*	HsScrap_Ti_103.184	6.3401	0.3616	2418.46	2419.53	7712.9	1	1905.5	60.5	1	K.NETHAEVLEQQNELCPYESK.F

*	HsSrcap_Ti_203.399	4.2855	0.3139	4291.17	4290.691	4633	5	240.6	18.1	3	K.E
*	HsSrcap_Ti_203.302	5.0154	0.3346	3087.02	3087.324	10024.4	1	738.1	34.6	8	K.EHENFLETIQEQQTTESAGQDLISIPK.A
*	HsSrcap_Ti_205.322	5.0728	0.3881	3088.31	3087.324	7549.1	1	833.2	29.8	4	K.EHENFLETIQEQQTTESAGQDLISIPK.A
*	HsSrcap_Ti_203.489	5.3697	0.3105	3726.22	3726.987	11860.3	1	1964.2	29	7	K.DAEDSLHEWQDINLEELETLESNLLAQQNSLK.A
*	HsSrcap_Ti_205.307	3.8708	0.3025	2307.44	2307.527	7917	1	661.6	47.1	2	K.FVEYYQYVDFHNQLGLDR.N
*	HsSrcap_Ti_203.191	2.6616	0.2705	1347.45	1348.46	6106.5	1	595.6	61.1	2	K.FSEWWHEAQK.N
*	HsScrap_Ti_104.199	3.5547	0.3452	1350.03	1348.46	6078.1	1	1172.7	83.3	4	K.FSEWWHEAQK.N
*	HsScrap_Ti_103.324	3.1104	0.2006	2034.15	2031.359	2987.5	1	302.4	50	3	R.TLQLTPGFPNPAVAEAYLK.P
*	HsSrcap_Ti_203.351	3.63	0.3927	2771.95	2772.171	5955.4	1	579.6	42	2	R.TLQLTPGFPNPAVAEAYLKPVVDDSK.G
*	HsSrcap_Ti_203.206	3.1445	0.269	1362.61	1363.556	5520.7	1	733.8	63.6	2	K.GSFLWGKPDLDK.I
*	HsSrcap_Ti_203.206	3.5695	0.2764	1365.76	1363.556	6529.8	1	1030.4	72.7	1	K.GSFLWGKPDLDK.I
*	HsSrcap_Ti_203.212	2.3592	0.1509	1377.56	1378.609	6111.1	1	630.9	63.6	2	R.TKTDESLFPVLK.Q
*	HsSrcap_Ti_203.212	4.1781	0.246	1378.74	1378.609	5293.7	2	900	77.3	2	R.TKTDESLFPVLK.Q
*	HsScrap_Ti_102.252	3.2398	0.2371	1149.45	1149.329	4730.6	1	1070.7	88.9	2	K.TDESLFPVLK.Q
*	HsSrcap_Ti_204.173	4.2061	0.21	1535.74	1535.695	8506.7	1	1410	73.1	1	K.RGITNTLEESSSLK.R
gi|24234747|r	11	71	32.80%	390	43062	5.3	interleukin enhancer binding factor 2 [Homo sapiens]				
*	HsSrcap_Ti_203.204	3.401	0.312	1733.41	1732.971	5313.5	1	577.7	56.7	18	R.VKPAPDETSFSEALLK.R
*	HsFLAG-Lin9_Ti_20	4.9447	0.4125	2255.8	2256.521	8971.3	1	1110.2	52.5	8	K.RNQDLAPNSAEQASILSLVTK.I
*	HsFLAG-FLJ20729_	5.4671	0.3197	2256.77	2256.521	7395.8	1	1481.2	38.8	12	K.RNQDLAPNSAEQASILSLVTK.I
*	HsFLAG-p53-DNA-D	4.9873	0.4681	2099.68	2100.334	4043	1	1131.3	71.1	2	R.NQDLAPNSAEQASILSLVTK.I
*	HsFLAG-Lin9_Ti_20	4.2003	0.2955	2582.66	2583.944	5840.5	2	433.2	40.9	12	K.INNVIDNLIVAPGTFEVQIEEVR.Q
*	HsFLAG-FLJ20729_	4.8721	0.2522	2584.59	2583.944	8350.2	1	1044.5	33	1	K.INNVIDNLIVAPGTFEVQIEEVR.Q
*	HsFLAG-p53-DNA-D	4.0925	0.3377	1770.56	1770.097	10386	1	1259.9	53.1	1	K.GTMTTGHNVADLVVILK.I
*	HsFLAG-p53-DNA-D	2.9953	0.2848	1409.59	1410.697	7051.4	1	691.3	57.7	3	K.ILPTLEAVAALGNK.V
*	HsFLAG-p53-DNA-D	5.0407	0.4288	1410.96	1410.697	5405.1	1	1489.5	88.5	12	K.ILPTLEAVAALGNK.V
*	HsFlag-DPCD_Ti_20	5.0165	0.3671	2872.88	2872.127	9554.5	1	1519.9	44.2	1	R.AQDPSEVLTMLTNETGFEISSSDATVK.I
*	HsFLAG-p53-DNA-D	3.7443	0.1131	1043.33	1042.267	7597.7	1	2071.4	94.4	1	K.VLQSALAAIR.H
gi|4506743|re	7	38	32.70%	208	24205	10.3	ribosomal protein S8 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_11	4.0752	0.2553	1348.14	1348.545	7376.4	1	1326.9	81.8	4	R.KYELGRPAANTK.I
*	HsFLAG-ARP6_Ti_1	3.2535	0.2702	1220.75	1220.371	9259.3	1	1421.1	80	4	K.YELGRPAANTK.I
*	HsFLAG-ARP6_Ti_1	4.4531	0.4105	1789.4	1788.843	6827.3	1	894.1	60.7	2	R.LDVGNFSWGSECCTR.K
	HsFlag-NUFIP_Ti_1	3.8149	0.3165	1719.65	1719.935	8511	1	1480.9	67.9	5	R.IIDVVYNASNNELVR.T
*	HsFLAG-ARP6_Ti_1	3.3778	0.3114	1620.41	1620.808	3975	1	412.4	66.7	13	R.QWYESHYALPLGR.K
*	HsFLAG-TCF3_Ti_1	3.2944	0.3427	1506.33	1507.684	5370.6	1	697.2	70.8	2	K.ISSLLEEQFQQGK.L
*	HsFLAG-ARP8_Ti_2	4.7193	0.3769	1507.23	1507.684	7946.1	1	1818.7	79.2	8	K.ISSLLEEQFQQGK.L
gi|89061489|r	26	205	32.60%	869	100139	9.9	PREDICTED: similar to Bcl-2-associated transcription factor 1 (Btf) isoform 1 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	4.2612	0.3994	2608.33	2609.676	5946.2	1	803	50	1	K.SQEEPKDTFEHDPSESIDEFNK.S
	HsFLAG-FLJ20309_	4.4768	0.3065	2609.29	2609.676	5563.1	1	1164.5	40.5	3	K.SQEEPKDTFEHDPSESIDEFNK.S
	HsFLAG-Lin9_Ti_20	3.3212	0.393	1909.47	1910.945	5751.3	1	598.7	60	1	K.DTFEHDPSESIDEFNK.S
	HsFLAG-ARP6_Ti_1	5.1513	0.412	2081.01	2082.191	4345.3	1	1197.2	65.8	14	K.SSATSGDIWPGLSAYDNSPR.S
	HsFLAG-ARP6_Ti_1	5.7567	0.5084	3149.59	3150.41	5943.5	1	989.4	33.3	5	R.SPHSPSPIATPPSQSSSCSDAPMLSTVHSAK.N
	HsFLAG-Lin9_Ti_20	3.2888	0.3921	1841.82	1842.925	8446.2	1	920.3	60	1	K.NTPSQHSHSIQHSPER.S
	HsFLAG-ARP6_Ti_1	2.5523	0.1984	967.27	968.101	4600.9	6	828.2	87.5	1	K.TIAPQNAPR.D

	HsH2AZ-FLAG_293_	2.8249	0.2658	1502.15	1502.534	2926	1	542.6	73.1	2	R.SSFYPDGGDQETAK.T
	HsFLAG-Lin9_Ti_20	5.2958	0.3655	2246.57	2246.308	7267	1	1898.4	69.4	4	K.GRAEGEWEDQEALDYFSDK.E
	HsFLAG-Lin9_Ti_20	5.0374	0.3337	2032.96	2033.069	9320.5	1	2207.5	71.9	1	R.AEGEWEDQEALDYFSDK.E
	HsFLAG-FLJ20309_	5.5489	0.5305	1922.24	1922.824	6865.1	1	1753.4	73.3	20	K.FNDSEGDDTEETEDYR.Q
	HsARP6-FLAG_Ti_1	4.0025	0.399	1467.31	1467.619	6423.2	1	915.3	75	17	K.ETGYVVERPSTTK.D
	HsFLAG-p53-DNA-D	4.3204	0.369	1573.66	1573.832	9737	1	1775.8	75	1	K.LKDLFDYSPPLHK.N
	HsFLAG-Lin9_Ti_20	3.5931	0.26	1332.32	1332.499	7653.8	1	1005.4	70	12	K.DLFDYSPPLHK.N
	HsFlag-DPCD_Ti_20	3.8989	0.261	1370.22	1370.566	8028.2	1	1481.2	81.8	15	K.MIASDSHRPEVK.L
	HsFLAG-ARP6_Ti_1	4.047	0.3734	1812.47	1813.079	5550.3	2	533.8	56.2	24	K.MAPVPLDDSNRPASLTK.D
	HsARP6-FLAG_Ti_1	3.247	0.2366	1439.34	1439.698	6648.9	1	1365.4	83.3	9	K.DRLLASTLVHSVK.K
	HsFlag-NUFIP_Ti_11	4.0313	0.1564	1439.98	1439.698	6001.1	1	1627.3	58.3	4	K.DRLLASTLVHSVK.K
	HsFLAG-UTX1_Ti_2	2.5908	0.1827	1169.61	1168.422	4573.5	8	374.5	60	8	R.LLASTLVHSVK.K
	HsFLAG-FLJ20309_	3.8371	0.2884	1169.73	1168.422	6485.1	1	1340.1	85	32	R.LLASTLVHSVK.K
	HsFLAG-Lin9_Ti_20	3.9334	0.3292	1296.14	1296.596	8716.5	1	1516.9	77.3	2	R.LLASTLVHSVKK.E
	HsFLAG-p53-DNA-D	3.9366	0.2838	1484.42	1484.739	9225.3	1	1148.9	66.7	4	R.SIFDHIKLPQASK.S
	HsFLAG-FLJ20729_	4.3567	0.3409	2048.13	2049.337	9388	1	952.6	50	5	K.STSESFIQHIVSLVHHVK.E
	HsFLAG-BC014022_	4.3344	0.463	2049.27	2049.337	4916.2	1	977.5	45.6	6	K.STSESFIQHIVSLVHHVK.E
	HsFLAG-ARP5_Ti_1	3.8223	0.3908	1897.48	1897.955	7861.5	1	982.7	60	4	R.GTFHDDRDDGVDYWAK.R
	HsFLAG-ARP6_Ti_2	4.9742	0.2722	2358.56	2359.391	6939.8	1	1704.2	63.2	9	K.YQGDGIVEDEEETMENNEEK.K
gi|51460917|	2	19	32.50%	114	11577	4.7	PREDICTED: similar to 60S acidic ribosomal protein P1 isoform 1 [Homo sapiens]				
gi|88957953|	2	19	32.50%	114	11577	4.7	PREDICTED: similar to 60S acidic ribosomal protein P1 isoform 3 [Homo sapiens]				
	HsFLAG-TCF3_Ti_1	3.2965	0.227	2404.75	2406.658	6988.5	1	700.3	50	1	K.LACIYSALILHDDEVTVTEDK.I
	HsFLAG-ARP6_Ti_1	3.9266	0.2884	1705.72	1703.981	4430.2	1	618.8	60	18	K.AAGVNVEPFWPGLFAK.A
gi|21361489|	18	96	32.40%	763	86267	8.6	enhancer of polycomb homolog 2 [Homo sapiens]				
*	HsTIP60_Ti_103.16	3.0184	0.2018	1020.21	1020.177	4967	1	845.3	87.5	1	R.AISAQQVFR.E
*	HsFLAG-TIP49b_Ti_	4.5642	0.3824	2341.01	2340.613	4564.1	1	792.1	60.5	6	K.KESMVIPVPEAESNVNYYNR.L
*	HsTIP60_Ti_104.238	3.658	0.2894	2212.2	2212.439	3563.4	1	439.6	55.6	4	K.ESMVIPVPEAESNVNYYNR.L
*	HsH2AZ-FLAG_293_	4.0291	0.2623	1389.36	1389.549	6578	1	971.7	70.8	1	K.ASSNQLVTLQEAK.L
*	HsH2AZ-FLAG_293_	3.8172	0.2298	1350.36	1349.567	5110.1	3	1150.5	90	6	K.LLLNEDDYLIK.A
*	HsTIP60_Ti_102.17	3.7725	0.3285	1455.46	1456.511	7079.8	1	1070.2	70.8	4	R.DGSTNNDPYVAFR.R
*	HsMRGBP-FLAG_Ti_	5.0443	0.4025	1863.49	1864.068	7079.5	1	1471.5	73.3	3	K.RYHLGDYGGEILNEVK.I
*	HsH2AZ-FLAG_293_	5.5498	0.3703	2150.81	2151.465	5027.1	1	1150.9	65.8	14	K.AEALITSQQPTPETLPVINK.S
*	HsMRGBP-FLAG_Ti_	3.3239	0.3043	1243.49	1242.346	6196.8	1	855.6	83.3	3	R.RAGCQYYAPR.L
*	HsYL1_Ti_103.1483.	5.4696	0.428	2060.29	2060.105	7219.4	1	1533.7	67.6	3	R.LDQANHSCENSELADLDK.L
*	HsH2AZ-FLAG_293_	2.8923	0.3222	1198.49	1198.374	5620.2	1	755.3	77.8	4	R.HCLTTLTVPR.R
*	HsH2AZ-FLAG_293_	4.5306	0.1583	1245.23	1245.462	7770.2	1	1861.3	95	12	R.LSLSEILSNIR.S
*	HsMRGBP-FLAG_Ti_	4.6959	0.4251	1768.76	1767.81	6094.5	1	1614.7	78.6	3	R.LLNLQDSDSEECTSR.K
*	HsFLAG-TIP49b_Ti_	4.6848	0.3504	1417.43	1417.649	7796.7	1	1814	80.8	8	K.RVSAASVALLNTSK.N
*	HsYL1_Ti_103.1279.	4.9097	0.4149	2081.84	2082.194	8020.8	1	768.4	47.4	5	K.EQNTGHNNINGVVQPSGTSK.T
*	HsMRGBP-FLAG_Ti_	4.6769	0.3636	2295.96	2296.644	6586.8	1	946.4	52.4	7	K.TLYSTNMALSSSPGISAVQLVR.T
*	HsYL1_Ti_104.1504.	3.6559	0.2482	1361.71	1359.627	5202.5	1	996.3	75	10	K.LATVAASMDRVPK.V
*	HsTIP60_Ti_104.17	2.8979	0.2743	1189.04	1189.354	3382.4	1	534.7	77.3	2	K.VTPSSAISSIAR.E
gi|4502491|re	4	42	32.30%	282	31362	4.8	complement component 1, q subcomponent binding protein precursor [Homo sapiens]				

*	HsFLAG-ARP6_Ti_1	4.0704	0.3394	1698.18	1698.87	6494.6	1	1811.6	84.6	8	K.AFVDFLSDEIKEER.K
*	HsFLAG-ARP6_Ti_1	4.7154	0.3807	2287.37	2288.557	6492.7	1	1104.9	57.9	6	K.VEEQEPELTSTPNFVVEVIK.N
*	HsFLAG-ARP6_Ti_1	5.5774	0.3822	3138.46	3138.291	10844.4	1	1977.8	34.6	4	K.ALVLDCHYPEDEVGQEDEAESDIFSIR.E
*	HsFLAG-p53-DNA-D	5.4367	0.4228	3441.71	3441.77	5612.1	1	882	30.2	24	R.GVDNTFADELVELSTALEHQEYITFLEDLK.S
gi|4506691|re	9	59	32.20%	146	16445	10.2	ribosomal protein S16 [Homo sapiens]				
	HsFlag-NUFIP_Ti_1(	2.904	0.1815	1187.59	1188.372	3118	1	273.3	70	3	K.GPLQSVQVFGR.K
	HsFlag-NUFIP_Ti_1(	4.3186	0.3903	1188.47	1188.372	7132	1	1293.4	80	16	K.GPLQSVQVFGR.K
*	HsFLAG-ARP6_Ti_1	3.3579	0.1449	1411.32	1411.662	3646.3	3	721.2	72.7	9	K.VNGRPLEMIEPR.T
*	HsFlag-NUFIP_Ti_1(	3.8007	0.219	1413.97	1411.662	6498.2	5	1264.9	54.5	2	K.VNGRPLEMIEPR.T
	HsFLAG-ARP6_Ti_1	2.388	0.1364	1095.61	1095.411	6978.4	1	694	72.2	1	K.LLEPVLLLGK.E
	HsFlag-NUFIP_Ti_1(	3.3932	0.185	1096.44	1095.411	3924.4	6	728	83.3	6	K.LLEPVLLLGK.E
	HsFlag-NUFIP_Ti_1(	3.4539	0.2966	1380.5	1380.714	6299.5	1	1250.7	86.4	5	K.LLEPVLLLGKER.F
*	HsFlag-NUFIP_Ti_1(	2.7732	0.2364	1241.76	1242.423	6137	2	571.5	59.1	4	K.GGGHVAQIYAIR.Q
*	HsFlag-NUFIP_Ti_1(	4.0204	0.285	1242.45	1242.423	6150.9	1	1269.4	77.3	13	K.GGGHVAQIYAIR.Q
gi|16579885|r	15	60	32.10%	427	47697	11.1	ribosomal protein L4 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.1777	0.1767	988.36	989.203	5059.3	1	556.6	75	3	K.NVTLPAVFK.A
*	HsFLAG-TIP49b_Ti_	6.9189	0.4809	2717.63	2717.874	9774.2	1	2428.7	40.6	4	K.NNRQPYAVSELAGHQTSAESWGTGR.A
*	HsFLAG-TCF3_Ti_1(	4.741	0.5423	2332.27	2333.479	7057.2	1	1033.2	54.8	2	R.QPYAVSELAGHQTSAESWGTGR.A
	HsFLAG-ARP6_Ti_1	5.5867	0.5563	2093.86	2094.487	4334	1	954.9	65.8	3	K.RYAICSALAASALPALVMSK.G
	HsFLAG-TCF3_Ti_1(	4.5736	0.5142	1938.49	1938.299	8166.2	1	1235.3	58.3	7	R.YAICSALAASALPALVMSK.G
*	HsFLAG-p53-DNA-D	5.452	0.343	2539	2536.888	8831.1	2	1433.9	36.9	1	K.GHRIEEVPELPLVVEDKVEGYK.K
	HsFlag-Ies6_293_Ti_	2.9087	0.1544	1609.37	1609.857	2346	7	439.1	69.2	1	R.IEEVPELPLVVEDK.V
*	HsFLAG-TCF3_Ti_1(	2.954	0.2849	2186.53	2186.507	5631.4	3	334.9	41.7	2	R.IEEVPELPLVVEDKVEGYK.K
*	HsFLAG-ARP6_Ti_1	4.4088	0.3261	1763.26	1762.97	6301.6	1	1588.3	78.6	6	R.RGPCIIYNEDNGIIK.A
*	HsFLAG-TCF3_Ti_1(	3.3252	0.3665	1269.62	1269.527	3056.9	1	685.6	86.4	9	R.NIPGITLLNVSK.L
	HsFLAG-ARP6_Ti_1	3.6129	0.2296	1281.88	1281.454	6318.2	1	1378.2	88.9	2	R.KLDELYGTWR.K
	HsFLAG-ARP6_Ti_1	2.8948	0.1593	1106.11	1104.269	5469.3	2	691.5	75	2	K.SNYNLPMHK.M
*	HsFLAG-ARP6_Ti_1	2.6945	0.084	956.54	957.118	8631	1	1115.9	70	7	K.AAAAAAALQAK.S
*	HsFLAG-ARP6_Ti_1	4.5522	0.1208	957.25	957.118	7441.3	1	2498.1	95	8	K.AAAAAAALQAK.S
*	HsVPS71-FLAG_Ti_:	5.061	0.3276	1416.55	1416.574	8820.3	1	2510.7	82.1	3	K.AAAAAAALQAKSDEK.A
gi|4758486|re	1	2	32.10%	109	12457	6.8	general transcription factor IIA, 2 (12kD subunit) [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.4058	0.1252	3927.48	3928.429	6461.1	1	1119.1	28.7	2	R.NTTLGNSLQESLDELIQSQQITPQLALQVLLQFDK.A
gi|12056465|r	8	81	31.80%	321	33784	10.2	fibrillarin [Homo sapiens]				
*	HsFLAG-TIP49b_Ti_	2.6929	0.1572	1981.26	1981.249	8963.7	8	463	43.3	2	K.NVMVEPHRHEGVFICR.G
*	HsFLAG-p53-DNA-D	3.1118	0.1175	961.27	961.103	4395.5	2	909.5	87.5	1	R.GKEDALVTK.N
	HsARP6-FLAG_Ti_1	4.5227	0.3922	1520.33	1519.828	5301.5	1	1088.6	71.4	6	K.LAAAILGGVDQIHIK.P
*	HsFLAG-TIP49b_Ti_	6.1047	0.4638	1872.49	1873.249	7382.3	1	1870.5	66.7	19	K.LAAAILGGVDQIHIKPGAK.V
*	HsFLAG-Lin9_Ti_20	3.7983	0.1885	1873.66	1873.249	6939.8	9	822.8	34.7	4	K.LAAAILGGVDQIHIKPGAK.V
*	HsFLAG-ARP6_Ti_1	7.7894	0.465	3417.7	3418.831	7774.5	1	1827.7	34.4	24	K.VLYLGAASGTTVSHVSDIVGPDGLVYAVEFSHR.S
	HsFLAG-FLJ20729_	3.5477	0.3144	1255.3	1255.506	7510.1	1	1217.3	80	16	R.IVALNAHTFLR.N
*	HsFLAG-Lin9_Ti_20	5.1605	0.3934	1535.57	1534.801	7444.7	1	1996.2	80.8	9	R.DHAVVVGVYRPPPK.V
gi|5803137|re	2	9	31.80%	157	17170	8.9	RNA binding motif protein 3 isoform a [Homo sapiens]				
gi|63054840|r	2	9	55.60%	90	9668	4.8	RNA binding motif protein 3 isoform b [Homo sapiens]				

	HsFLAG-p53-DNA-D	4.8768	0.3	3495.95	3496.898	7412.6	1	963	28.2	7	K.LFVGGLNFNTDEQALEDHFSSFGPISEVVVVK.D
	HsFLAG-p53-DNA-D	4.4205	0.4586	1984.33	1983.252	7608.5	1	1162.3	55.9	2	R.GFGFITFTNPEHASVAMR.A
gi|38372923|r	3	4	31.70%	205	22764	5.5	basigin isoform 4 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	5.5517	0.4627	3515.64	3517.817	6968.8	1	763.8	26.7	1	R.VDSDDQWGEYSCVFLPEPMGTANIQLHGPPR.V
	HsFLAG-ARP6_Ti_1	5.1703	0.4656	1805.05	1805.964	6259.5	1	2075	80	1	K.SSEHINEGETAMLVCK.S
	HsFLAG-ARP6_Ti_1	4.433	0.3832	2117.57	2117.298	5643.6	1	1325.1	70.6	2	R.SELHIENLNMEADPGQYR.C
gi|4759160|re	5	41	31.70%	126	13916	10.3	small nuclear ribonucleoprotein polypeptide D3 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	4.6692	0.3176	2416.54	2415.588	11360.4	1	1640.2	37.5	3	K.VLHEAEGHIVTCETNTGEVYR.G
*	HsFlag-NUFIP_Ti_1	6.7218	0.5018	2416.96	2415.588	7484.3	1	1877.2	65	25	K.VLHEAEGHIVTCETNTGEVYR.G
*	HsFlag-VPS71_Ti_1	2.4371	0.2153	1218.61	1219.426	5612	1	472.9	66.7	4	R.VAQLEQVYIR.G
*	HsFLAG-p53-DNA-D	3.7425	0.1769	1219.04	1219.426	9954.9	1	1599.2	83.3	8	R.VAQLEQVYIR.G
*	HsFlag-VPS71_Ti_1	2.2754	0.1083	1089.58	1090.409	6537.1	4	854.8	75	1	R.FLILPDMLK.N
gi|4506769|re	3	5	31.70%	101	11457	6.8	S100 calcium-binding protein A7 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.3768	0.3806	1385.53	1385.56	7241.7	1	1375.9	77.3	2	K.KGTNYLADVFEK.K
*	HsFLAG-FLJ20729_	4.825	0.2672	2312	2313.612	8577.9	1	1247	38.2	2	K.KIDFSEFLSLLGDIATDYHK.Q
*	HsFLAG-p53-DNA-D	3.7409	0.3327	2314.2	2313.612	9197.5	1	931.3	50	1	K.KIDFSEFLSLLGDIATDYHK.Q
gi|50053795|r	16	98	31.60%	611	69151	5.7	eukaryotic translation initiation factor 4B [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	5.0351	0.511	2277.71	2277.447	7648.8	1	1190.4	52.3	5	K.TISLTDFLAEDGGTGGGSTYVSK.P
*	HsFlag-FLJ90652_2	4.9436	0.4624	2340.67	2342.607	6349.9	1	1262.4	60	23	K.SPPYTAFLGNLPYDVTEESIK.E
*	HsFLAG-FLJ20729_	4.6182	0.2412	2342.57	2342.607	9082.3	2	1347.9	36.2	2	K.SPPYTAFLGNLPYDVTEESIK.E
*	HsFLAG-p53-DNA-D	4.965	0.324	2922.64	2922.263	7167.8	1	1103.2	35.4	4	K.SPPYTAFLGNLPYDVTEESIKEFFR.G
*	HsMRGBP-FLAG_Ti_	2.7724	0.1656	1195.59	1195.321	6583.5	2	759.3	72.2	1	R.LPREPSNPER.L
*	HsFLAG-p53-DNA-D	5.7874	0.3817	2947.51	2948.169	7966.7	1	1536.6	48.1	22	K.GFGYAEFEDLDSLLSALSLNEESLGNR.R
*	HsMRGBP-FLAG_Ti_	5.0467	0.1381	2950.53	2948.169	10039.1	1	1574.3	31.7	2	K.GFGYAEFEDLDSLLSALSLNEESLGNR.R
*	HsFlag-VPS71_Ti_1	4.9707	0.3273	3104.52	3104.357	5434.3	1	872.8	31.5	11	K.GFGYAEFEDLDSLLSALSLNEESLGNRR.I
*	HsFlag-VPS71_Ti_1	4.1192	0.2945	1358.71	1358.494	5532.5	1	1459.3	86.4	8	R.IRVDVADQAQDK.D
*	HsMRGBP-FLAG_Ti_	3.4433	0.3326	1608.91	1608.707	3914.8	1	634.6	65.4	3	R.ARPATDSFDDYPPR.R
*	HsFLAG-ARP5_Ti_1	3.1881	0.2788	1316.5	1316.373	6016.6	1	861.1	80	2	R.RGDDSFGDKYR.D
*	HsARP6-FLAG_Ti_1	3.9198	0.4048	1532.11	1532.74	5358.3	1	1090.8	73.3	8	R.AASIFGGAKPVDTAAR.E
*	HsMRGBP-FLAG_Ti_	4.9695	0.3042	3222.02	3220.483	7281.3	1	776.3	28.7	3	K.SLENETLNKEEDCHSPTSKPPKPDQPLK.V
*	HsFlag-NUFIP_Ti_2	3.6027	0.0825	2191.47	2191.369	10191.3	1	1075.4	34.7	1	K.EEDCHSPTSKPPKPDQPLK.V
*	HsFlag-VPS71_Ti_1	2.6719	0.2771	1294.88	1295.395	3197.4	6	372.3	62.5	2	K.VAPAQPSEEGPGR.K
*	HsFlag-VPS71_Ti_1	3.4736	0.2024	1447.71	1446.618	7402.2	3	1241.9	70.8	1	R.KDENKVDGMNAPK.G
gi|4759276|re	8	41	31.60%	475	51841	7.9	RNA, U3 small nucleolar interacting protein 2 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_2	3.3941	0.1608	1130.15	1130.286	5460.9	5	1007	93.8	1	R.LKEDVLEQR.G
*	HsFlag-NUFIP_Ti_1	4.4019	0.3453	2430.97	2431.714	7309.9	1	1477.2	56.8	1	R.GHQLSITCLVVTPDDSAIFSAAK.D
*	HsFlag-NUFIP_Ti_1	3.1555	0.2603	1402.53	1402.466	6514.8	1	767.8	68.2	2	R.GTHQLYSTSHDR.S
*	HsFlag-NUFIP_Ti_1	5.4616	0.4749	3076.3	3077.38	5091.8	1	1270	37	13	K.VWNVAENSYVETLFGHQDAVAALDALSR.E
*	HsFlag-NUFIP_Ti_11	5.1034	0.4372	3500.34	3500.856	5260	1	1303.9	35.2	12	R.GEPGLEQPFWISSVAALLNTDLVATGSHSSCVR.L
*	HsFlag-NUFIP_Ti_1	5.3448	0.4261	2058.66	2059.42	5561.5	1	1124.2	70.6	6	R.QLDLLCDIPLVGFINSLK.F
*	HsFlag-NUFIP_Ti_2	3.6668	0.4162	1794.1	1793.933	7532.5	1	771.8	53.1	2	K.FSSSGDFLVAGVGQEHR.L
*	HsFlag-NUFIP_Ti_1	2.3072	0.2668	950.46	951.114	3209.1	3	220.2	55.6	4	R.RVPVPPAAGS.-
gi|5031857|re	8	16	31.60%	332	36689	8.3	lactate dehydrogenase A [Homo sapiens]				

*	HsFlag-VPS71_Ti_1	4.6167	0.2271	2074.84	2075.326	9802.4	1	1317.2	56.2	2	K.DQLIYNLLKEEQTPQNK.I
*	HsH2AZ-FLAG_293_	5.4577	0.4296	1658.46	1658.843	7050.7	1	1979.3	78.6	6	K.DLADELALVDVIEDK.L
	HsFlag-VPS71_Ti_1	3.4513	0.3412	1249.89	1249.332	4382.8	1	752.9	77.3	2	R.VIGSGCNLDSAR.F
*	HsFlag-VPS71_Ti_1	2.9815	0.2364	1265.74	1265.449	5763.1	2	553.1	70	1	K.QVVESAYEVIK.L
*	HsFlag-VPS71_Ti_1	4.2519	0.4505	2114.8	2113.433	6846	1	1126.9	55.3	1	K.GYTSWAIGLSVADLAESIMK.N
*	HsFLAG-p53-DNA-D	2.598	0.1525	1168.42	1168.443	7309.1	1	1214.3	83.3	1	R.RVHPVSTMIK.G
*	HsH2AZ-FLAG_293_	3.0188	0.2594	1135.29	1135.216	7635.8	1	1483.1	94.4	2	K.VTLTSEEEAR.L
*	HsFlag-VPS71_Ti_1	2.6653	0.3028	1119.62	1119.263	5204.5	1	471.7	61.1	1	K.SADTLWGIQK.E
gi|33636750|	25	44	31.40%	1292	141383	5.1	likely ortholog of mouse ubiquitin-conjugating enzyme E2-230K [Homo sapiens]				
*	HsFlag-FLJ90652_2	2.491	0.3211	1243.35	1244.436	2137.6	1	188.9	70	1	R.LLFSHDLVSGR.Y
*	HsFlag-FLJ90652_2	3.2525	0.2516	1244.08	1244.436	7175.7	1	951.7	75	2	R.LLFSHDLVSGR.Y
*	HsFlag-FLJ90652_2	2.3423	0.2062	1105.34	1106.266	5797.8	4	497.1	62.5	2	R.VQWYPEGVK.Q
*	HsFlag-FLJ90652_2	5.3377	0.4745	3565.03	3565.926	6897.8	1	1955.3	34.7	3	K.LYDVCPHVSDSGLFFDDSYGFYPGQVLIGPAK.I
*	HsFlag-FLJ90652_2	4.2847	0.2482	1351.04	1351.588	6745.5	1	1459.2	81.8	2	K.IFSSVQWLSGVK.P
*	HsFlag-FLJ90652_2	5.3554	0.4806	2503.8	2503.694	4594.2	1	639.3	50	4	K.SFCPGGTDSVSPPPSVITQENLGR.V
*	HsFlag-FLJ90652_2	2.766	0.2322	1103.92	1104.177	7295.8	2	886.8	81.2	1	R.LGCFDHAQR.Q
*	HsFlag-FLJ90652_2	3.409	0.3912	1521.58	1522.794	6793.4	1	1094.8	75	1	R.CLYVFPAKVEPAK.I
*	HsFlag-FLJ90652_2	2.5194	0.1858	1442.41	1442.516	5874.5	3	421.8	59.1	1	R.IMSCSPDTQCSR.D
*	HsFlag-FLJ90652_2	5.7586	0.309	2819.39	2817.009	8868.1	1	1439.7	35.9	2	R.SNDLFPVHHLDNNEFCPGDFVVDK.R
*	HsFlag-FLJ90652_2	5.0538	0.4124	2397.97	2398.607	8394	1	1684.4	39.3	2	K.RVQSCPDPAVYGVVQSGDHIGR.T
*	HsFlag-FLJ90652_2	3.6056	0.3314	3289.74	3289.493	7794.5	4	480.8	24.1	1	K.LRPSGDDVELIGEEEDVSVYDIADHPDFR.F
*	HsFlag-FLJ90652_2	3.5085	0.1501	2307.16	2307.439	8664.8	8	764.3	32.1	1	R.IGNTEDGAPHKEDEPSVGQVAR.V
*	HsFlag-FLJ90652_2	3.6963	0.3379	2308.41	2307.439	9517.9	1	664.3	40.5	1	R.IGNTEDGAPHKEDEPSVGQVAR.V
*	HsFlag-FLJ90652_2	3.5682	0.4793	1999.43	1999.268	3905.1	1	748.5	67.6	2	K.IEEPPIPPLEQPVAPEDK.G
*	HsFlag-FLJ90652_2	4.2931	0.3773	2613.67	2613.943	7045.3	1	641.8	43.5	3	K.NMTVEQLLTGSPTSPTVEPEKPTR.E
*	HsFlag-FLJ90652_2	1.8593	0.2874	907.36	908.042	4353.7	2	290.4	68.8	1	K.PGVTFTSAK.G
*	HsFlag-FLJ90652_2	3.8379	0.3311	1895.04	1896.109	6415.1	1	621	53.1	5	K.GEVFSVLEFAPSNHSFK.K
*	HsFlag-FLJ90652_2	2.3042	0.1344	1186.45	1187.381	5107.7	1	459.5	61.1	1	K.KIEFQPPEAK.K
*	HsFlag-FLJ90652_2	5.2809	0.403	4032.23	4033.461	7037.7	1	1753.4	31.8	2	R.TPYEDGLYLFDIQLPNIYPAVPPHFCYLSQCSGR.L
*	HsFlag-FLJ90652_2	3.3143	0.2328	1152.38	1153.194	6774.5	1	1373.5	83.3	2	R.GLQEGYENSR.C
*	HsFlag-FLJ90652_2	3.9502	0.237	1569.22	1569.798	8418.6	1	1588.7	79.2	1	R.IESWLETHALLEK.A
*	HsFlag-FLJ90652_2	3.6813	0.3087	2307.03	2308.464	9548.7	1	620.9	40.5	1	R.DHTDQTSETAPDASVPPSVKPK.K
*	HsFlag-FLJ90652_2	3.3723	0.221	1639.16	1638.904	5868.1	1	757.4	60.7	1	K.SGYPDIGFPLFPLSK.G
*	HsFlag-FLJ90652_2	4.6637	0.3444	1637.61	1635.793	5113.6	1	929.3	71.4	1	R.AALLEAGMPECTEDK.-
gi|5454064|re	13	26	31.40%	669	69492	9.7	RNA binding motif protein 14 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.2507	0.1971	1557.77	1556.768	9823.4	1	933.3	57.7	1	R.AIEALHGHELRPGR.A
*	HsFLAG-ARP6_Ti_1	5.1888	0.3915	1753.94	1752.931	5538.3	1	2233.4	90	3	K.IFVGNVSAACTSQELR.S
*	HsFLAG-UTX1_Ti_2	3.2243	0.3842	1157.52	1157.312	6753.4	1	1146.4	77.3	4	K.KGPGLAVQSGDK.T
*	HsFLAG-Lin9_Ti_20	4.2998	0.2303	3688.06	3687.877	9204.7	1	602.5	20.1	1	Q
*	HsFLAG-Lin9_Ti_20	3.6133	0.2897	1609.76	1609.822	5516.9	1	754	64.3	2	R.ASYVAPLTAQPATYR.A
*	HsFLAG-Lin9_Ti_20	2.3044	0.2343	1219.47	1220.371	5698.2	1	384.3	63.6	1	R.AQPSVSLGAAYR.A
*	HsFLAG-Lin9_Ti_20	3.0212	0.2475	1246	1246.409	5603.3	1	814.5	72.7	1	R.AQPSVSLGAPYR.G
*	HsFLAG-Lin9_Ti_20	4.5109	0.4856	2465.02	2466.629	7183.7	1	985.2	47.8	3	R.TQSSASLAASYAAQQHPQAAASYR.G

*	HsFLAG-ARP6_Ti_1	3.9724	0.3264	2466.46	2466.629	4636	1	659.2	32.6	1	R.TQSSASLAASYAAQQHPQAAASYR.G
*	HsFLAG-Lin9_Ti_20	3.552	0.1737	3696.14	3696.943	6642.1	1	475.2	20.8	1	T
*	HsFLAG-ARP6_Ti_1	3.9119	0.2204	1223.58	1223.374	7771.7	1	1594	94.4	2	R.RLSESQLSFR.R
*	HsFlag-NUFIP_Ti_2	3.3825	0.3179	1301.38	1301.404	5767.5	1	983.8	80	5	R.RLPDAHSDYAR.Y
*	HsFLAG-p53-DNA-D	2.3823	0.2128	1148.47	1149.269	6910.2	1	437.9	66.7	1	R.AAQMHSGYQR.R
gi|9507215|re	16	335	31.20%	449	50094	5.1	tubulin, alpha 8 [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.8546	0.3066	2415.78	2416.655	9887	1	636.1	42.5	25	R.QLFHPEQLITGKEDAANNYAR.G
	HsSrcap_Ti_204.213	5.0964	0.4219	2416.38	2416.655	6002.3	1	934.1	37.5	18	R.QLFHPEQLITGKEDAANNYAR.G
	HsScrap_Ti_106.239	2.55	0.1652	1877.45	1876.082	6295.5	1	349.4	53.6	1	R.RNLDIERPTYTNLNR.L
	HsFlag-ZnF-HIT2_Ti_	2.9442	0.2517	1719.52	1719.895	6354.4	3	522.7	57.7	12	R.NLDIERPTYTNLNR.L
	HsFLAG-ARP6_Ti_1	5.0973	0.4595	1487.62	1488.768	7314.4	1	1783.7	80.8	94	R.LISQIVSSITASLR.F
	HsFLAG-Lin9_Ti_20	3.9906	0.2202	1487.96	1488.768	5903.2	1	1035.4	48.1	1	R.LISQIVSSITASLR.F
	HsFLAG-ARP6_Ti_1	5.8116	0.4265	2410.46	2410.689	5990.7	1	1327.4	60	74	R.FDGALNVDLTEFQTNLVPYPR.I
	HsSrcap_Ti_205.279	4.5969	0.4286	1755.42	1755.98	5429.1	1	785.6	65.4	26	K.RTIQFVDWCPTGFK.V
	HsSrcap_Ti_205.280	4.8872	0.2348	1757.48	1755.98	8327.5	1	2242.3	57.7	10	K.RTIQFVDWCPTGFK.V
	HsSrcap_Ti_202.300	2.6402	0.345	1598.54	1599.793	6635.7	1	411.8	50	2	R.TIQFVDWCPTGFK.V
	HsFLAG-TCF3_Ti_1	4.0211	0.3559	1599.41	1599.793	6154.4	1	984.8	70.8	8	R.TIQFVDWCPTGFK.V
	HsFLAG-ARP6_Ti_2	4.0719	0.4153	1825.6	1826.103	3498.4	1	615.9	58.8	34	K.VGINYQPPTVVPGGDLAK.V
	HsFLAG-ARP6_Ti_1	6.0682	0.4321	1865.52	1866.108	10861.7	1	2782.2	75	18	R.AVCMLSNTTAIAEAWAR.L
	HsFLAG-ARP6_Ti_1	4.4765	0.3204	1867.57	1866.108	8904.4	1	1596.3	45.3	7	R.AVCMLSNTTAIAEAWAR.L
	HsFLAG-ARP6_Ti_1	3.7547	0.214	2330.07	2331.521	8623.8	3	888.4	34.2	2	R.AFVHWYVGEGMEEGEFSEAR.E
	HsFLAG-ARP6_Ti_1	4.334	0.4395	2330.87	2331.521	6787.1	1	1352.6	57.9	3	R.AFVHWYVGEGMEEGEFSEAR.E
gi|4503727|re	4	9	31.20%	224	25177	9.3	FK506-binding protein 3 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.4803	0.3876	1745.48	1745.889	7949	1	1643.5	75	2	K.FLQEHGSDSFLAEHK.L
*	HsFLAG-p53-DNA-D	4.5417	0.4451	1688.62	1688.88	6535.1	1	1601.2	76.9	4	K.DHLVTAYNHLFETK.R
*	HsFLAG-p53-DNA-D	5.1844	0.3927	3143.54	3143.403	7508.6	1	1362.1	32.4	2	K.KGDVVHCWYTGTLQDGTVFDTNIQTSAK.K
*	HsFLAG-Lin9_Ti_20	3.9855	0.2235	1562.42	1562.765	8869.5	1	1442.6	70.8	1	K.ARLEIEPEWAYGK.K
gi|4826860|re	4	30	31.20%	128	14174	8.5	NHP2 non-histone chromosome protein 2-like 1 [Homo sapiens]				
gi|51317376|r	4	30	31.20%	128	14174	8.5	NHP2 non-histone chromosome protein 2-like 1 [Homo sapiens]				
	HsFlag-NUFIP_Ti_2	2.8918	0.2857	1200.07	1200.38	3897.2	1	666.1	85	3	K.AYPLADAHLTK.K
	HsFLAG-p53-DNA-D	5.3073	0.2419	1609.58	1609.829	7969.3	1	2338.8	87.5	17	K.KLLDLVQQSCNYK.Q
	HsFlag-NUFIP_Ti_2	4.8054	0.2836	1480.51	1481.655	7566.6	1	1605	81.8	2	K.LLDLVQQSCNYK.Q
	HsFlag-NUFIP_Ti_2	4.7989	0.3919	1718.5	1718.967	9050.1	1	1508.8	66.7	8	R.ACGVSRPVIACSVTIK.E
gi|67003578|r	3	6	31.00%	116	13001	5	hypothetical protein LOC91750 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	3.5954	0.2866	2261.21	2261.539	3826.1	1	694.3	55	2	R.ASPDLWPEQLPGVAEFAASFK.S
*	HsFLAG-Lin9_Ti_20	4.5682	0.4102	1677	1677.855	7690.6	1	2306.4	57.1	2	R.GLQNLAYQLGLDESR.E
*	HsFLAG-Lin9_Ti_20	5.6686	0.4672	1677.57	1677.855	8851.3	1	2203.4	78.6	2	R.GLQNLAYQLGLDESR.E
gi|47604944|r	20	73	30.90%	929	103709	8.2	SCY1-like 2 protein [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	2.9696	0.2715	1210.33	1211.366	3539.5	1	511.5	72.7	1	R.HIASGGNGLAWK.I
*	HsFlag-DPCD_Ti_20	2.6301	0.1351	958.23	958.109	7560.2	1	910.2	92.9	1	K.RGVQQLTR.L
*	HsFlag-NUFIP_Ti_2	3.6945	0.2038	1422.1	1422.624	6113.1	1	1175.6	81.8	6	R.LLTVQHPLEESR.D
*	HsFLAG-Lin9_Ti_20	4.9889	0.3791	3679.47	3677.077	7372.1	1	521.9	23.4	2	R.DCLAFCTEPVFASLANVLGNWENLPSPISPDIK.D
*	HsFLAG-Lin9_Ti_20	4.1218	0.3774	4083.32	4083.516	5775.4	2	344.7	18.6	1	R.DCLAFCTEPVFASLANVLGNWENLPSPISPDIKDYK.L

*	HsFLAG-p53-DNA-D	4.8343	0.3183	1964.86	1965.257	6806.9	1	1669.9	70.6	8	K.YGLLQVSEGLSFLHSSVK.M
*	HsFLAG-FLJ20729_	4.9162	0.3182	1965.15	1965.257	6071.3	1	1665.4	47.1	1	K.YGLLQVSEGLSFLHSSVK.M
*	HsFLAG-p53-DNA-D	4.3221	0.3705	1693.67	1694.002	6430.6	1	1110.8	67.9	4	K.MVHGNITPENIILNK.S
*	HsFLAG-p53-DNA-D	4.809	0.422	2012.82	2013.36	6932.8	1	1584.9	70.6	8	K.LLLNVTPTVRPDADQMTK.I
*	HsFLAG-p53-DNA-D	5.5757	0.2857	2493.11	2493.821	9628.4	1	1889.5	60	18	K.IPFFDDVGAVTLQYFDTLFQR.D
*	HsFLAG-p53-DNA-D	3.9916	0.2938	2493.56	2493.821	8732.7	1	877.1	30	2	K.IPFFDDVGAVTLQYFDTLFQR.D
*	HsFlag-NUFIP_Ti_20	3.2746	0.1565	1226.02	1226.545	3867.6	2	709.2	80	1	K.LILPELGPVFK.Q
*	HsFLAG-Lin9_Ti_20	3.7796	0.3112	1711.57	1712.086	6637.4	1	969.3	69.2	4	K.QQEPIQILLIFLQK.M
*	HsFLAG-FLJ20729_	5.1627	0.2996	2059.59	2060.444	4210.4	1	1079	75	1	K.WFVLDDILPFLQQIPSK.E
*	HsFLAG-FLJ20729_	3.7107	0.2373	2060.24	2060.444	4605	1	1056	50	1	K.WFVLDDILPFLQQIPSK.E
*	HsFLAG-Lin9_Ti_20	6.394	0.3865	3078.56	3078.625	9591.1	1	1528.7	32.7	1	K.VLPHLIPLSIENNLNLNQFNSFISVIK.E
*	HsFlag-NUFIP_Ti_20	3.8763	0.2821	1755.67	1755.042	8703.5	1	1234.6	69.2	1	K.TKLEQLHIMQEQQK.S
*	HsFLAG-Lin9_Ti_20	4.0711	0.2909	2692.91	2693.884	8286.2	1	694.6	39.6	2	K.VFNNIGADLLTGSESENKEDGLQNK.H
*	HsFLAG-p53-DNA-D	3.7551	0.4131	1858.91	1859.179	5758.4	1	545.6	50	8	K.SQQPLKPQVHTPVATVK.Q
*	HsFLAG-FLJ20729_	4.97	0.4781	2357	2357.65	11365	1	1376.7	50	2	K.DLTDTLMDNMSSLTSLSVSTPK.S
gi|4759156|re	6	8	30.90%	282	31280	9.8	small nuclear ribonucleoprotein polypeptide A [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	6.5065	0.3794	2171.67	2171.544	9213.5	1	3252.6	75	1	K.SLYAIFSQFGQILDILVSR.S
	HsFLAG-p53-DNA-D	1.82	0.1028	909.35	910.104	9474.6	8	664.6	71.4	1	R.GQAFVIFK.E
*	HsFLAG-p53-DNA-D	3.136	0.2165	1605.04	1604.882	3787.7	1	550.6	66.7	1	R.SMQGFPFYDKPMR.I
*	HsFlag-NUFIP_Ti_10	4.2514	0.5136	2728.21	2729.188	6354.3	1	690.6	37.5	1	K.AVQGGGATPVVGAVQGPVPGMPPMTQAPR.I
*	HsFlag-NUFIP_Ti_11	4.3363	0.3247	2728.5	2729.188	6928.6	1	1191.8	33.9	3	K.AVQGGGATPVVGAVQGPVPGMPPMTQAPR.I
*	HsFlag-NUFIP_Ti_10	2.7718	0.3402	1990.99	1990.139	11572	1	701.6	47.1	1	R.HDIAFVEFDNEVQAGAAR.D
gi|62414289|r	10	55	30.70%	466	53652	5.1	vimentin [Homo sapiens]				
*	HsSrcap_Ti_202.184	2.6889	0.3017	1429.68	1429.572	4460.4	1	342.5	61.5	1	R.SLYASSPGGVYATR.S
*	HsFLAG-FLJ20729_	5.7262	0.5172	2127.51	2127.356	8862.2	1	2190.9	66.7	5	R.LLQDSVDFSLADAINTEFK.N
*	HsARP6-FLAG_Ti_1	3.9579	0.1378	1170.38	1170.435	4950.3	2	1136.4	88.9	7	K.ILLAELEQLK.G
*	HsFLAG-ARP6_Ti_1	5.5042	0.2926	1534.76	1534.793	7614.2	1	1964.1	83.3	10	R.KVESLQEEIAFLK.K
	HsSrcap_Ti_202.206	2.4671	0.1093	1309.47	1310.406	4889.5	4	284.9	61.1	2	K.NLQEAEEWYK.S
*	HsFLAG-Lin9_Ti_20	3.2248	0.2877	1490.51	1491.648	7095.9	1	584.6	62.5	1	R.QVQSLTCEVDALK.G
*	HsFlag-DPCD_Ti_20	3.1021	0.2203	2188.87	2188.33	8830.7	1	871.1	47.2	1	R.EMEENFAVEAANYQDTIGR.L
*	HsFLAG-ARP6_Ti_1	3.4401	0.3115	1572.05	1571.86	4788.4	1	613.9	65.4	25	R.ISLPLPNFSSLNLR.E
*	HsFLAG-ARP6_Ti_1	3.3663	0.2945	1670.44	1669.829	4163.8	1	632.6	67.9	1	R.ETNLDSLPLVDTHSK.R
*	HsFLAG-Lin9_Ti_20	3.4172	0.2643	1837.34	1837.854	9044.7	1	1086.2	60	2	R.DGQVINETSQHHDDLE.-
gi|88954948|r	11	72	30.70%	293	31435	10.1	PREDICTED: similar to ribosomal protein S2 isoform 1 [Homo sapiens]				
gi|88954974|r	11	72	38.60%	233	25623	9.7	PREDICTED: similar to ribosomal protein S2 isoform 8 [Homo sapiens]				
gi|88954969|r	11	72	38.60%	233	25623	9.7	PREDICTED: similar to ribosomal protein S2 isoform 7 [Homo sapiens]				
gi|88954965|r	11	72	40.90%	220	24156	9.6	PREDICTED: similar to 40S ribosomal protein S2 isoform 6 [Homo sapiens]				
	HsFlag-NUFIP_Ti_10	2.3266	0.2989	1551.76	1552.851	8692.8	1	499.1	54.2	2	K.SLEEIYLFSLPIK.E
	HsFlag-NUFIP_Ti_10	4.7238	0.3286	1553.49	1552.851	7279.5	1	1555.3	79.2	20	K.SLEEIYLFSLPIK.E
	HsFlag-NUFIP_Ti_10	4.6322	0.1477	1718.33	1717.965	5982.5	1	1223	68.8	20	K.AFVAIGDYNGHVGLGVK.C
	HsFLAG-p53-DNA-D	2.7185	0.1177	1136.75	1137.334	5462.5	3	610.7	72.2	2	K.IGKPHTVPCK.V
	HsFlag-NUFIP_Ti_10	2.118	0.3256	1025.62	1026.221	7555.2	1	739.8	70	1	R.GTGIVSAPVPK.K
	HsFlag-NUFIP_Ti_10	2.7662	0.2751	1847.94	1846.133	8752.3	1	659.6	53.3	1	K.KLLMMAGIDDCYTSAR.G

	HsFlag-NUFIP_Ti_1	3.7738	0.3008	1719	1717.959	8689.1	1	1086.5	64.3	1	K.LLMMAGIDDCYTSAR.G
	HsFLAG-TCF3_Ti_1	2.0447	0.2449	1386.49	1387.575	7244.3	6	375.5	50	1	K.TYSYLTPDLWK.E
	HsFLAG-ARP6_Ti_1	3.2281	0.3305	1386.78	1387.575	6225.5	1	872.2	75	6	K.TYSYLTPDLWK.E
	HsFlag-NUFIP_Ti_1	3.641	0.3159	1464.48	1464.618	5566.5	1	1336.9	59.1	1	K.SPYQEFTDHLVK.T
	HsFLAG-ARP6_Ti_1	3.9707	0.4151	1464.63	1464.618	7813.3	1	1641.1	81.8	17	K.SPYQEFTDHLVK.T
gi|32483377|r	4	17	30.70%	238	25839	7.5	peroxiredoxin 3 isoform b [Homo sapiens]				
gi|5802974|re	4	17	28.50%	256	27693	7.8	peroxiredoxin 3 isoform a precursor [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	5.3529	0.4914	1754.58	1755.042	7331.3	1	1667.4	68.8	2	K.NGGLGHMNIALLSDLTK.Q
	HsFLAG-ARP6_Ti_1	4.9511	0.389	1462.09	1463.674	10227.1	1	2751.2	84.6	5	R.DYGVLLEGSGLALR.G
	HsFLAG-p53-DNA-D	3.4987	0.3651	1208.07	1207.375	5037.4	1	882.1	80	6	K.HLSVNDLPVGR.S
	HsFLAG-ARP6_Ti_1	6.4953	0.4398	3387.08	3387.696	6755.8	1	851.6	28.3	4	K.AFQYVETHGEVCPANWTPDSPTIKPSPAASK.E
gi|4506685|re	6	24	30.50%	151	17222	10.5	ribosomal protein S13 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.6998	0.2605	1092.23	1092.24	5663.1	2	532.3	72.2	1	K.GLSQSALPYR.R
*	HsFlag-NUFIP_Ti_11	3.8264	0.2559	1382.45	1382.69	5086.4	1	1048	79.2	10	K.KGLTPSQIGVILR.D
*	HsFlag-NUFIP_Ti_11	3.6541	0.0966	1383.14	1382.69	6193.7	2	1643.1	54.2	1	K.KGLTPSQIGVILR.D
*	HsFLAG-ARP6_Ti_1	3.1198	0.27	1255.87	1254.516	5671	1	711.8	72.7	3	K.GLTPSQIGVILR.D
*	HsFlag-NUFIP_Ti_1	3.4221	0.3113	1694.75	1694.968	4965.4	1	679.1	67.9	8	K.GLAPDLPEDLYHLIK.K
*	HsFlag-NUFIP_Ti_11	2.5431	0.1641	1008.81	1010.227	3136.9	1	440.8	92.9	1	K.RVLPPNWK.Y
gi|14141152|r	15	121	30.40%	730	77516	8.7	heterogeneous nuclear ribonucleoprotein M isoform a [Homo sapiens]				
*	HsFlag-DPCD_Ti_20	3.0341	0.2506	1868.3	1869.013	4531.9	1	631.1	55.3	3	K.MEEESGAPGVPSGNGAPGPK.G
	HsFLAG-Lin9_Ti_20	3.9908	0.1035	1265.5	1265.495	5736.4	4	1053.9	80	4	R.AFITNIPFDVK.W
	HsFLAG-FLJ20729_	4.763	0.4557	1755.55	1754.005	7306.9	1	1412.6	66.7	20	K.VGEVTYVELLMDAEGK.S
	HsFLAG-Lin9_Ti_20	3.7365	0.3153	1427.35	1427.64	5103.8	1	1041.9	79.2	15	R.LGSTVFVANLDYK.V
	HsYL1_Ti_104.2680.	5.0772	0.499	2179.86	2179.575	4416.4	1	546.4	47.7	13	K.GIGMGNIGPAGMGMEGIGFGINK.M
	HsFLAG-ARP6_Ti_1	3.7162	0.4333	1715.34	1715.972	8013.8	1	1396.7	65.6	2	K.MGGMEGPFGGGMENMGR.F
	HsFLAG-ARP6_Ti_1	3.3665	0.1101	1115.31	1115.315	6008.8	3	1204.1	88.9	2	R.INEILSNALK.R
	HsFLAG-TCF3_Ti_1	2.9756	0.2641	1286.84	1285.359	6343.5	1	572.7	60.7	2	K.QGGGGGGGSVPGIER.M
	HsFlag-NUFIP_Ti_2	3.8298	0.4043	1102.14	1102.271	6207.4	1	1495.7	95	8	R.MGAGLGHGMDR.V
	HsFlag-VPS71_Ti_1	5.0445	0.4576	1614.57	1614.875	7122.9	1	1947.2	82.1	16	R.MGPLGLDHMASSIER.M
	HsFLAG-ARP6_Ti_1	3.3774	0.353	1125.65	1126.334	5463.2	1	1193.7	90	2	R.MGAGMGFGLER.M
	HsFLAG-ARP6_Ti_1	3.6363	0.3546	1429.67	1428.708	4978.6	1	1033.5	75	13	R.MGPAMGPALGAGIER.M
	HsFlag-NUFIP_Ti_11	4.781	0.3808	2035.68	2036.173	7115.2	1	1076.5	50	11	R.GNFGGSFAGSFGGAGGHAPGVAR.K
	HsFLAG-TCF3_Ti_1	1.9639	0.1102	1167.52	1168.337	5513.6	5	311.9	62.5	1	R.NLPFDFTWK.M
	HsFLAG-ARP6_Ti_1	4.8317	0.3881	1566.16	1566.72	7132.9	1	2587.8	91.7	9	K.FNECGHVLYADIK.M
gi|88970681|r	4	6	30.40%	135	14926	8.2	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein K isoform 2 [Homo sapiens]				
	HsFlag-VPS71_Ti_1	2.0636	0.0937	729.55	729.855	4751.3	5	414.1	71.4	1	K.NAGAVIGK.G
*	HsFLAG-FLJ20729_	2.8333	0.104	1662.57	1662.926	4411.5	1	429.4	62.5	1	K.KIIPTLEEYQHYK.G
	HsFlag-VPS71_Ti_1	3.1261	0.2606	1099.29	1099.108	4459.9	5	727	81.2	2	K.GSDFDCELR.L
	HsFlag-VPS71_Ti_1	2.976	0.1126	1333.59	1333.484	6995.3	1	634.1	75	2	K.ELRENTQTTIK.L
gi|4506715|re	3	27	30.40%	69	7841	10.7	ribosomal protein S28 [Homo sapiens]				
gi|89042507|r	3	27	18.90%	111	12494	10.4	PREDICTED: similar to 40S ribosomal protein S28 [Homo sapiens]				
gi|89035017|r	3	27	30.40%	69	7841	10.7	PREDICTED: similar to 40S ribosomal protein S28 [Homo sapiens]				
gi|89034184|r	3	27	30.40%	69	7841	10.7	PREDICTED: similar to 40S ribosomal protein S28 [Homo sapiens]				

gi|88959151|r	3	27	30.40%	69	7841	10.7	PREDICTED: similar to 40S ribosomal protein S28 [Homo sapiens]				
gi|88953906|r	3	27	30.40%	69	7841	10.7	PREDICTED: similar to 40S ribosomal protein S28 [Homo sapiens]				
	HsFlag-NUFIP_Ti_1	1.9578	0.2089	1099.46	1100.188	4432.6	2	342.5	62.5	1	R.VEFMDDTSR.S
	HsFlag-NUFIP_Ti_1	2.566	0.1086	1100.3	1100.188	3757.8	3	620.7	87.5	2	R.VEFMDDTSR.S
	HsFLAG-ARP6_Ti_1	4.2033	0.305	1360.97	1361.492	7714.1	1	1559.1	81.8	24	R.EGDVLTLLESER.E
gi|4826998|re	24	203	30.30%	707	76150	9.4	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated) [Homo sapiens]				
*	HsFLAG-p53-DNA-D	1.99	0.1853	882.28	882.946	5835.6	1	662	78.6	2	K.ISDSEGFK.A
*	HsFLAG-FLJ20729_	3.9043	0.4204	1808.07	1809.026	3514.7	1	845.6	76.7	8	R.LFVGNLPADITEDEFK.R
*	HsFLAG-p53-DNA-D	3.5028	0.2239	1966.76	1965.213	4199.7	1	671.4	62.5	2	R.LFVGNLPADITEDEFKR.L
*	HsFlag-VPS71_Ti_1	2.8505	0.3281	1252.61	1253.397	4670.3	1	435.5	60	3	K.YGEPGEVFINK.G
*	HsFlag-VPS71_Ti_1	4.151	0.3225	1253.75	1253.397	3358.2	1	809.4	90	5	K.YGEPGEVFINK.G
*	HsFLAG-p53-DNA-D	2.5664	0.4197	1143.53	1144.319	5629.1	1	621	75	9	R.FATHAAALSVR.N
*	HsARP6-FLAG_Ti_1	3.4993	0.443	1144.32	1144.319	5954.8	1	1151.6	85	13	R.FATHAAALSVR.N
*	HsFLAG-UTX1_Ti_2	5.6627	0.4674	2640.25	2640.909	10322.2	1	1805.8	52.3	52	R.NLSPYVSNELLEEAFSQFGPIER.A
*	HsFlag-VPS71_Ti_1	4.1189	0.2123	2643.45	2640.909	7124.3	1	1080.3	34.1	1	R.NLSPYVSNELLEEAFSQFGPIER.A
	HsFlag-VPS71_Ti_1	2.2093	0.2393	886.64	887.024	5875.5	7	596.8	78.6	3	R.AVVIVDDR.G
*	HsFLAG-p53-DNA-D	2.8244	0.2759	1245.55	1246.452	5146	3	336.7	54.5	1	K.GIVEFASKPAAR.K
*	HsFLAG-FLJ20309_	3.1298	0.3592	1246.58	1246.452	8598.2	1	1365.6	72.7	2	K.GIVEFASKPAAR.K
*	HsFlag-VPS71_Ti_1	4.7104	0.4347	1483.1	1481.655	6886.7	1	1724	87.5	2	R.CSEGVFLLTTTPR.P
*	HsFlag-DPCD_Ti_20	6.803	0.3878	3599.3	3598.992	9184.5	1	1309	29	29	R.CSEGVFLLTTTPRPVIVEPLEQLDDEDGLPEK.L
*	HsFLAG-p53-DNA-D	6.0004	0.4467	2135.71	2136.361	4805	1	1336.6	75	5	R.PVIVEPLEQLDDEDGLPEK.L
*	HsFLAG-FLJ20729_	4.411	0.4574	1764.31	1763.863	7357.8	1	1166.3	69.2	6	R.FAQHGTFEYEYSQR.W
*	HsFlag-NUFIP_Ti_2	4.3111	0.3892	2428.37	2429.623	6071.1	1	784.4	36.8	2	K.DKLESEMEDAYHEHQANLLR.Q
*	HsFlag-VPS71_Ti_1	5.7419	0.4642	2428.73	2429.623	7480.2	1	1706	63.2	3	K.DKLESEMEDAYHEHQANLLR.Q
*	HsFLAG-p53-DNA-D	4.4269	0.3024	1573.43	1573.782	9875.8	1	1730	81.8	10	R.RMEELHNQEMQK.R
*	HsFlag-VPS71_Ti_1	3.0196	0.1888	1418.02	1417.595	8433.9	1	1299.8	85	1	R.MEELHNQEMQK.R
*	HsFlag-VPS71_Ti_1	4.2912	0.4615	1773.64	1772.963	5697.5	1	692	52.8	5	R.MGGGGAMNMGDPYGSGGQK.F
*	HsFLAG-p53-DNA-D	2.917	0.29	1341.54	1342.457	4208.2	1	297.4	57.1	4	R.FGQGGAGPVGGQGPR.G
*	HsFlag-FLJ90652_2	4.1451	0.3488	1342.27	1342.457	7729.3	1	1644	75	33	R.FGQGGAGPVGGQGPR.G
*	HsFlag-DPCD_Ti_20	2.6433	0.3217	1120.25	1121.256	6080	1	582.3	68.2	2	R.GMGPGTPAGYGR.G
gi|66392203|r	6	11	30.30%	267	30137	8.9	NME1-NME2 protein [Homo sapiens]				
	HsFLAG-p53-DNA-D	2.7564	0.1325	1151.25	1150.366	8005	2	1179.8	83.3	1	K.DRPFFAGLVK.Y
	HsFLAG-ARP6_Ti_1	4.4463	0.3575	1787.15	1787.041	6441.4	1	868.6	59.4	6	R.VMLGETNPADSKPGTIR.G
	HsFLAG-ARP6_Ti_1	2.7383	0.1994	1176.6	1176.404	6052.6	1	776.7	72.2	1	K.DRPFFPGLVK.Y
	HsFLAG-ARP6_Ti_1	2.624	0.3073	2092.81	2094.495	8056.3	2	389.4	38.9	1	K.YMNSGPVVAMVWEGLNVVK.T
	HsFlag-VPS71_Ti_1	2.2232	0.1557	1069.51	1070.191	3866.3	1	448.7	72.2	1	R.NIIHGSDSVK.S
	HsFlag-FLJ90652_2	2.6675	0.1514	1897.5	1897.178	4522.1	1	255.6	50	1	K.EISLWFKPEELVDYK.S
gi|4757834|re	5	11	30.30%	211	23772	6.7	BCL2-associated athanogene 2 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.3644	0.2279	1329.24	1329.536	7598.8	1	1793.2	90	2	R.LLESLDQLELR.V
*	HsFLAG-ARP6_Ti_1	4.3282	0.3823	2059.49	2058.375	8884.7	1	813.7	53.1	3	K.EILLEMIHSIQNSQDMR.Q
*	HsFLAG-ARP6_Ti_1	6.0812	0.5095	2429.63	2430.661	6815.6	1	1876.2	45.2	3	K.SHLMSLYSACSSEVPHGPVDQK.F
*	HsFLAG-ARP6_Ti_1	4.2431	0.4419	2430.09	2430.661	8077.2	1	1567.7	57.1	2	K.SHLMSLYSACSSEVPHGPVDQK.F
*	HsFLAG-ARP6_Ti_1	2.6134	0.2211	1607.9	1608.798	5472.7	2	736.3	65.4	1	K.FQSIVIGCALEDQK.K

gi|5032179|re	10	17	30.10%	835	88550	5.8	tripartite motif-containing 28 protein [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	6.4146	0.4971	3600.21	3600.813	9727	1	1545.4	26.4	2	K.RSTAPSAAASASASAAASSPAGGGAEALELLEHCGVCR.E
*	HsFLAG-TCF3_Ti_1	5.2709	0.3579	4112.79	4114.343	6986.8	1	533.2	21.3	2	PVCK.Q
*	HsFLAG-ARP6_Ti_1	4.2842	0.3278	1520.61	1521.629	7889.2	1	1668.7	81.8	2	K.DHQYQFLEDAVR.N
*	HsFLAG-ARP6_Ti_1	2.8208	0.2355	1309.19	1309.467	3590	1	595.5	83.3	1	K.FQWDLNAWTK.S
*	HsFLAG-p53-DNA-D	3.852	0.2874	2019.82	2020.314	7206.6	1	840	55.3	1	K.IVAERPGTNSTGPAPMAPPR.A
*	HsFlag-VPS71_Ti_1	3.5158	0.2705	3559.24	3559.713	5851.7	1	389	20.6	1	K.QGSGSSQPMEVQEGYGFGSGDDPYSSAEPHVSGVK.R
*	HsFLAG-ARP6_Ti_1	3.6087	0.2324	2244.7	2244.55	7701.6	1	1106.7	55.3	1	R.VSLERLDLDLTADSQPPVFK.V
*	HsFLAG-ARP6_Ti_1	4.2418	0.3219	1954.25	1954.187	3088.8	1	551.2	65.6	3	K.VFPGSTTEDYNLIVIER.G
*	HsFLAG-ARP6_Ti_1	4.0545	0.4168	1850.29	1850.931	7027.5	1	1180.6	61.1	3	K.EEDGSLSLDGADSTGVVAK.L
*	HsFLAG-Lin9_Ti_20	3.6188	0.2319	4307.8	4307.869	7076.1	1	381.3	18.9	1	R.VLLALFCHEPCRPLHQLATDSTFSLDQPGGTLDLTLIR.A
gi|28144916|r	9	18	30.10%	246	28383	8.7	hypothetical protein LOC55957 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.8148	0.196	1770.92	1772.021	7430.6	1	1872.8	51.8	1	K.ARNQLDAVLQCLLEK.S
*	HsFLAG-Lin9_Ti_20	4.5435	0.2246	1772.6	1772.021	9194.7	1	1499.6	64.3	2	K.ARNQLDAVLQCLLEK.S
*	HsFLAG-Lin9_Ti_20	3.1659	0.3054	1543.55	1544.755	7314.5	1	599.9	58.3	2	R.NQLDAVLQCLLEK.S
*	HsFLAG-Lin9_Ti_20	5.1866	0.2175	1544.4	1544.755	7118.1	1	2020.6	87.5	4	R.NQLDAVLQCLLEK.S
*	HsFLAG-Lin9_Ti_20	4.339	0.4437	2110.9	2111.325	6309	1	1359.8	67.6	3	R.SVDLAQFSENTPLYPICR.A
*	HsFLAG-Lin9_Ti_20	3.5587	0.156	2111.4	2111.325	7220.3	2	926.2	38.2	1	R.SVDLAQFSENTPLYPICR.A
*	HsFLAG-Lin9_Ti_20	3.1454	0.3369	2870.84	2871.992	6766.5	1	381.8	34	2	R.ERECSPSSPLPPLPEDEEGSEVTNSK.S
*	HsFLAG-Lin9_Ti_20	4.7504	0.4091	2871.01	2871.992	4772.8	1	667.7	34	2	R.ERECSPSSPLPPLPEDEEGSEVTNSK.S
*	HsFLAG-Lin9_Ti_20	2.5866	0.1663	1529.16	1529.702	5344.2	3	600.4	60.7	1	K.LPPPTPPGPPGDACR.S
gi|10440560|r	2	32	30.10%	136	15404	11.1	H3 histone family, member I [Homo sapiens]				
gi|4504295|re	2	32	30.10%	136	15404	11.1	H3 histone family, member K [Homo sapiens]				
gi|4504291|re	2	32	30.10%	136	15404	11.1	H3 histone family, member H [Homo sapiens]				
gi|4504289|re	2	32	30.10%	136	15404	11.1	H3 histone family, member F [Homo sapiens]				
gi|4504287|re	2	32	30.10%	136	15404	11.1	H3 histone family, member D [Homo sapiens]				
gi|4504285|re	2	32	30.10%	136	15404	11.1	H3 histone family, member C [Homo sapiens]				
gi|4504281|re	2	32	30.10%	136	15404	11.1	H3 histone family, member A [Homo sapiens]				
gi|21071021|r	2	32	30.10%	136	15404	11.1	H3 histone family, member B [Homo sapiens]				
	HsFLAG-p53-DNA-D	2.6769	0.2307	1034.28	1033.219	4212.4	4	520	81.2	3	R.YRPGTVALR.E
	HsFLAG-ARP6_Ti_1	6.0271	0.4076	3589.51	3588.986	6964.5	1	1309.3	30.6	29	R.FQSSAVMALQEACEAYLVGLFEDTNLCAIHAK.R
gi|31742503|r	2	25	30.10%	136	15388	11.3	H3 histone family, member M [Homo sapiens]				
gi|88943489|r	2	25	30.10%	136	15388	11.3	PREDICTED: similar to CG31613-PA [Homo sapiens]				
gi|88943485|r	2	25	22.80%	180	20527	10.2	PREDICTED: similar to H3 histone, family 2 isoform 2 [Homo sapiens]				
	HsFLAG-p53-DNA-D	2.6769	0.2307	1034.28	1033.219	4212.4	4	520	81.2	3	R.YRPGTVALR.E
	HsFLAG-p53-DNA-D	6.028	0.3893	3514.79	3515.926	6193.6	1	1018.7	29	22	R.FQSSAVMALQEASEAYLVGLFEDTNLCAIHAK.R
gi|4504279|re	2	46	30.10%	136	15328	11.3	H3 histone, family 3A [Homo sapiens]				
gi|88976633|r	2	46	30.10%	136	15226	11	PREDICTED: similar to H3 histone, family 3B [Homo sapiens]				
gi|4885385|re	2	46	30.10%	136	15328	11.3	H3 histone, family 3B [Homo sapiens]				
	HsFLAG-p53-DNA-D	2.6769	0.2307	1034.28	1033.219	4212.4	4	520	81.2	3	R.YRPGTVALR.E
	HsFLAG-p53-DNA-D	6.2359	0.3312	3440.67	3439.813	5190.8	1	958.2	29.8	43	R.FQSAAIGALQEASEAYLVGLFEDTNLCAIHAK.R
gi|5730085|re	2	3	30.10%	113	12452	5.1	t-complex-associated-testis-expressed 1-like 1 [Homo sapiens]				
*	HsFLAG-FLJ20729_	3.121	0.3675	1674.39	1675.795	5169	1	785.7	63.3	1	K.EAIESAIGGNAYQHSK.V

*	HsFLAG-p53-DNA-D	5.1487	0.4171	2089.8	2090.341	7986.4	1	826.3	55.9	2	K.VNQWTTNVVEQTLSQLTK.L
gi|4506699|re	4	30	30.10%	83	9111	8.5	ribosomal protein S21 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	4.3289	0.4386	1557.48	1557.719	8954.4	1	1974.2	80.8	25	K.DHASIQMNVAEVDK.V
*	HsFlag-NUFIP_Ti_1	2.3055	0.3363	1557.69	1557.719	7327	1	462.7	50	1	K.DHASIQMNVAEVDK.V
*	HsFlag-NUFIP_Ti_1	3.5081	0.3019	1280.68	1279.411	5878.5	1	842.1	75	2	R.RMGESDDSILR.L
*	HsFlag-NUFIP_Ti_1	3.6214	0.2971	1123.35	1123.223	6366	1	1567.8	94.4	2	R.MGESDDSILR.L
gi|35493811|r	13	62	30.00%	530	59380	10.1	RNA-binding region containing protein 2 isoform a [Homo sapiens]				
gi|4757926|re	13	62	30.30%	524	58657	10.1	RNA-binding region containing protein 2 isoform b [Homo sapiens]				
gi|35493829|r	13	62	42.60%	373	40541	6.3	RNA-binding region containing protein 2 isoform c [Homo sapiens]				
gi|35493822|r	13	62	43.30%	367	39818	6.6	RNA-binding region containing protein 2 isoform d [Homo sapiens]				
gi|35493817|r	13	62	42.60%	373	40541	6.3	RNA-binding region containing protein 2 isoform c [Homo sapiens]				
	HsFlag-VPS71_Ti_1	2.2452	0.1315	1271.55	1272.397	7516.2	1	518.2	60	1	R.DLEEFFSTVGK.V
	HsFlag-VPS71_Ti_1	3.0667	0.1704	1272.35	1272.397	7380.2	1	1607	85	1	R.DLEEFFSTVGK.V
	HsFLAG-Lin9_Ti_20	5.8847	0.5014	2392.42	2392.758	8327.9	1	2341.7	44.3	4	K.GIAYVEFVDVSSVPLAIGLTGQR.V
	HsFLAG-ARP6_Ti_1	3.7127	0.3607	2392.72	2392.758	4166.3	1	389.6	45.5	2	K.GIAYVEFVDVSSVPLAIGLTGQR.V
	HsFLAG-Lin9_Ti_20	3.3374	0.378	1551.64	1552.855	6905.2	1	1042.4	67.9	2	R.VLGVPIIVQASQAEK.N
	HsFlag-VPS71_Ti_1	4.6031	0.428	1552.66	1552.855	3122	1	965.1	85.7	15	R.VLGVPIIVQASQAEK.N
	HsFLAG-p53-DNA-D	2.6372	0.3265	1908.3	1909.21	10604.1	1	784.4	50	1	R.LYVGSLHFNITEDMLR.G
	HsFLAG-Lin9_Ti_20	3.7222	0.3436	1581.67	1582.673	7191.2	1	1074.8	69.2	3	K.GYGFITFSDSECAK.K
	HsFlag-NUFIP_Ti_1	4.6828	0.2298	1776.53	1775.076	8755	1	942	56.7	8	K.ALEQLNGFELAGRPMK.V
	HsFlag-DPCD_Ti_20	5.2913	0.515	1831.2	1830.857	7497.3	1	1497.3	68.8	11	R.TDASSASSFLDSDELER.T
	HsFlag-NUFIP_Ti_1	5.6312	0.3446	1692.76	1692.925	7470.1	1	2321.6	78.1	9	K.CPSIAAAIAAVNALHGR.W
	HsFlag-NUFIP_Ti_1	5.4069	0.3385	1693.02	1692.925	8351.9	1	2142.5	51.6	2	K.CPSIAAAIAAVNALHGR.W
	HsFlag-NUFIP_Ti_1	5.0329	0.3463	3348.92	3349.931	5596.8	1	543.9	26.7	3	K.MITAAYVPLPTYHNLFPDSMTATQLLVPSR.R
gi|73760405|r	9	52	30.00%	454	50670	9.4	thymopoietin isoform beta [Homo sapiens]				
	HsFLAG-KIAA0515_	2.5085	0.142	1700.23	1698.874	4238.1	8	409.2	53.3	1	K.SELVANNVTLPAGEQR.K
	HsFLAG-p53-DNA-D	4.7959	0.3471	1719.67	1719.981	7762.8	1	1475.9	73.1	9	K.DVYVQLYLQHLTAR.N
	HsFLAG-UTX1_Ti_2	3.7274	0.3961	1252.53	1252.416	6178.6	1	1455	81.8	21	R.NRPPLPAGTNSK.G
	HsFlag-NUFIP_Ti_2	5.4352	0.4378	2571.48	2571.72	7444.5	1	1550	36	8	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S
	HsFLAG-p53-DNA-D	4.1052	0.2686	2688.36	2689.887	10107.3	1	620.4	34.1	1	R.QEDKDDLDVTELTNEDLLDQLVK.Y
	HsFlag-Ies6_293_Ti_	4.6388	0.3556	2190.38	2189.378	7580	1	1027.3	55.6	3	K.DDLDVTELTNEDLLDQLVK.Y
	HsARP6-FLAG_Ti_1	3.1637	0.357	1330.97	1331.514	3923.2	1	937.3	75	6	K.YGVNPGPIVGTTR.K
	HsFLAG-FLJ20729_	2.5442	0.253	1647.67	1648.767	4565.1	1	1021.1	73.3	1	R.SSTPLPTISSSAENTR.Q
*	HsFLAG-p53-DNA-D	3.8296	0.2533	1793.71	1794.06	5369.3	1	597.8	56.7	2	K.HASPILPITEFSDIPR.R
gi|21464101|r	5	16	30.00%	247	28303	4.9	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide [Homo sapie				
*	HsFlag-VPS71_Ti_1	3.8428	0.2903	2237.08	2236.534	6488.9	1	1404.6	41.7	1	K.ELEAVCQDVLSLLDNYLIK.N
*	HsFlag-VPS71_Ti_1	5.0578	0.4411	2237.94	2236.534	6758.2	1	1598.3	66.7	5	K.ELEAVCQDVLSLLDNYLIK.N
*	HsFlag-NUFIP_Ti_1	4.5024	0.2803	3014.22	3014.373	6321	1	585.1	27	1	R.LGLALNYSVFYYEIQNAPEQACHLAK.T
*	HsFlag-VPS71_Ti_1	5.5011	0.5145	2133.65	2132.242	6140.9	1	1584.4	69.4	7	K.TAFDDAIAELDTLNEDSYK.D
	HsFLAG-FLJ20729_	3.7624	0.1371	1189.5	1190.444	6163.6	5	1616.1	88.9	2	K.DSTLIMQLLR.D
gi|12667788|r	41	132	29.80%	1960	226530	5.6	myosin, heavy polypeptide 9, non-muscle [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.6294	0.3973	1673.41	1673.869	6947.8	1	1668.4	78.6	2	K.NFINNPLAQADWAAK.K
	HsFLAG-ARP6_Ti_1	4.3483	0.3981	2286.24	2287.556	7047.8	1	714	47.4	1	K.VEDMAELTCLNEASVLHNLK.E

	HsFLAG-Lin9_Ti_20	3.8076	0.3868	2125.48	2126.205	8110.7	1	708	44.7	1	R.EDQSILCTGESGAGKTENTK.K
*	HsFLAG-ARP6_Ti_1	4.5418	0.4442	1479.5	1479.719	7111.8	1	1578.7	79.2	13	K.VIQYLAYVASSHK.S
*	HsFLAG-ARP6_Ti_1	3.9069	0.3458	2385.79	2386.707	6199.5	1	572.3	45	3	R.INFDVNGYIVGANIETYLLEK.S
*	HsFLAG-ARP6_Ti_1	4.3698	0.431	1641.22	1641.824	4550.2	1	1025.1	75	6	R.FLSNGHVTIPGQQDK.D
*	HsFLAG-ARP8_Ti_1	5.0671	0.3467	1487.47	1487.826	7530.6	1	2342.9	88.5	8	R.VISGVLQLGNIVFK.K
*	HsFLAG-ARP6_Ti_1	3.4316	0.3787	1615.6	1616	8617.2	2	756.1	57.1	2	R.VISGVLQLGNIVFKK.E
	HsFLAG-ARP6_Ti_1	2.7773	0.2777	1592.1	1592.678	3561.8	1	582.7	64.3	2	R.NTDQASMPDNTAAQK.V
*	HsFLAG-ARP6_Ti_1	4.1401	0.2788	1572.34	1572.805	6559.9	1	1490.5	76.9	11	K.VSHLLGINVTDFTR.G
*	HsFLAG-ARP6_Ti_1	3.6056	0.2127	1573.07	1572.805	5273.7	1	1147.5	55.8	1	K.VSHLLGINVTDFTR.G
	HsFLAG-ARP6_Ti_1	3.9279	0.1225	2468.62	2468.789	8469.2	1	1635.8	41.7	1	K.LQQLFNHTMFILEQEEYQR.E
*	HsFlag-FLJ90652_2	2.5276	0.2003	2111.94	2111.411	10019.4	4	559.9	41.7	1	K.PAGPPGILALLDEECWFPK.A
	HsFLAG-ARP6_Ti_1	3.8076	0.3428	1296.43	1295.447	6649.5	1	1344	85	2	K.ADFCIIHYAGK.V
*	HsFlag-VPS71_Ti_1	4.8672	0.449	2020.93	2019.364	6795	1	1114.6	55.3	3	R.IIGLDQVAGMSETALPGAFK.T
	HsFLAG-BC014022_	4.6953	0.3416	1578.18	1575.852	3947.8	1	735	69.2	4	K.AGKLDPHLVLDQLR.C
	HsFLAG-Lin9_Ti_20	2.6215	0.2311	1319.1	1319.547	3341.6	1	429.6	75	2	K.LDPHLVLDQLR.C
*	HsFLAG-ARP6_Ti_1	3.0349	0.175	1559.4	1559.806	5442.3	1	582.9	66.7	2	R.QRYEILTPNSIPK.G
	HsFLAG-ARP6_Ti_1	4.1988	0.3798	1224.38	1224.359	6572.6	1	1434.4	85	2	R.AGVLAHLEEER.D
*	HsFLAG-ARP6_Ti_1	2.707	0.1912	1554.02	1553.731	8257	1	711.4	62.5	1	K.ITDVIIGFQACCR.G
*	HsFLAG-ARP6_Ti_1	3.9852	0.273	1770.49	1770.903	9984	1	1608.9	69.2	3	K.KQELEEICHDLEAR.V
*	HsFLAG-ARP6_Ti_1	4.8331	0.4046	1889.26	1890.064	8109.1	1	1475.6	67.9	1	K.KLEEEQIILEDQNCK.L
*	HsFLAG-Lin9_Ti_20	5.0507	0.3448	2616.22	2616.882	9036.1	1	1486.8	50	1	R.KLEGDSTDLSDQIAELQAQIAELK.M
	HsFLAG-ARP6_Ti_1	3.1298	0.1302	1258.36	1258.417	6831.5	4	1016.2	80	1	K.KEEELQAALAR.V
*	HsFLAG-ARP8_Ti_1	4.5317	0.427	2034.89	2035.126	5625.6	1	1340.6	71.9	4	R.ELESQISELQEDLESER.A
*	HsFLAG-BC014022_	5.1663	0.4208	3017.96	3019.243	9497.3	1	1341.5	29.8	7	R.DLGEELEALKTELEDTLDSTAAQQELR.S
*	HsFLAG-ARP6_Ti_1	5.6319	0.4465	1841.02	1840.985	8176.4	1	2777.5	83.3	2	K.HSQAVEELAEQLEQTK.R
*	HsFLAG-ARP6_Ti_1	4.9074	0.2596	1413.2	1413.657	7931.4	1	2164.3	90.9	2	K.KVEAQLQELQVK.F
*	HsFLAG-FLJ20729_	3.7484	0.3549	1948.88	1947.15	9231.5	1	543.6	41.2	1	K.LQVELDNVTGLLSQSDSK.S
*	HsFlag-VPS71_Ti_1	5.0882	0.2717	2493.9	2494.631	7501.9	1	995.2	52.5	2	K.DFSALESQLQDTQELLQEENR.Q
*	HsFLAG-BC014022_	5.2812	0.2268	2207.92	2208.436	6887.2	1	2222.6	51.5	2	K.TRLQQELDDLLVDLDHQR.Q
*	HsFLAG-ARP6_Ti_1	3.7197	0.2867	1952.25	1951.144	8912.3	1	783.5	50	2	R.LQQELDDLLVDLDHQR.Q
	HsFLAG-Lin9_Ti_20	3.416	0.1163	1220.85	1221.396	6427.8	2	1186.2	83.3	2	K.KFDQLLAEEK.T
*	HsFLAG-ARP6_Ti_1	3.4576	0.2093	1361.48	1361.556	5616.8	2	859.4	80	1	K.RALEQQVEEMK.T
	HsFLAG-ARP6_Ti_1	6.8581	0.5173	1962.21	1963.059	10191.7	1	3429.4	81.2	12	K.TQLEELEDELQATEDAK.L
*	HsFLAG-ARP6_Ti_1	4.3601	0.3797	1349.14	1349.394	7782.1	1	1641.7	79.2	1	R.DELADEIANSSGK.G
*	HsFlag-VPS71_Ti_1	6.5893	0.3644	2474.24	2473.61	9557.5	1	2713.3	65	8	R.IAQLEEELEEEQGNTELINDR.L
*	HsFLAG-Lin9_Ti_20	4.6125	0.4088	1871.64	1871.057	6933.4	1	1367.4	70	2	K.ANLQIDQINTDLNLER.S
*	HsFLAG-Lin9_Ti_20	4.2187	0.2786	1531.46	1531.66	9225.1	1	1672.7	75	2	K.IAQLEEQLDNETK.E
*	HsFLAG-ARP6_Ti_1	3.8266	0.1314	1488.36	1488.554	9069.5	1	1407	72.7	2	K.RQLEEAEEEAQR.A
*	HsFLAG-BC014022_	3.703	0.0856	1156.23	1156.373	6193.5	2	1149.9	88.9	6	R.RGDLPFVVPR.R
gi|21735625|r	6	26	29.80%	245	27745	4.8	tyrosine 3/tryptophan 5 -monooxygenase activation protein, zeta polypeptide [Homo sapiens]				
gi|4507953|re	6	26	29.80%	245	27745	4.8	tyrosine 3/tryptophan 5 -monooxygenase activation protein, zeta polypeptide [Homo sapiens]				
	HsH2AZ-FLAG_293_	4.6302	0.3489	1550.08	1549.591	7406.4	1	1856.9	80.8	2	K.SVTEQGAELSNEER.N
	HsFLAG-ARP6_Ti_1	4.1705	0.2529	1420.28	1419.581	8018.9	1	2144.9	86.4	3	R.DICNDVLSLLEK.F

	HsFlag-FLJ90652_2	5.9546	0.4468	2041.92	2042.21	10329.5	1	2605.9	70.6	2	K.GIVDQSQQAYQEAFEISK.K
	HsFlag-VPS71_Ti_1	5.2604	0.3881	2132.76	2133.27	6134	1	1616.9	69.4	13	K.TAFDEAIAELDTLSEESYK.D
	HsFlag-FLJ90652_2	4.9556	0.3922	2133.81	2133.27	8417.6	1	1560.2	43.1	4	K.TAFDEAIAELDTLSEESYK.D
	HsFLAG-FLJ20729_	3.7624	0.1371	1189.5	1190.444	6163.6	5	1616.1	88.9	2	K.DSTLIMQLLR.D
gi|4506587|re	2	4	29.80%	121	13569	5.1	replication protein A3, 14kDa [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.8323	0.3012	2138.37	2137.514	7046	5	477.2	38.9	1	R.INAGMLAQFIDKPVCFVGR.L
*	HsFlag-NUFIP_Ti_1	5.0477	0.425	2039.5	2040.329	6062.5	1	1460.8	71.9	3	K.IIHDFPQFYPLGIVQHD.-
gi|32996737|r	13	51	29.70%	558	63811	9.4	lin-9 homolog [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	2.6368	0.1896	1609.48	1609.693	8717	9	628.5	54.2	1	R.LFSDEDDRQINTR.S
*	HsFLAG-Lin9_Ti_20	2.9468	0.3523	1824.22	1824.996	7980.5	1	752.1	62.5	1	K.WCIYEWFYSNIDK.P
*	HsFLAG-Lin9_Ti_20	5.5564	0.4489	2363.79	2364.577	8126.4	1	2341.6	64.3	2	R.GVHDGLFTGQIDAVDTLNATYR.V
*	HsFLAG-Lin9_Ti_20	4.7232	0.2661	2364.71	2364.577	9508.8	1	1731.2	39.3	2	R.GVHDGLFTGQIDAVDTLNATYR.V
*	HsFLAG-Lin9_Ti_20	6.5631	0.4503	2757.66	2759.137	9140.1	1	1962.1	39.1	4	R.LHYTPPLQSPIIDNDPLLGQSPWR.S
*	HsFLAG-Lin9_Ti_20	4.7986	0.3754	2758.89	2759.137	6374	1	901.3	52.2	7	R.LHYTPPLQSPIIDNDPLLGQSPWR.S
*	HsFLAG-Lin9_Ti_20	5.3038	0.3808	2366.58	2367.661	7857.9	1	1706.9	40.5	6	K.ISGSDTETLGGFPVEFLIQVTR.L
*	HsFLAG-Lin9_Ti_20	5.4332	0.3978	2366.75	2367.661	5697.5	1	1224.4	59.5	15	K.ISGSDTETLGGFPVEFLIQVTR.L
*	HsFLAG-Lin9_Ti_20	3.6424	0.3609	1458.02	1458.672	4524.4	1	823.5	81.8	2	K.SYSMPISIEFQR.R
*	HsFLAG-Lin9_Ti_20	4.889	0.2076	1690.2	1690.98	9638.6	1	2260.2	80.8	2	R.RYATIVLELEQLNK.D
*	HsFLAG-Lin9_Ti_20	5.1317	0.2041	1534.5	1534.793	8904.3	1	2279.5	87.5	6	R.YATIVLELEQLNK.D
*	HsFLAG-Lin9_Ti_20	4.0714	0.2626	2825.83	2825.045	4752.2	1	557.1	43.5	2	K.VQQYCYELAPDQGLQPADQPTDMR.R
*	HsFLAG-Lin9_Ti_20	5.0463	0.4115	2442.81	2443.555	6161	1	1089.4	54.8	1	R.HANSSTGQPCVENENLTDLISR.L
gi|10835067|r	11	65	29.70%	408	46837	7.1	autoantigen La [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	5.4497	0.4566	2073.27	2073.281	9091.2	1	2583	76.7	8	K.ICHQIEYYFGDFNLPR.D
*	HsFlag-NUFIP_Ti_1	4.7497	0.3623	2073.32	2073.281	7427.7	1	1805.9	48.3	12	K.ICHQIEYYFGDFNLPR.D
*	HsFLAG-ARP6_Ti_1	3.7385	0.2196	1544.23	1543.862	3912.9	1	750.2	79.2	2	K.LDEGWVPLEIMIK.F
*	HsFLAG-ARP6_Ti_1	4.4448	0.3285	1550.61	1550.792	5446.1	1	1111.5	76.9	17	R.LTTDFNVIVEALSK.S
*	HsFlag-NUFIP_Ti_1	4.4422	0.2972	1746.81	1746.958	9125.6	1	2553.6	78.6	5	R.RSPSKPLPEVTDEYK.N
*	HsFLAG-ARP6_Ti_1	3.9396	0.3675	1590.1	1590.77	3510.9	1	741.2	76.9	1	R.SPSKPLPEVTDEYK.N
*	HsFLAG-ARP6_Ti_1	4.224	0.3868	1500.42	1499.704	6590.8	1	1062.5	69.2	7	K.GSIFVVFDSIESAK.K
*	HsFLAG-ARP6_Ti_1	3.0313	0.1269	1034.69	1034.2	4074.2	1	880.5	87.5	1	K.KFVETPGQK.Y
*	HsFLAG-ARP6_Ti_1	4.3649	0.3176	1831.64	1832.103	6344.2	1	804.6	57.1	9	K.ETDLLILFKDDYFAK.K
*	HsFLAG-ARP6_Ti_1	3.7839	0.3619	1547.71	1547.702	10127	1	1802.1	75	2	K.EVTWEVLEGEVEK.E
*	HsFLAG-ARP6_Ti_1	4.4832	0.1867	1445.09	1445.613	6820.8	1	1624.4	86.4	1	K.KIIEDQQESLNK.W
gi|21536286|r	7	23	29.70%	381	42644	5.6	brain creatine kinase [Homo sapiens]				
*	HsFLAG-p53-DNA-D	2.9477	0.1632	1255.07	1255.332	9226	4	734.7	65	2	R.HGGYKPSDEHK.T
*	HsFLAG-ARP6_Ti_1	3.1695	0.1914	2294.39	2296.513	9759.8	1	629.2	41.7	2	K.SMTEAEQQQLIDDHFLFDK.P
*	HsFLAG-p53-DNA-D	4.7688	0.2781	3588.3	3590.104	10507.6	1	961.9	23.4	1	K.SMTEAEQQQLIDDHFLFDKPVSPLLLASGMAR.D
*	HsFLAG-RPB5MP_2	4.0375	0.3673	1558.22	1558.781	6667.1	1	1529.3	83.3	7	R.FCTGLTQIETLFK.S
*	HsFLAG-ARP6_Ti_1	3.8253	0.3359	2955.1	2956.311	8573.9	1	963.2	31.2	1	K.DYEFMWNPHLGYILTCPSNLGTGLR.A
*	HsFLAG-ARP6_Ti_1	4.7289	0.299	1850.08	1850.18	7181.4	1	2030.7	71.9	9	R.LGFSEVELVQMVVDGVK.L
*	HsFLAG-FLJ20729_	3.2056	0.2353	1658.65	1657.879	7189.6	1	1055.7	67.9	1	R.LEQGQAIDDLMPAQK.-
gi|15055539|r	9	82	29.70%	293	31324	10.2	ribosomal protein S2 [Homo sapiens]				
	HsFLAG-UTX1_Ti_2	5.0805	0.2697	3686.33	3688.293	8796.6	1	1045.8	26.6	2	K.SLEEIYLFSLPIKESEIIDFFLGASLKDEVLK.I

	HsFlag-NUFIP_Ti_10	3.0626	0.2662	1570.14	1569.795	9463.4	1	965.7	61.5	7	K.ESEIIDFFLGASLK.D
	HsFlag-NUFIP_Ti_11	4.9436	0.3844	2154.19	2154.465	7120.9	1	1375.2	61.1	31	K.ESEIIDFFLGASLKDEVLK.I
	HsFlag-NUFIP_Ti_10	4.6322	0.1477	1718.33	1717.965	5982.5	1	1223	68.8	20	K.AFVAIGDYNGHVGLGVK.C
	HsFLAG-p53-DNA-D	2.7185	0.1177	1136.75	1137.334	5462.5	3	610.7	72.2	2	K.IGKPHTVPCK.V
	HsFlag-NUFIP_Ti_10	2.7662	0.2751	1847.94	1846.133	8752.3	1	659.6	53.3	1	K.KLLMMAGIDDCYTSAR.G
	HsFlag-NUFIP_Ti_10	3.7738	0.3008	1719	1717.959	8689.1	1	1086.5	64.3	1	K.LLMMAGIDDCYTSAR.G
	HsFlag-NUFIP_Ti_10	3.641	0.3159	1464.48	1464.618	5566.5	1	1336.9	59.1	1	K.SPYQEFTDHLVK.T
	HsFLAG-ARP6_Ti_1	3.9707	0.4151	1464.63	1464.618	7813.3	1	1641.1	81.8	17	K.SPYQEFTDHLVK.T
gi|50592996|r	18	365	29.60%	450	50433	4.9	tubulin, beta, 4 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	4.2213	0.2479	1617.4	1616.87	4265.9	1	1041.3	78.6	14	R.AILVDLEPGTMDSVR.S
	HsFLAG-TCF3_Ti_10	7.1819	0.4728	1959.62	1960.151	9139.8	1	3610.1	82.4	73	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-ARP6_Ti_1	4.9251	0.2887	1959.94	1960.151	7005.8	1	1288.7	41.2	34	K.GHYTEGAELVDSVLDVVR.K
	HsFLAG-TIP49b_Ti_	5.684	0.3213	2087.63	2088.325	8116.7	1	2259	51.4	39	K.GHYTEGAELVDSVLDVVRK.E
	HsSrcap_Ti_206.286	6.4593	0.361	2087.84	2088.325	9352.8	1	2739.4	72.2	25	K.GHYTEGAELVDSVLDVVRK.E
	HsFlag-VPS71_Ti_10	2.5434	0.1418	1319.6	1320.59	6897.3	9	431	59.1	1	R.IMNTFSVVPSPK.V
	HsFLAG-ARP6_Ti_1	4.5585	0.3954	1320.55	1320.59	7624	1	1689.8	86.4	26	R.IMNTFSVVPSPK.V
	HsFLAG-ARP6_Ti_1	2.1817	0.2119	1130.19	1131.277	3484.6	1	331.1	72.2	1	R.FPGQLNADLR.K
	HsFLAG-ARP6_Ti_1	3.1035	0.1934	1133.31	1131.277	4537.1	1	968.3	94.4	20	R.FPGQLNADLR.K
	HsFLAG-ARP6_Ti_1	2.7216	0.2275	1259.45	1259.451	6377.3	1	1130.1	85	3	R.FPGQLNADLRK.L
	Hs293Flag-Ies2_Ti_1	4.1115	0.2404	1271.88	1272.594	7432.2	1	1437.4	85	9	R.KLAVNMVPFPR.L
	HsFLAG-Lin9_Ti_20	3.7432	0.2947	1144.31	1144.42	4934.2	1	1119.4	94.4	37	K.LAVNMVPFPR.L
	HsTIP60_Ti_106.282	3.611	0.2365	1693.78	1692.968	3399.3	1	640.9	75	3	R.ALTVPELTQQMFDAK.N
	HsFLAG-ARP6_Ti_1	3.1514	0.3044	1065.99	1066.201	5998.7	1	1325.1	87.5	4	K.NMMAACDPR.H
	HsFLAG-ARP6_Ti_1	4.0978	0.3327	1699.12	1697.888	5299.1	1	715	61.5	39	K.NSSYFVEWIPNNVK.V
*	HsFLAG-ARP6_Ti_1	5.1249	0.4531	1875.46	1875.147	4879.6	1	1335.9	71.9	20	K.MSSTFIGNSTAIQELFK.R
	HsFLAG-ARP6_Ti_1	4.1879	0.3996	1386.16	1386.612	7897.9	1	1417.6	85	10	K.RISEQFTAMFR.R
	HsFLAG-ARP6_Ti_1	3.7061	0.3498	1229.27	1230.424	8240.8	1	1542.7	88.9	7	R.ISEQFTAMFR.R
gi|88947729|r	10	92	29.50%	275	29765	9.9	PREDICTED: similar to ribosomal protein S2 isoform 3 [Homo sapiens]				
gi|88981109|r	10	92	28.90%	280	29883	9.6	PREDICTED: similar to ribosomal protein S2 [Homo sapiens]				
gi|88976655|r	10	92	28.90%	280	29883	9.6	PREDICTED: similar to ribosomal protein S2 [Homo sapiens]				
	HsFlag-NUFIP_Ti_10	2.3266	0.2989	1551.76	1552.851	8692.8	1	499.1	54.2	2	K.SLEEIYLFSLPIK.E
	HsFlag-NUFIP_Ti_10	4.7238	0.3286	1553.49	1552.851	7279.5	1	1555.3	79.2	20	K.SLEEIYLFSLPIK.E
	HsFLAG-UTX1_Ti_20	5.0805	0.2697	3686.33	3688.293	8796.6	1	1045.8	26.6	2	K.SLEEIYLFSLPIKESEIIDFFLGASLKDEVLK.I
	HsFlag-NUFIP_Ti_10	3.0626	0.2662	1570.14	1569.795	9463.4	1	965.7	61.5	7	K.ESEIIDFFLGASLK.D
	HsFlag-NUFIP_Ti_11	4.9436	0.3844	2154.19	2154.465	7120.9	1	1375.2	61.1	31	K.ESEIIDFFLGASLKDEVLK.I
	HsFlag-NUFIP_Ti_10	4.6322	0.1477	1718.33	1717.965	5982.5	1	1223	68.8	20	K.AFVAIGDYNGHVGLGVK.C
	HsFLAG-p53-DNA-D	2.7185	0.1177	1136.75	1137.334	5462.5	3	610.7	72.2	2	K.IGKPHTVPCK.V
	HsFlag-NUFIP_Ti_10	2.118	0.3256	1025.62	1026.221	7555.2	1	739.8	70	1	R.GTGIVSAPVPK.K
	HsFLAG-TCF3_Ti_10	2.0447	0.2449	1386.49	1387.575	7244.3	6	375.5	50	1	K.TYSYLTPDLWK.E
	HsFLAG-ARP6_Ti_1	3.2281	0.3305	1386.78	1387.575	6225.5	1	872.2	75	6	K.TYSYLTPDLWK.E
gi|15431288|r	7	25	29.50%	217	24831	9.9	ribosomal protein L10a [Homo sapiens]				
*	HsFLAG-TCF3_Ti_10	4.278	0.4128	1893.48	1893.98	5896.7	1	929.7	63.3	6	K.FSVCVLGDQQHCDEAK.A
	HsFLAG-ARP6_Ti_1	3.6821	0.3099	1451.75	1452.709	3332.1	1	599.9	75	3	K.AVDIPHMDIEALK.K

	HsFLAG-TCF3_Ti_1	3.2863	0.3849	1452.57	1452.709	4736.4	1	653.1	62.5	1	K.AVDIPHMDIEALK.K
*	HsFLAG-TCF3_Ti_1	2.6306	0.3626	1484.51	1485.72	5109.6	1	645.5	62.5	1	K.KYDAFLASESLIK.Q
*	HsFLAG-p53-DNA-D	4.9719	0.3862	1485.04	1485.72	8882.3	1	2007.7	83.3	9	K.KYDAFLASESLIK.Q
*	HsFLAG-ARP6_Ti_1	2.3659	0.1078	811.47	812	4900.2	1	644.5	85.7	4	R.ILGPGLNK.A
*	HsFlag-NUFIP_Ti_1	4.5888	0.381	1601.51	1601.861	8613.4	1	1672.4	73.1	1	K.FPSLLTHNENMVAK.V
gi|13376798|	15	38	29.40%	721	79136	6.7	hypothetical protein LOC80304 [Homo sapiens]				
*	HsFLAG-TIP49a_Ti_	3.5811	0.3199	3437.21	3437.849	4789.1	1	515.9	26.7	1	K.VIGQFECVCGLSWAPPVADDTPVLLAVQHEK.H
*	HsFLAG-TIP49a_Ti_	4.8946	0.4468	1886.57	1887.127	6499.3	1	2102.5	80	5	K.HVTVWQLCPSPMESSK.W
*	HsFLAG-TIP49b_Ti_	2.9571	0.2943	1690.51	1689.964	3563.3	5	313.9	53.6	3	R.GSLPILPQGCVWHPK.C
*	HsFLAG-TIP49b_Ti_	3.7469	0.4164	1517.11	1517.617	6285	1	1025.5	77.3	1	R.IHCACWTQDGLR.L
*	HsFLAG-TIP49a_Ti_	5.3902	0.5167	3615.81	3616.833	6941.6	1	1157.7	27.4	1	K.EATDSETNSEVSVSSSYLEPLDLTHIHFNQHK.S
*	HsFLAG-TIP49b_Ti_	4.538	0.3863	1816.56	1817.018	6190.5	1	1184.1	71.4	2	K.KLIESLSPDFCHQNK.G
*	HsFLAG-TIP49a_Ti_	3.813	0.3135	1688.58	1688.844	4316.4	1	517.5	61.5	3	K.LIESLSPDFCHQNK.G
*	HsFLAG-TIP49a_Ti_	4.5919	0.3693	3053.42	3053.359	6214.7	1	775.3	39.3	1	K.EIQSPLSSICDGSIALDAEPVTQPASLPR.H
*	HsFLAG-TIP49b_Ti_	2.5236	0.3372	1661.74	1662.756	9012.3	1	625.9	50	1	R.HSSTPDHTSTLEPPR.L
*	HsFLAG-TIP49b_Ti_	3.189	0.3188	2157	2157.351	7586.7	1	610	44.4	1	R.HSSTPDHTSTLEPPRLPQR.K
*	HsFLAG-TIP49a_Ti_	4.5597	0.4233	2338.75	2338.665	6828.9	1	1586.3	65.8	6	K.SSSVYPLSQDLPYVHIIYQK.P
*	HsFLAG-TIP49b_Ti_	3.3205	0.1626	1032.21	1032.194	5145.2	1	745	87.5	4	K.RAVLLCDGK.L
*	HsFLAG-TIP49a_Ti_	2.3727	0.3092	1418.33	1419.534	4750.3	1	608	61.5	2	R.DSFSHSPGAVSSLK.V
*	HsFLAG-TIP49a_Ti_	3.6366	0.3292	1419.47	1419.534	5254	1	1096	73.1	6	R.DSFSHSPGAVSSLK.V
*	HsFLAG-TIP49a_Ti_	3.6447	0.1502	1420.47	1419.534	3975.2	1	1090	50	1	R.DSFSHSPGAVSSLK.V
gi|28882049|	5	8	29.10%	320	35244	5.5	replication factor C 2 (40kD) isoform 2 [Homo sapiens]				
gi|31563534|	5	8	26.30%	354	39157	6.4	replication factor C 2 (40kD) isoform 1 [Homo sapiens]				
	HsFlag-VPS71_Ti_1	4.8491	0.3074	1641.87	1641.824	7392.6	1	1744.4	78.6	2	K.APGSAGHYELPWVEK.Y
	HsFLAG-Lin9_Ti_20	3.791	0.2708	1634.88	1634.873	5383.5	2	606.2	53.1	3	R.EGNVPNIIIAGPPGTGK.T
	HsFLAG-Lin9_Ti_20	2.5792	0.1565	2565.95	2563.829	11724.2	2	377.5	27.3	1	R.QALNNLQSTFSGFGFINSENVFK.V
	HsFLAG-Lin9_Ti_20	4.3778	0.3391	2465.49	2465.86	8696.4	1	992.4	47.5	1	K.ILAHLWHLGYSPEDIIGNIFR.V
	HsFLAG-FLJ20729_	3.1863	0.3257	1756.31	1757.101	10557.7	1	1507.3	59.4	1	K.IAEGVNSLLQMAGLLAR.L
gi|12025678|	18	72	29.00%	911	104854	5.4	actinin, alpha 4 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.2973	0.3143	1392.39	1393.511	7905.9	1	1434.5	85	3	K.TFTAWCNSHLR.K
*	HsFLAG-p53-DNA-D	3.8131	0.1304	2094.64	2094.564	6579.7	8	1083	39.7	1	K.LMLLLEVISGERLPKPER.G
*	HsFLAG-ARP6_Ti_1	4.1101	0.3682	1485.92	1486.673	8357.5	1	1858.8	81.8	3	K.NVNVQNFHISWK.D
	HsFLAG-p53-DNA-D	3.8606	0.3388	1227.36	1227.409	9249.4	2	1758.7	85	5	K.DGLAFNALIHR.H
*	HsFLAG-FLJ20729_	3.7047	0.2019	1777.13	1776.897	11174.4	1	1346.4	63.3	3	K.DDPVTNLNNAFEVAEK.Y
	HsFLAG-FLJ20729_	3.9341	0.4516	2007.79	2009.287	7496.6	1	1006	55.9	4	K.AIMTYVSSFYHAFSGAQK.A
	HsFLAG-p53-DNA-D	3.8305	0.2522	1216.95	1216.423	7573.3	1	1642.6	94.4	1	K.LASDLLEWIR.R
*	HsFLAG-p53-DNA-D	2.9305	0.1524	1482.57	1482.723	3679.1	5	328.9	63.6	1	R.TIPWLEDRVPQK.T
	HsFLAG-p53-DNA-D	4.1643	0.2635	1422.27	1422.58	8347.1	1	1715	85	2	K.GYEEWLLNEIR.R
*	HsFLAG-Lin9_Ti_20	3.78	0.31	1760.12	1759.882	9766.6	1	1529.4	67.9	2	K.ICDQWDALGSLTHSR.R
*	HsFLAG-p53-DNA-D	4.5407	0.4627	1920.05	1921.158	7732.8	1	1215	58.8	4	K.LSGSNPYTTVTPQIINSK.W
*	HsFLAG-Lin9_Ti_20	2.9807	0.1785	1327.66	1326.452	5690.9	1	741.8	80	1	K.RDHALLEEQSK.Q
*	HsFLAG-p53-DNA-D	4.3204	0.4115	1774.55	1775.017	5825.8	1	527.7	53.3	4	R.QFASQANVVGPWIQTK.M
*	HsFLAG-p53-DNA-D	6.4581	0.4839	3324.99	3326.774	7199	1	1027.9	29.6	8	R.SIVDYKPNLDLLEQQHQLIQEALIFDNK.H

	HsFLAG-Lin9_Ti_20	4.3758	0.2651	1387.59	1387.622	9291.5	1	1782.9	81.8	18	R.VGWEQLLTTIAR.T
	HsFLAG-p53-DNA-D	3.8681	0.3006	1430.49	1430.601	7341.8	1	1291	81.8	1	R.TINEVENQILTR.D
*	HsFLAG-p53-DNA-D	4.7342	0.4433	1742.33	1742.834	9255.5	1	1652.2	66.7	8	R.ETTDTDTADQVIASFK.V
*	HsFLAG-FLJ20729_	3.6005	0.3151	1794.13	1794.032	5659.7	1	741.9	62.5	3	R.MAPYQGPDAVPGALDYK.S
gi|23503295|r	4	15	28.80%	215	24942	5.6	casein kinase 2, beta polypeptide [Homo sapiens]				
*	HsFlag-FLJ90652_2	4.396	0.4174	2007.37	2009.056	8007.5	1	1468.6	66.7	5	R.GNEFFCEVDEDYIQDK.F
*	HsFlag-VPS71_Ti_1	3.9783	0.3627	1688.85	1688.883	4450.6	1	595.6	61.5	8	K.FNLTGLNEQVPHYR.Q
*	HsFlag-FLJ90652_2	3.1355	0.1964	2563.53	2562.965	5648.5	1	411.8	38.6	1	R.VYCENQPMLPIGLSDIPGEAMVK.L
*	HsFLAG-FLJ20729_	3.0875	0.1863	1085.1	1085.254	6436.1	2	963.4	93.8	1	K.RPANQFVPR.L
gi|17105394|r	4	19	28.80%	156	17695	10.4	ribosomal protein L23a [Homo sapiens]				
gi|89057257|r	4	19	29.00%	155	17662	10.4	PREDICTED: similar to 60S ribosomal protein L23a [Homo sapiens]				
gi|42662048|r	4	19	29.00%	155	17662	10.4	PREDICTED: similar to 60S ribosomal protein L23a [Homo sapiens]				
	HsFLAG-p53-DNA-D	2.5907	0.2465	1108.51	1109.268	7567.5	1	812.6	70	1	K.EAPAPPKAEAK.A
	HsFLAG-ARP6_Ti_1	3.0594	0.0817	973.1	973.16	6484.4	8	1172	92.9	1	K.LDHYAIIK.F
	HsFlag-NUFIP_Ti_11	3.0603	0.1562	1749.37	1748.029	9456.3	1	1055.2	60.7	4	K.KIEDNNTLVFIVDVK.A
	HsFLAG-ARP6_Ti_1	3.8137	0.2535	1243.37	1242.418	6728.3	5	943.7	75	13	K.VNTLIRPDGEK.K
gi|24234750|r	15	28	28.60%	894	95339	8.8	interleukin enhancer binding factor 3 isoform a [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.9785	0.3355	2672.32	2672.886	8722.3	2	993.3	31.8	5	K.HSSVYPTQEELEAVQNMVSHTER.A
	HsFLAG-Lin9_Ti_20	4.5489	0.251	1389.13	1388.61	8620.1	1	1959.6	81.8	2	K.GDLDLELVLLCK.E
	HsFLAG-ARP6_Ti_1	2.6646	0.2087	1760.83	1760.087	6856.2	3	464.9	46.7	1	K.EPPLSLTIHLTSPVVR.E
	HsFlag-DPCD_Ti_20	4.4375	0.4439	1910.45	1911.119	5474.4	1	905	61.8	4	K.VLAGETLSVNDPPDVLDR.Q
	HsFLAG-p53-DNA-D	3.7266	0.2137	1601.08	1601.821	7002.9	1	716.2	60	3	K.SIGTANRPMGAGEALR.R
	HsFlag-VPS71_Ti_1	3.8493	0.5107	2512.62	2511.779	5562	1	823.4	52.3	1	R.VLECLASGIVMPDGSGIYDPCEK.E
	HsFLAG-Lin9_Ti_20	2.8367	0.1287	1302.19	1302.56	5057	6	603	75	1	R.LNQLKPGLQYK.L
	HsFLAG-p53-DNA-D	4.1644	0.2193	3317.78	3318.726	10731.7	1	800.6	23.4	1	K.LVSQTGPVHAPIFTMSVEVDGNSFEASGPSKK.T
	HsFLAG-FLJ20729_	3.5325	0.2583	1444.53	1444.646	5050.3	1	709.8	65.4	1	K.VLQDMGLPTGAEGR.D
	HsFLAG-Lin9_Ti_20	3.5628	0.3446	1435.93	1436.518	5269.2	2	829.9	70.8	1	K.YELISETGGSHDK.R
	HsFLAG-Lin9_Ti_20	3.0347	0.2429	1436.72	1436.518	6065.3	2	519.9	58.3	1	K.YELISETGGSHDK.R
	HsFLAG-Lin9_Ti_20	2.8883	0.3412	1414.42	1415.629	3656.1	1	601.2	75	1	K.LFPDTPLALDANK.K
*	HsFLAG-Lin9_Ti_20	4.9938	0.2924	3254.31	3255.224	8779.2	1	1530.8	30.8	1	K.GYNHGQGSYSYSNSYNSPGGGGGSDYNYESK.F
*	HsFLAG-Lin9_Ti_20	3.9319	0.4471	3012.79	3013.98	5575.1	1	567.7	33.3	1	R.SGGNSYGSGGASYNPGSHGGYGGGSGGGSSYQGK.Q
*	HsFLAG-FLJ20309_	4.5575	0.3727	3014.72	3013.98	6254.3	1	1053.1	29.5	4	R.SGGNSYGSGGASYNPGSHGGYGGGSGGGSSYQGK.Q
gi|5174449|re	11	76	28.60%	213	22487	10.8	H1 histone family, member X [Homo sapiens]				
*	HsFLAG-p53-DNA-D	2.2447	0.2539	945.41	946.048	5382.5	1	468.5	65	2	K.AGGSAALSPSK.K
*	HsFLAG-p53-DNA-D	2.604	0.2144	1073.51	1074.222	7617.9	8	539.4	59.1	1	K.AGGSAALSPSKK.R
*	HsFLAG-ARP6_Ti_1	3.9093	0.3762	1210.11	1208.4	5679.4	1	1230	88.9	3	K.YSQLVVETIR.R
*	HsFLAG-ARP6_Ti_1	2.8366	0.2421	1364.02	1364.588	6687.3	1	816.2	75	1	K.YSQLVVETIRR.L
*	HsFLAG-ARP6_Ti_1	3.0976	0.2265	1247.22	1247.356	5679.6	1	1047.2	88.9	1	K.VPWFDQQNGR.T
*	HsFLAG-ARP6_Ti_1	4.0999	0.2668	1343.21	1342.578	7412.5	1	1522.6	81.8	5	K.ALVQNDTLLQVK.G
*	HsFLAG-p53-DNA-D	3.6651	0.3187	1488.7	1488.69	3590	1	729.8	48.3	2	R.RGAPAAATAPAPTAHK.A
*	HsFlag-NUFIP_Ti_11	3.8219	0.3753	1488.71	1488.69	6467.6	1	1610.5	80	14	R.RGAPAAATAPAPTAHK.A
*	HsFlag-NUFIP_Ti_11	3.1306	0.261	1488.82	1488.69	4145.7	4	260	53.3	1	R.RGAPAAATAPAPTAHK.A
*	HsFlag-NUFIP_Ti_1	2.6303	0.263	1331.68	1332.502	5578.7	1	370	46.4	1	R.GAPAAATAPAPTAHK.A

*	HsFLAG-p53-DNA-D	4.3704	0.3122	1332.17	1332.502	4746	2	957.8	75	45	R.GAPAAATAPAPTAHK.A
gi|13376840|r	4	16	28.50%	305	33581	5.5	WD repeat domain 61 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.216	0.3966	3006.92	3006.298	7312.2	1	793	26.8	1	K.SIDAGPVDAWTLAFSPDSQYLATGTHVGK.V
*	HsFLAG-FLJ20309_	5.4244	0.3926	2052.75	2053.363	7092.8	1	1451.1	60.5	13	K.YLASGAIDGIINIFDIATGK.L
*	HsFLAG-Lin9_Ti_20	2.7617	0.2676	2258.26	2258.487	9316.2	4	389.1	32.5	1	R.SLTFSPDSQLLVTASDDGYIK.I
*	HsFLAG-p53-DNA-D	5.3233	0.4661	2105.79	2105.283	9622.5	1	1545	62.5	1	R.TCVHTFFDHQDQVWGVK.Y
gi|89036252|r	7	58	28.50%	295	32744	4.5	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma lamini				
	HsFlag-NUFIP_Ti_1	3.2111	0.1384	1136.52	1136.334	3726.7	3	871.1	83.3	9	K.SDGIYIINLK.R
	HsFlag-NUFIP_Ti_1	4.2588	0.3692	1204.09	1204.371	8028.8	1	1826.1	83.3	7	K.FAAATGATPIAGR.F
	HsFlag-NUFIP_Ti_1	4.4753	0.5023	1699.48	1699.907	3408.4	1	560.3	71.4	8	R.FTPGTFTNQIQAAFR.E
	HsFlag-NUFIP_Ti_1	3.0509	0.2708	913.3	913.105	4232	2	978	92.9	1	R.LLVVTDPR.A
	HsFlag-NUFIP_Ti_1	5.5581	0.4986	2997.06	2998.285	6353.2	1	838.2	44.2	10	R.ADHQPLTEASYVNLPTIALCNTDSPLR.Y
	HsFlag-NUFIP_Ti_1	5.9107	0.4253	2997.29	2998.285	8807.5	1	1816.3	36.5	19	R.ADHQPLTEASYVNLPTIALCNTDSPLR.Y
	HsFlag-NUFIP_Ti_1	3.4062	0.1796	1307.4	1307.455	4319.8	1	1167.2	90	4	R.YVDIAIPCNNK.G
gi|15809016|r	4	15	28.50%	172	19779	4.8	myosin regulatory light chain MRCL2 [Homo sapiens]				
gi|5453740|re	4	15	28.70%	171	19794	4.8	myosin regulatory light chain MRCL3 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.7386	0.2618	2090.98	2092.331	8215.1	1	679.6	47.1	4	R.ATSNVFAMFDQSQIQEFK.E
	HsFLAG-ARP6_Ti_1	5.5389	0.4091	2351.6	2351.454	8064	1	1704.8	63.2	7	R.NAFACFDEEATGTIQEDYLR.E
	HsFLAG-ARP6_Ti_1	3.5554	0.0846	1389.37	1389.553	7205.6	1	1288.9	80	3	K.KGNFNYIEFTR.I
	HsFLAG-Lin9_Ti_20	3.6641	0.2473	1261.06	1261.379	7716.4	1	1026.9	77.8	1	K.GNFNYIEFTR.I
gi|14150100|r	4	9	28.40%	190	20713	9.5	hypothetical protein LOC84284 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_11	3.6056	0.3785	1209.35	1209.434	4141	1	1020	86.4	3	R.HVFLTGPPGVGK.T
*	HsFLAG-TIP49b_Ti_	3.5109	0.283	1422.49	1421.64	7331.1	1	1226.1	75	2	R.RIGFDVVTLSGTR.G
*	HsFLAG-p53-DNA-D	3.0702	0.3874	1836.54	1837.21	8170	1	587.5	44.1	2	R.QTLSTPGTIILGTIPVPK.G
*	HsFLAG-ARP6_Ti_1	3.1564	0.3382	1225.36	1225.474	6096.4	1	1191.7	85	2	K.GKPLALVEEIR.N
gi|4506625|re	5	7	28.40%	148	16561	11	ribosomal protein L27a [Homo sapiens]				
gi|88999528|r	5	7	28.40%	148	16622	11.1	PREDICTED: similar to 60S ribosomal protein L27a [Homo sapiens]				
gi|51465328|r	5	7	28.40%	148	16622	11.1	PREDICTED: similar to 60S ribosomal protein L27a [Homo sapiens]				
	HsFLAG-TCF3_Ti_1	1.8218	0.0822	968.47	969.087	3573.2	3	373.3	78.6	1	K.YHPGYFGK.V
	HsFLAG-TCF3_Ti_1	4.2422	0.3947	1576.72	1579.719	6651.7	2	933.5	70.8	3	K.RNQSFCPTVNLDK.L
	HsFLAG-ARP6_Ti_1	3.3083	0.2751	1233.94	1233.41	7037.8	1	1249.6	88.9	1	K.LWTLVSEQTR.V
	HsFLAG-TCF3_Ti_1	2.4015	0.2709	1111.63	1112.315	5138.6	1	375.7	65	1	K.TGAAPIIDVVR.S
	HsFlag-Ies6_293_Ti_	2.9366	0.2691	1112.32	1112.315	3419.5	4	703.3	85	1	K.TGAAPIIDVVR.S
gi|5031741|re	8	32	28.20%	412	45746	6.5	DnaJ subfamily A member 2 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_2	3.506	0.3726	1626.23	1626.803	10141.2	2	1021.5	57.7	2	K.EISFAYEVLSNPEK.R
*	HsFLAG-ARP6_Ti_1	3.1183	0.2884	1782.56	1782.991	8369.8	1	813.7	53.6	2	K.EISFAYEVLSNPEKR.E
*	HsFLAG-TCF3_Ti_1	3.3031	0.368	1340.18	1338.392	7894	1	1115.3	70.8	1	K.NVLCSACSGQGGK.S
*	HsFLAG-ARP6_Ti_1	4.6091	0.4645	2641.62	2641.978	3982.1	1	478.2	45.8	4	R.ITFTGEADQAPGVEPGDIVLLLQEK.E
*	HsFLAG-ARP6_Ti_1	5.0314	0.4403	2642.03	2641.978	7527	1	1412.3	36.5	2	R.ITFTGEADQAPGVEPGDIVLLLQEK.E
*	HsFLAG-ARP6_Ti_1	3.7669	0.4279	1730.19	1731.011	6852.1	1	1027.9	60.7	6	K.IGLVEALCGFQFTFK.H
*	HsFLAG-TCF3_Ti_1	4.5211	0.2368	1864.47	1864.024	3541.4	2	625.1	67.9	3	K.FDVQFFPENNWINPDK.L
*	HsSrcap_Ti_203.430	6.0596	0.3599	3786.34	3786.138	4595.9	1	1034	33.6	12	K.LSELEDLLPSRPEVPNIIGETEEVELQEFDSTR.G
gi|55956788|r	26	504	28.00%	710	76615	4.7	nucleolin [Homo sapiens]				

*	HsFLAG-p53-DNA-D	2.6334	0.1417	857.53	858.069	5301.9	1	728.4	78.6	1	K.KVVVSPTK.K
*	HsFLAG-p53-DNA-D	2.5362	0.1858	985.56	986.243	4621.6	1	522.4	68.8	1	K.KVVVSPTKK.V
*	HsFLAG-p53-DNA-D	2.5478	0.229	884.49	885.095	5094.5	1	597.6	75	2	K.KVAVATPAK.K
*	HsFLAG-p53-DNA-D	2.7786	0.2781	1012.53	1013.269	5051.3	1	697.1	72.2	2	K.KVAVATPAKK.A
*	HsFLAG-p53-DNA-D	2.4188	0.2195	756.48	756.921	4773.7	1	446.7	78.6	6	K.VAVATPAK.K
*	HsFLAG-p53-DNA-D	1.9051	0.0949	884.57	885.095	4048.5	2	405.1	68.8	1	K.VAVATPAKK.A
*	HsFLAG-FLJ20729_	1.8885	0.0947	756.36	756.921	4173.7	1	328.6	71.4	1	K.ALVATPGK.K
*	HsFLAG-p53-DNA-D	4.9982	0.322	2697.56	2698.051	7203.3	1	1416.4	37	1	K.KQKVEGTEPTTAFNLFVGNLNFNK.S
*	HsFLAG-ARP6_Ti_1	4.3962	0.4259	2568.38	2569.877	6485.5	1	424	36.4	3	K.QKVEGTEPTTAFNLFVGNLNFNK.S
*	HsFlag-NUFIP_Ti_10	4.8198	0.2578	2569.4	2569.877	8031.4	1	978.7	30.7	9	K.QKVEGTEPTTAFNLFVGNLNFNK.S
*	HsFlag-NUFIP_Ti_10	5.7412	0.3568	2312.4	2313.572	8442.5	1	1831.4	41.2	12	K.VEGTEPTTAFNLFVGNLNFNK.S
*	HsFlag-NUFIP_Ti_10	5.4967	0.4623	2312.87	2313.572	7677.7	1	1786	62.5	72	K.VEGTEPTTAFNLFVGNLNFNK.S
*	HsFLAG-p53-DNA-D	5.4367	0.4275	1777.06	1777.925	7233.3	1	2435.4	85.7	5	R.KFGYVDFESAEDLEK.A
*	HsFlag-NUFIP_Ti_10	5.2007	0.4287	1648.68	1649.751	5788.2	1	1901.2	88.5	36	K.FGYVDFESAEDLEK.A
*	HsFLAG-ARP6_Ti_1	2.9113	0.1789	1177.41	1177.386	6150	1	1000.4	88.9	2	K.VFGNEIKLEK.P
*	HsFLAG-ARP6_Ti_1	3.7221	0.2555	1448.65	1448.659	6584.6	1	1273.4	81.8	1	K.NLPYKVTQDELK.E
*	HsFLAG-ARP6_Ti_1	3.7449	0.2104	1179.4	1179.272	4847.7	1	1189	94.4	3	K.EVFEDAAEIR.L
*	HsFLAG-ARP6_Ti_1	5.9768	0.5068	2501.02	2502.778	6712.4	1	1306.5	57.1	213	K.TLVLSNLSYSATEETLQEVFEK.A
*	HsFlag-NUFIP_Ti_11	4.1613	0.2913	2504.79	2502.778	8463	1	1087.2	33.3	5	K.TLVLSNLSYSATEETLQEVFEK.A
*	HsFLAG-ARP6_Ti_1	5.359	0.4852	1595.29	1595.748	8296.2	1	2243.9	80.8	91	K.GYAFIEFASFEDAK.E
*	HsFLAG-p53-DNA-D	3.1404	0.1662	1326.25	1323.397	7682	2	898.4	68.2	2	K.GLSEDTTEETLK.E
*	HsFLAG-ARP6_Ti_1	4.3525	0.4223	2201.31	2201.306	9160.2	1	1149.7	50	5	K.GLSEDTTEETLKESFDGSVR.A
*	HsFLAG-p53-DNA-D	2.9462	0.2576	1193.12	1193.299	9370.7	8	766.5	65	1	R.IVTDRETGSSK.G
*	HsFLAG-ARP6_Ti_1	4.437	0.3574	1562.38	1562.632	5761.8	1	1192.9	76.9	23	K.GFGFVDFNSEEDAK.A
*	HsFLAG-ARP6_Ti_1	3.5707	0.3841	1308.36	1308.359	6549.4	1	1208.9	81.8	5	K.EAMEDGEIDGNK.V
*	HsFLAG-ARP6_Ti_1	3.0222	0.2075	1058.1	1058.266	6503.7	6	1164.7	87.5	1	K.VTLDWAKPK.G
gi|38149981|r	5	27	28.00%	225	25486	9.7	small nuclear ribonucleoprotein polypeptide B'' [Homo sapiens]				
gi|4507123|re	5	27	28.00%	225	25486	9.7	small nuclear ribonucleoprotein polypeptide B'' [Homo sapiens]				
	HsFlag-NUFIP_Ti_11	5.9391	0.4309	2107.76	2108.488	9852.4	1	2598.2	69.4	18	R.SLYALFSQFGHVVDIVALK.T
	HsFLAG-p53-DNA-D	1.82	0.1028	909.35	910.104	9474.6	8	664.6	71.4	1	R.GQAFVIFK.E
	HsFlag-NUFIP_Ti_11	3.2912	0.2762	1569.58	1569.864	6104.5	1	594.2	66.7	1	R.QLQGFPFYGKPMR.I
	HsFlag-NUFIP_Ti_10	4.1464	0.2931	2471.26	2470.707	9410.7	1	1352.6	34.1	2	R.LVPGRHDIAFVEFENDGQAGAAR.D
	HsFlag-NUFIP_Ti_10	4.6272	0.4734	1947.58	1948.059	11279.1	1	1524.4	58.8	5	R.HDIAFVEFENDGQAGAAR.D
gi|41151097|r	5	8	28.00%	214	24627	10.1	PREDICTED: similar to ribosomal protein L10 isoform 1 [Homo sapiens]				
gi|89057215|r	5	8	28.00%	214	24627	10.1	PREDICTED: similar to ribosomal protein L10 isoform 4 [Homo sapiens]				
gi|89057211|r	5	8	28.00%	214	24627	10.1	PREDICTED: similar to ribosomal protein L10 isoform 1 [Homo sapiens]				
gi|89052350|r	5	8	28.00%	214	24627	10.1	PREDICTED: similar to ribosomal protein L10 isoform 4 [Homo sapiens]				
gi|5174431|re	5	8	28.00%	214	24577	10.1	ribosomal protein L10 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	4.0774	0.1893	3085.9	3084.304	9054.3	1	960.4	29.8	1	K.VDEFPLCGHMVSDEYEQLSSEALEAAR.I
	HsFLAG-TIP49b_Ti_	2.6148	0.2343	1188.58	1189.36	4646.5	5	278.5	59.1	1	R.GAFGKPQGTVAR.V
	HsFlag-ZnF-HIT2_Ti_	2.7464	0.0938	1189.2	1189.36	2900.2	3	508.7	77.3	1	R.GAFGKPQGTVAR.V
	HsFLAG-ARP6_Ti_1	3.7083	0.2544	1254.49	1253.549	4746	2	958.1	80	2	R.VHIGQVIMSIR.T
	HsFLAG-ARP6_Ti_1	3.2865	0.233	1114.51	1115.284	4796.7	1	893.2	83.3	3	K.RLIPDGCGVK.Y

gi|4502551|re	5	10	27.90%	315	37107	4.6	calumenin precursor [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.6379	0.2602	1461.03	1461.577	7417.4	1	760.3	68.2	1	K.DRVHHEPQLSDK.V
*	HsFLAG-ARP6_Ti_1	3.6553	0.3473	1665.32	1665.883	6722.6	1	739.4	57.7	2	K.DGFVTVDELKDWIK.F
*	HsFLAG-ARP6_Ti_1	3.4034	0.3545	2280.11	2280.365	8853.8	2	770.8	44.7	2	K.NATYGYVLDDPDPDDGFNYK.Q
*	HsFLAG-ARP6_Ti_1	5.1459	0.3862	1535.17	1535.706	8107.2	1	1940.8	83.3	2	K.DIVVQETMEDIDK.N
*	HsFLAG-ARP6_Ti_1	3.9472	0.275	3360.61	3361.531	6423.9	1	576.1	24.1	3	K.NADGFIDLEEYIGDMYSHDGNTDEPEWVK.T
gi|17999537|r	47	178	27.80%	2335	273686	8.8	U5 snRNP-specific protein [Homo sapiens]				
*	HsFlag-ZnF-HIT2_Ti_	4.6866	0.4406	2165.48	2166.454	4090.9	1	666.2	57.5	4	R.GPGNPVPGPLAPLPDYMSEEK.L
*	HsFlag-ZnF-HIT2_Ti_	5.7503	0.4358	2534.82	2534.868	6112.8	1	1295.8	60	36	R.LANQLLTDLVDDNYFYLFDLK.A
*	HsFLAG-p53-DNA-D	5.2639	0.4461	2122.89	2123.197	10508.9	1	2002.5	65.6	6	R.DINLQDEDWNEFNDINK.I
*	HsFLAG-Lin9_Ti_20	3.5359	0.2146	2457.46	2458.733	4649	1	787.6	40	1	K.TEDPDLPAFYFDPLINPISHR.H
*	HsFlag-ZnF-HIT2_Ti_	4.0853	0.4478	2457.8	2458.733	5345.5	1	795.4	55	11	K.TEDPDLPAFYFDPLINPISHR.H
*	HsFlag-DPCD_Ti_20	3.6947	0.0883	2750.88	2750.972	6895.7	6	879	34.1	1	K.SQEPLPDDDEEFELPEFVEPFLK.D
*	HsFLAG-p53-DNA-D	4.6693	0.3917	2750.9	2750.972	5609.1	1	650.3	45.5	10	K.SQEPLPDDDEEFELPEFVEPFLK.D
*	HsFlag-ZnF-HIT2_Ti_	2.0347	0.2976	1122.27	1123.22	3378.4	7	204.9	61.1	1	R.EHCPAGQPVK.V
*	HsFlag-ZnF-HIT2_Ti_	3.8126	0.3336	1123.43	1122.238	6905	1	1047	87.5	2	R.FGNAFHLCR.E
*	HsFlag-ZnF-HIT2_Ti_	2.6153	0.3113	1770.74	1772.146	8445.6	1	543.6	46.7	1	R.AAVMHDILDMMPEGIK.Q
*	HsFLAG-FLJ20729_	3.6462	0.2031	1354.35	1354.552	9605.2	1	1605.4	85	5	R.TILQHLSEAWR.C
*	HsARP6-FLAG_Ti_1	2.5375	0.2585	1550.11	1550.9	4111.9	1	399.4	57.7	1	K.VPGLPTPIENMILR.Y
*	HsFlag-ZnF-HIT2_Ti_	3.5081	0.3663	1536.36	1535.618	6992.1	1	1230.5	77.3	3	K.ADWWTNTAHYNR.E
*	HsFlag-ZnF-HIT2_Ti_	4.3483	0.3964	2823.53	2823.23	5704.6	1	536.4	39.1	3	K.EVGIEFMDLYSHLVPVYDVEPLEK.I
*	HsFlag-ZnF-HIT2_Ti_	3.3042	0.2833	2007.72	2008.191	8843	1	1118.6	56.7	1	K.ITDAYLDQYLWYEADK.R
*	HsFlag-ZnF-HIT2_Ti_	2.7848	0.1703	1421.6	1421.571	8498.7	1	630.4	63.6	1	K.DMNHTNSYGIIR.G
*	HsFlag-ZnF-HIT2_Ti_	2.7365	0.2062	811.28	810.888	4287.8	2	873	100	1	K.HDVNLGR.A
*	HsFlag-ZnF-HIT2_Ti_	4.001	0.3608	1887.54	1888.037	5870.6	1	971.4	64.3	2	K.DNPNLLFNMCGFECR.I
*	HsSrcap_Ti_202.013	3.1271	0.2878	1403.55	1403.535	5403.8	1	527.2	68.2	1	K.DGVWNLQNEVTK.E
*	HsSrcap_Ti_202.013	3.9705	0.2155	1403.66	1403.535	7800.9	1	1525.8	81.8	3	K.DGVWNLQNEVTK.E
*	HsFLAG-p53-DNA-D	4.8737	0.2591	1685.94	1684.971	8156.2	1	1462.8	71.4	4	R.EAVVNTQELLDLLVK.C
*	HsFLAG-FLJ20729_	2.9461	0.2674	1666.75	1667.022	7735.2	1	694.3	57.7	1	K.MPSRFFPPVVFYTPK.E
*	HsFlag-ZnF-HIT2_Ti_	2.6867	0.3262	1174.13	1174.302	4174.6	1	666.3	94.4	1	K.QTDVGITHFR.S
*	HsFlag-ZnF-HIT2_Ti_	4.2986	0.4106	1889.27	1890.078	4656	1	887.6	66.7	4	R.SGMSHEEDQLIPNLYR.Y
*	HsFLAG-p53-DNA-D	3.7003	0.3362	1798.43	1798.949	4994	1	885.3	73.1	1	R.YIQPWESEFIDSQR.V
*	HsFlag-ZnF-HIT2_Ti_	3.8178	0.1457	1086.47	1086.196	8298.8	1	1900.1	100	1	K.RQEAIAQNR.R
*	HsFLAG-p53-DNA-D	2.275	0.2592	847.35	847.946	5005.9	1	598.1	83.3	4	R.HTLAYDK.G
*	HsFlag-ZnF-HIT2_Ti_	2.9409	0.1694	1400.53	1400.542	3976.8	3	363.7	72.2	1	K.QNPFWWTHQR.H
*	HsFlag-ZnF-HIT2_Ti_	2.508	0.0951	1093.01	1093.23	3898.8	3	659.8	92.9	1	K.LWNLNNYR.T
*	HsFLAG-p53-DNA-D	4.696	0.3067	2172.8	2173.532	7060.8	1	1747.4	63.2	5	R.TDMIQALGGVEGILEHTLFK.G
*	HsFlag-VPS71_Ti_1	4.9576	0.3721	2174.92	2173.532	4920.4	1	1451.4	48.7	11	R.TDMIQALGGVEGILEHTLFK.G
*	HsFLAG-p53-DNA-D	4.0557	0.3816	1761.22	1761.974	4564	1	862.7	73.1	3	K.GTYFPTWEGLFWEK.A
*	HsFlag-ZnF-HIT2_Ti_	3.8151	0.2931	1473.26	1473.672	4881	1	724.8	70.8	13	K.WNVSRPSLLADSK.D
*	HsARP6-FLAG_Ti_1	4.5116	0.361	2350.87	2351.71	9268.9	1	896.8	33.8	2	K.TFEGNLTTKPINGAIFIFNPR.T
*	HsFlag-ZnF-HIT2_Ti_	2.7728	0.2392	1240.35	1240.448	7403	1	981.8	80	1	K.IIHTSVWAGQK.R
*	HsFlag-VPS71_Ti_1	3.288	0.317	2165.37	2164.611	7343.9	1	697.8	47.2	1	K.GMLDPLEVHLLDFPNIVIK.G

*	HsScrap_Ti_102.280	2.7903	0.1692	1491.94	1491.694	3826.6	5	501.7	62.5	1	K.GSELQLPFQACLK.V
*	HsFLAG-p53-DNA-D	4.8416	0.4401	2084.06	2084.394	7485.2	1	1618.2	71.9	11	K.ATEPQMVLFNLYDDWLK.T
*	HsScrap_Ti_102.214	2.0039	0.1636	1007.61	1008.159	6878.3	9	530	68.8	1	K.DLILADYGK.K
*	HsFlag-ZnF-HIT2_Ti_	2.9884	0.3456	1263.24	1263.35	7768.3	1	941	75	2	K.EQSQLTATQTR.T
*	HsFlag-ZnF-HIT2_Ti_	5.5754	0.4715	2346.9	2347.454	5641.3	1	597.6	52.5	2	K.HGDEIITSTTSNYETQTFSSK.T
*	HsFlag-ZnF-HIT2_Ti_	3.5418	0.2131	1067.34	1066.249	5664.7	1	1074.9	88.9	3	R.AISAANLHLR.T
*	HsFlag-ZnF-HIT2_Ti_	3.5932	0.288	1393.41	1392.508	5884.8	1	802.3	72.7	1	R.TNHIYVSSDDIK.E
*	HsScrap_Ti_102.231	3.2775	0.3963	2018.4	2018.277	4375.9	1	698.1	58.3	1	R.AQIAGYLYGVSPPDNPQVK.E
*	HsFLAG-Lin9_Ti_20	4.3123	0.3628	3196.15	3198.679	5990.6	1	506.4	26.9	1	R.CIVMVPQWGTHQTVHLPGQLPQHEYLK.E
*	HsFLAG-p53-DNA-D	5.3937	0.333	3171.15	3172.496	9575.8	1	1533.4	32.4	5	K.EMEPLGWIHTQPNESPQLSPQDVTTHAK.I
*	HsFlag-ZnF-HIT2_Ti_	5.2254	0.5091	2134.51	2135.394	3988.2	1	973.6	69.4	2	K.TIIITCSFTPGSCTLTAYK.L
gi|4503483|re	17	65	27.70%	858	95338	6.8	eukaryotic translation elongation factor 2 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	5.039	0.3362	2204.76	2205.469	8754.9	1	1316.9	55.6	9	K.STAISLFYELSENDLNFIK.Q
*	HsFLAG-ARP6_Ti_1	5.4798	0.3529	2221.68	2221.515	4724.7	1	1089.1	67.6	7	R.ALLELQLEPEELYQTFQR.I
*	HsFlag-VPS71_Ti_1	4.3955	0.2899	1496.18	1495.768	7966.1	1	1554.3	81.8	5	R.TFCQLILDPIFK.V
*	HsFLAG-p53-DNA-D	4.0357	0.2235	1715.53	1715.941	8378.4	1	1063.5	60.7	1	K.LDSEDKDKEGKPLLK.A
*	HsFLAG-p53-DNA-D	4.9107	0.4085	2602.03	2602.11	8099.7	1	953.3	45.7	2	R.WLPAGDALLQMITIHLPSPVTAQK.Y
*	HsFlag-VPS71_Ti_1	2.4397	0.1857	1107.62	1108.323	7088	3	595.5	65	2	R.VFSGLVSTGLK.V
*	HsFLAG-FLJ20729_	4.4833	0.3619	2760.33	2761.154	7616	1	1097.7	32.3	2	R.YVEPIEDVPCGNIVGLVGVDQFLVK.T
*	HsFLAG-TCF3_Ti_1	3.4009	0.3853	2760.96	2761.154	4925.5	1	514.4	39.6	2	R.YVEPIEDVPCGNIVGLVGVDQFLVK.T
*	HsFlag-VPS71_Ti_1	5.5375	0.2056	2144.24	2144.349	8882.9	1	2043.3	43.4	4	K.ARPFPDGLAEDIDKGEVSAR.Q
*	HsFLAG-p53-DNA-D	4.6262	0.2852	2234.84	2234.523	8103.9	5	843.2	34.2	1	R.KIWCFGPDGTGPNILTDITK.G
*	HsFlag-VPS71_Ti_1	4.991	0.281	2235.11	2234.523	5278.2	1	968.7	60.5	5	R.KIWCFGPDGTGPNILTDITK.G
*	HsFLAG-ARP6_Ti_1	4.9471	0.4587	2105.27	2106.349	7293.4	1	1433	63.9	4	K.IWCFGPDGTGPNILTDITK.G
*	HsFLAG-p53-DNA-D	5.2811	0.3383	2992.75	2991.482	9757.9	1	1977.1	35	3	R.LMEPIYLVEIQCPEQVVGGIYGVLNR.K
*	HsFlag-VPS71_Ti_1	4.5343	0.5346	2118.92	2119.446	8848	1	642.7	44.4	2	K.RGHVFEESQVAGTPMFVVK.A
*	HsFLAG-p53-DNA-D	5.9946	0.4724	1963.8	1963.259	8919.5	1	2378	73.5	2	R.GHVFEESQVAGTPMFVVK.A
*	HsFlag-VPS71_Ti_1	2.5065	0.2507	1800.62	1801.009	4019.8	5	279.7	53.3	1	K.AYLPVNESFGFTADLR.S
*	HsFlag-VPS71_Ti_1	3.4979	0.243	1446.88	1445.656	4984	1	754.1	75	13	K.EGIPALDNFLDKL.-
gi|30410781|r	9	18	27.60%	591	69423	5.1	hypothetical protein LOC65095 isoform 2 [Homo sapiens]				
gi|30410783|r	9	18	23.00%	709	83251	5.2	hypothetical protein LOC65095 isoform 1 [Homo sapiens]				
	HsFlag-NUFIP_Ti_1	5.8131	0.4517	2241.17	2241.284	8992.7	1	2025	61.9	2	R.AFVEDSEDEDGAGEGGSSLLQK.R
	HsFlag-NUFIP_Ti_1	5.5113	0.388	3278.11	3276.528	6170.9	1	925.7	32.1	1	K.VTGNEMLGLEEGDLEDDFDPAQHDQLMQK.C
	HsFlag-NUFIP_Ti_1	5.6778	0.4196	1974.71	1975.208	6381.2	1	1659	69.4	5	K.SPFAAAVGQEKPVFEPGDK.T
	HsFlag-NUFIP_Ti_1	3.5953	0.3034	1529.74	1528.615	9818.3	1	1682.4	85	1	K.TFEEYLDEYYR.L
	HsFlag-NUFIP_Ti_1	4.321	0.4365	2180.99	2181.367	4361.2	1	573	55.3	2	R.TVVPCDFGLSTEEILAADDK.E
	HsFlag-NUFIP_Ti_1	5.201	0.3777	2130.53	2131.273	8695.7	1	1597.8	63.9	2	K.SLCREEAETPAEATGKPQR.D
	HsFlag-NUFIP_Ti_1	3.2821	0.2791	1614.23	1614.709	6531.7	2	511.9	53.6	1	R.EEAETPAEATGKPQR.D
	HsFlag-NUFIP_Ti_1	3.7945	0.2236	2912.72	2913.229	6592.5	1	676.4	26.9	1	R.QLPALDGSLMGPESPPAQEEEAPVSPHK.K
	HsFlag-NUFIP_Ti_1	3.8622	0.3999	1637.7	1637.901	5941.6	1	1177.1	71.4	3	R.LLGPTVMLGGCEFSR.Q
gi|13514813|r	14	94	27.50%	662	73272	7.2	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3 [Homo sapiens]				
gi|13514817|r	14	94	27.50%	662	73272	7.2	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	2.6822	0.2384	1758.19	1758.839	4642.3	1	335.6	46.4	1	K.SDEDDWSKPLPPSER.L

	HsFLAG-Lin9_Ti_20	4.3046	0.327	1886.56	1884.053	7043.5	1	1263	65.6	2	R.LEQELFSGGNTGINFEK.Y
	HsFLAG-UTX1_Ti_2	5.6118	0.4035	2333.45	2333.69	5601.8	1	1423.2	64.3	31	K.TAAFLLPILSQIYSDGPGEALR.A
	HsFLAG-FLJ20729_	5.8628	0.4188	2333.63	2333.69	7327.4	1	1607.5	41.7	11	K.TAAFLLPILSQIYSDGPGEALR.A
	HsFLAG-Lin9_Ti_20	4.5686	0.378	1888.62	1889.131	4301.3	1	1131.7	68.8	6	R.VRPCVVYGGADIGQQIR.D
	HsFLAG-Lin9_Ti_20	3.8519	0.3501	1180.51	1181.346	7286.3	1	1429.5	80	4	R.GCHLLVATPGR.L
	HsFlag-VPS71_Ti_1	3.9446	0.3609	1338.59	1337.595	6421.6	1	1768.7	90	2	R.MLDMGFEPQIR.R
	HsARP6-FLAG_Ti_1	3.7593	0.3244	1558.09	1558.774	10252.4	1	1538	70.8	5	R.DFLDEYIFLAVGR.V
	HsARP6-FLAG_Ti_1	4.6193	0.2146	1448.84	1448.706	7288.5	1	1680	83.3	7	K.RSFLLDLLNATGK.D
	HsMRGBP-FLAG_Ti_	2.948	0.2414	1302.65	1301.404	4049.2	4	372.7	72.2	2	R.DREEALHQFR.S
	HsFlag-VPS71_Ti_1	4.0613	0.3726	1169.5	1169.41	7511.7	1	1599.5	86.4	4	K.SPILVATAVAAR.G
	HsFLAG-Lin9_Ti_20	5.282	0.3126	2084.06	2084.296	7080.3	1	1409.6	45.3	4	K.HVINFDLPSDIEEYVHR.I
	HsFLAG-Lin9_Ti_20	4.0995	0.3965	1526.33	1525.704	7758	1	1233.5	73.1	14	R.VGNLGLATSFFNER.N
	HsFLAG-Lin9_Ti_20	4.0757	0.1322	1129.21	1129.339	6372	1	1422.3	83.3	1	K.DLLDLLVEAK.Q
gi|15431293|	6	28	27.50%	204	24146	11.6	ribosomal protein L15 [Homo sapiens]				
gi|88998872|	6	28	27.50%	204	24174	11.6	PREDICTED: similar to ribosomal protein L15 isoform 6 [Homo sapiens]				
gi|88998870|	6	28	27.50%	204	24174	11.6	PREDICTED: similar to ribosomal protein L15 isoform 5 [Homo sapiens]				
gi|88998868|	6	28	27.50%	204	24174	11.6	PREDICTED: similar to ribosomal protein L15 isoform 4 [Homo sapiens]				
gi|88998866|	6	28	27.50%	204	24174	11.6	PREDICTED: similar to ribosomal protein L15 isoform 3 [Homo sapiens]				
gi|88998864|	6	28	27.50%	204	24174	11.6	PREDICTED: similar to ribosomal protein L15 isoform 1 [Homo sapiens]				
gi|88992466|	6	28	27.50%	204	24174	11.6	PREDICTED: similar to ribosomal protein L15 isoform 5 [Homo sapiens]				
gi|88992463|	6	28	27.50%	204	24174	11.6	PREDICTED: similar to ribosomal protein L15 isoform 4 [Homo sapiens]				
gi|88992460|	6	28	27.50%	204	24174	11.6	PREDICTED: similar to ribosomal protein L15 isoform 3 [Homo sapiens]				
gi|88992455|	6	28	27.50%	204	24174	11.6	PREDICTED: similar to ribosomal protein L15 isoform 1 [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.4669	0.3893	1705.98	1706.945	5136.2	1	587.5	56.7	4	K.GATYGKPVHHGVNQLK.F
	HsFLAG-TCF3_Ti_1	2.9071	0.105	1019.36	1019.1	6187.1	2	802.5	81.2	1	R.SLQSVAEER.A
	HsFLAG-TCF3_Ti_1	3.5508	0.2919	1505.67	1505.8	4277.4	1	497.7	68.2	2	K.FFEVILIDPFHK.A
	HsFLAG-ARP6_Ti_1	4.0112	0.3449	1507.39	1505.8	7328.1	1	1464.6	77.3	19	K.FFEVILIDPFHK.A
	HsFLAG-ARP6_Ti_1	2.9027	0.0985	1259.62	1259.407	7648.9	4	827.1	72.2	1	R.RNPDTQWITK.P
	HsFLAG-ARP6_Ti_1	2.2907	0.1611	1011.5	1012.116	5473	6	313.1	68.8	1	K.FHHTIGGSR.R
gi|18104948|	4	22	27.50%	160	18565	10.5	ribosomal protein L21 [Homo sapiens]				
gi|89031623|	4	22	27.50%	160	18565	10.5	PREDICTED: similar to ribosomal protein L21 isoform 1 [Homo sapiens]				
gi|89026818|	4	22	27.50%	160	18595	10.5	PREDICTED: similar to 60S ribosomal protein L21 [Homo sapiens]				
gi|89025818|	4	22	27.50%	160	18595	10.5	PREDICTED: similar to 60S ribosomal protein L21 [Homo sapiens]				
gi|88952736|	4	22	27.50%	160	18535	10.5	PREDICTED: similar to 60S ribosomal protein L21 [Homo sapiens]				
gi|88943726|	4	22	27.50%	160	18535	10.5	PREDICTED: similar to 60S ribosomal protein L21 [Homo sapiens]				
gi|51466076|	4	22	27.50%	160	18595	10.5	PREDICTED: similar to 60S ribosomal protein L21 [Homo sapiens]				
	HsFLAG-TCF3_Ti_1	2.8912	0.1988	1244.58	1244.497	4521.2	1	938.3	85	1	K.HGVVPLATYMR.I
	HsFLAG-TCF3_Ti_1	5.6281	0.369	1641.7	1641.911	8391.5	1	3083.2	89.3	15	R.VYNVTQHAVGIVVNK.Q
	HsFLAG-TCF3_Ti_1	4.0386	0.4119	1642.74	1641.911	4018.4	1	755.8	46.4	4	R.VYNVTQHAVGIVVNK.Q
	HsFLAG-ARP6_Ti_1	3.8836	0.2912	2079.33	2079.372	6852.4	1	1079.5	55.9	2	R.TNGKEPELLEPIPYEFMA.-
gi|33504573|	10	28	27.40%	430	46039	6.8	hypothetical protein LOC347918 [Homo sapiens]				
*	HsMRGBP-FLAG_Ti_	4.0801	0.3861	2588.77	2588.843	4851.5	1	664.9	46.2	5	R.AGAPGPGLGLCSSSPTGDFVDASVLVR.Q
	HsYL1-FLAG_Ti_20	4.4456	0.4387	2578.03	2578.946	5095.8	1	557.9	40.7	3	R.TPGVLLPGAGGAAGFGMTSPPPPTSPSR.T

	HsTIP60_Ti_106.011	3.8731	0.4046	2029.09	2028.372	3245.1	4	214.6	42.5	2	R.TAVPPGLSSLPLTSVGNTGMK.K
	HsMRGBP-FLAG_Ti_	4.6866	0.4365	2030.87	2028.372	6675.5	1	1003.2	37.5	1	R.TAVPPGLSSLPLTSVGNTGMK.K
	HsTIP60_Ti_106.223	4.1117	0.3041	1828.51	1828.152	2939.6	1	504.9	70	7	K.KLEEIPPASPEMAQMR.K
	HsMRGBP-FLAG_Ti_	3.9763	0.1089	1831.09	1828.152	7435.3	1	1379.4	46.7	1	K.KLEEIPPASPEMAQMR.K
*	HsMRGBP-FLAG_Ti_	2.9954	0.3717	1801.89	1801.981	6093.2	2	292.8	50	1	K.QCLDYHHQEMQALK.E
*	HsMRGBP-FLAG_Ti_	3.0535	0.2848	1479.77	1479.722	5812.6	2	769	72.7	2	K.ERLYGPLQAYLR.Q
*	HsMRGBP-FLAG_Ti_	2.2368	0.2324	1193.7	1194.419	4069.3	6	215.8	61.1	2	R.LYGPLQAYLR.Q
*	HsTIP60_Ti_106.269	3.6626	0.3514	1194.34	1194.419	4634.8	1	1085.8	94.4	4	R.LYGPLQAYLR.Q
gi|4506725|re	6	21	27.40%	263	29598	10.2	ribosomal protein S4, X-linked X isoform [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	2.8737	0.2189	1565.27	1565.815	7188.8	8	520.7	53.6	1	K.LTGVFAPRPSTGPHK.L
*	HsFLAG-TCF3_Ti_1(	4.9113	0.3653	1543.89	1543.902	7045.7	1	1418.7	81.8	6	K.LRECLPLIIFLR.N
*	HsFLAG-ARP6_Ti_1	2.6548	0.2161	1274.74	1274.555	5736.3	1	741.8	77.8	2	R.ECLPLIIFLR.N
*	HsFLAG-ARP6_Ti_1	3.2528	0.2909	1886.52	1887.155	2585	1	348.3	59.4	1	R.TDITYPAGFMDVISIDK.T
	HsFLAG-Lin9_Ti_20(	3.2081	0.2935	1216.15	1216.385	4827.1	1	718.5	75	10	K.GIPHLVTHDAR.T
*	HsFLAG-ARP6_Ti_1	3.8681	0.3932	1782.94	1783.963	7659.8	1	1249	62.5	1	K.FDTGNLCMVTGGANLGR.I
gi|4506649|re	13	47	27.30%	403	46109	10.2	ribosomal protein L3 isoform a [Homo sapiens]				
gi|76496472|r	13	47	31.10%	354	40152	10.2	ribosomal protein L3 isoform b [Homo sapiens]				
	HsFlag-NUFIP_Ti_11	3.2997	0.2948	984.44	984.146	5502.5	1	1018.6	87.5	5	R.HGSLGFLPR.K
	HsFLAG-TCF3_Ti_1(	3.5276	0.341	2248.77	2248.586	6857.1	1	820.7	52.6	2	K.SFPKDDPSKPVHLTAFLGYK.A
	HsFlag-NUFIP_Ti_11	2.8079	0.2717	1245.66	1246.495	4978	1	580.5	65	1	K.PVHLTAFLGYK.A
	HsFlag-NUFIP_Ti_11	3.0391	0.271	1246.5	1246.495	6114.4	1	1156.6	90	2	K.PVHLTAFLGYK.A
	HsFlag-NUFIP_Ti_1(	2.8107	0.2026	885.35	885.072	6106.8	1	922.4	92.9	3	K.AGMTHIVR.E
	HsFLAG-TCF3_Ti_1(	2.4432	0.33	1435.42	1436.527	7822.8	1	759.9	59.1	1	K.TVFAEHISDECK.R
	HsFlag-Ies6_293_Ti_	4.3793	0.4165	1436.43	1436.527	7493.7	1	1516.8	77.3	3	K.TVFAEHISDECK.R
	HsFLAG-TCF3_Ti_1(	2.8895	0.2963	1592.34	1592.715	4290.2	3	300.2	58.3	2	K.TVFAEHISDECKR.R
	HsFLAG-ARP6_Ti_1	5.3632	0.3225	2972.21	2973.371	5804.2	1	953.4	34	12	R.ERLEQQVPVNQVFGQDEMIDVIGVTK.G
	HsFLAG-TCF3_Ti_1(	2.5634	0.0995	2686.2	2688.068	8932.3	3	390.4	34.8	1	R.LEQQVPVNQVFGQDEMIDVIGVTK.G
	HsFLAG-TCF3_Ti_1(	2.885	0.3254	1342.28	1343.346	4127	1	403.9	68.2	2	K.NNASTDYDLSDK.S
	HsFLAG-TCF3_Ti_1(	3.3355	0.2174	1344.58	1343.346	5415.3	1	763.7	72.7	4	K.NNASTDYDLSDK.S
	HsFLAG-ARP6_Ti_1	4.9234	0.5678	2439.12	2438.803	8481.2	1	1326.1	52.4	9	K.SINPLGGFVHYGEVTNDFVMLK.G
gi|88983853|r	9	38	27.30%	282	29700	7.3	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-stran				
gi|88988325|r	9	38	27.50%	280	29862	7.3	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-stran				
gi|88988321|r	9	38	25.30%	304	32483	7.7	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-stran				
gi|88988318|r	9	38	27.40%	281	30152	7.6	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-stran				
gi|88988315|r	9	38	26.20%	294	31200	7.6	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-stran				
gi|88988312|r	9	38	32.00%	241	26480	8.7	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-stran				
gi|88983868|r	9	38	28.70%	268	28363	7.1	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-stran				
gi|88983865|r	9	38	26.40%	292	30983	7.3	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-stran				
gi|88983863|r	9	38	28.60%	269	28652	7.3	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-stran				
gi|88983861|r	9	38	27.30%	282	29700	7.3	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-stran				
gi|88983858|r	9	38	33.60%	229	24980	8.4	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein) (Single-stran				
	HsFLAG-p53-DNA-D	5.3975	0.5236	2148.33	2149.383	10346	1	1878.8	60.5	7	R.GFGFVTYATVEEVDAAMNAR.P
	HsFlag-VPS71_Ti_1(	4.819	0.4507	2511.61	2511.814	7887.6	1	891.3	45.5	4	R.GFGFVTYATVEEVDAAMNARPHK.V

	HsFLAG-p53-DNA-D	3.6762	0.3178	2939.29	2939.275	6079.2	1	609.8	27.9	1	R.GFGFVTYATVEEVDAAMNARPHKVDGR.V
	HsFLAG-Lin9_Ti_20	1.9907	0.1215	1437.61	1439.568	4567	1	387.3	50	1	R.EDSERPGAHLTVK.K
	HsFLAG-p53-DNA-D	3.6907	0.1927	1220.14	1219.439	7676.3	1	1667.5	88.9	3	K.IEVIEIMTDR.G
	HsFlag-VPS71_Ti_1	3.9174	0.2864	1486.86	1486.553	7688.4	1	1598.8	81.8	14	K.YHTVNGHNCEVR.K
	HsFLAG-Lin9_Ti_20	2.9389	0.1647	1613.63	1614.727	7325.1	1	1020.3	70.8	1	K.YHTVNGHNCEVRK.A
	HsFlag-VPS71_Ti_1	2.7146	0.3137	1375.54	1376.468	7140	1	628.8	57.7	5	R.SSGPYGGGGQYFAK.P
	HsFlag-VPS71_Ti_1	3.9291	0.3126	1377.7	1376.468	4784.6	1	826	73.1	2	R.SSGPYGGGGQYFAK.P
gi|5803227|re	5	16	27.30%	245	27764	4.8	tyrosine 3/tryptophan 5 -monooxygenase activation protein, theta polypeptide [Homo sapiens]				
*	HsFlag-FLJ90652_2	5.1215	0.3731	1533.06	1533.592	9087.1	1	2196.7	80.8	2	K.AVTEQGAELSNEER.N
*	HsFLAG-ARP6_Ti_1	3.9315	0.3609	1392.74	1392.599	7309.1	1	1301.2	81.8	6	R.SICTTVLELLDK.Y
*	HsFlag-FLJ90652_2	2.2161	0.0957	1320.64	1321.473	3472.2	1	251.2	63.6	1	K.YLIANATNPESK.V
*	HsFlag-NUFIP_Ti_1	4.3829	0.3824	2146.5	2146.269	9362.6	1	1146.9	52.8	5	K.TAFDEAIAELDTLNEDSYK.D
	HsFLAG-FLJ20729_	3.7624	0.1371	1189.5	1190.444	6163.6	5	1616.1	88.9	2	K.DSTLIMQLLR.D
gi|34740329|r	9	31	27.20%	378	39595	9	heterogeneous nuclear ribonucleoprotein A3 [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.9132	0.2993	1777.94	1777.891	3752.1	1	572.7	67.9	1	R.RGEEGHDPKEPEQLR.K
	HsFLAG-p53-DNA-D	2.7316	0.1269	1772.11	1771.965	8658.5	1	502.7	46.7	1	K.LFIGGLSFETTDDSLR.E
	HsFLAG-p53-DNA-D	3.6475	0.2575	2442.24	2442.687	9603	1	816.1	42.5	1	K.LFIGGLSFETTDDSLREHFEK.W
	HsFLAG-p53-DNA-D	2.1595	0.113	1380.59	1381.572	3881.9	2	380.7	58.3	1	R.EDSVKPGAHLTVK.K
	HsFLAG-p53-DNA-D	3.2006	0.2159	1381.63	1381.572	4205.4	1	573.7	75	5	R.EDSVKPGAHLTVK.K
	HsFLAG-p53-DNA-D	5.5285	0.4202	2011.71	2012.27	8142.8	1	2395.8	78.1	2	K.KIFVGGIKEDTEEYNLR.D
	HsFLAG-ARP6_Ti_1	5.033	0.4053	1883.55	1884.096	6764.5	1	1528.2	73.3	5	K.IFVGGIKEDTEEYNLR.D
	HsFLAG-p53-DNA-D	4.583	0.4053	1714.27	1714.828	5890.2	1	1426.3	78.6	7	R.GFAFVTFDDHDTVDK.I
*	HsFLAG-p53-DNA-D	5.2172	0.5395	1911.28	1911.896	6582.2	1	1356	61.9	8	R.SSGSPYGGGYGSGGGSGGYGSR.R
gi|4506617|re	5	25	27.20%	184	21397	10.2	ribosomal protein L17 [Homo sapiens]				
gi|89039066|r	5	25	27.20%	184	21313	10.1	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 5 [Homo sapiens]				
gi|89039064|r	5	25	27.20%	184	21313	10.1	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 4 [Homo sapiens]				
gi|89039062|r	5	25	27.20%	184	21313	10.1	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 3 [Homo sapiens]				
gi|89039060|r	5	25	27.20%	184	21313	10.1	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 2 [Homo sapiens]				
gi|89039058|r	5	25	27.20%	184	21313	10.1	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 1 [Homo sapiens]				
gi|89038352|r	5	25	27.20%	184	21313	10.1	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 2 [Homo sapiens]				
gi|89038350|r	5	25	27.20%	184	21313	10.1	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 1 [Homo sapiens]				
gi|88947794|r	5	25	27.20%	184	21399	10.1	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 2 [Homo sapiens]				
gi|88947792|r	5	25	27.20%	184	21399	10.1	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 1 [Homo sapiens]				
gi|88943958|r	5	25	27.20%	184	21455	10.2	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 6 [Homo sapiens]				
gi|88943956|r	5	25	27.20%	184	21455	10.2	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 5 [Homo sapiens]				
gi|88943954|r	5	25	27.20%	184	21455	10.2	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 4 [Homo sapiens]				
gi|88943952|r	5	25	27.20%	184	21455	10.2	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 3 [Homo sapiens]				
gi|88943950|r	5	25	27.20%	184	21455	10.2	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 2 [Homo sapiens]				
gi|88943948|r	5	25	27.20%	184	21455	10.2	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 1 [Homo sapiens]				
gi|88942753|r	5	25	27.20%	184	21399	10.1	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 2 [Homo sapiens]				
gi|88942751|r	5	25	27.20%	184	21399	10.1	PREDICTED: similar to 60S ribosomal protein L17 (L23) isoform 1 [Homo sapiens]				
	HsFLAG-TCF3_Ti_1	2.0848	0.0929	1163.51	1164.257	4934.9	5	337.3	61.1	1	R.YSLDPENPTK.S
	HsFLAG-TCF3_Ti_1	2.8854	0.1696	1188.53	1189.458	4935.8	3	662	72.2	2	K.SAEFLLHMLK.N

	HsFLAG-ARP6_Ti_1	3.963	0.2328	1190.16	1189.458	6824.3	1	1316.6	83.3	7	K.SAEFLLHMLK.N
	HsFLAG-ARP6_Ti_1	5.0694	0.4051	1779.5	1780.031	7365.1	1	1490.2	66.7	13	K.GLDVDSLVIEHIQVNK.A
	HsFLAG-ARP6_Ti_1	3.4639	0.1992	1624.45	1624.831	3983.5	1	792.3	80.8	2	K.EQIVPKPEEEVAQK.K
gi|4759154|re	6	10	27.10%	258	28970	5.8	synaptosomal-associated protein 29 [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	3.5526	0.3651	1118.91	1118.232	6637.6	1	1010.4	80	2	K.VGVASSEELAR.Q
*	HsFLAG-TCF3_Ti_1	2.2149	0.1893	1230.55	1231.437	8493.3	6	467.6	55	1	K.SVFGGLVNYFK.S
*	HsFLAG-TCF3_Ti_1	3.2331	0.2242	1231.27	1231.437	6363.5	1	1215	85	2	K.SVFGGLVNYFK.S
*	HsFLAG-TCF3_Ti_1	4.1324	0.4672	2294.47	2295.471	5394	1	881.6	57.5	2	K.SKPVETPPEQNGTLTSQPNNR.L
*	HsFLAG-TCF3_Ti_1	3.0227	0.294	1256.51	1256.373	6311.4	1	1280.8	75	1	R.GAGSAMSTDAYPK.N
*	HsFLAG-TCF3_Ti_1	5.2348	0.4119	1520.97	1520.698	7376.7	1	1811	80.8	2	K.IDSNLDELSMGLGR.L
gi|5031635|re	4	10	27.10%	166	18502	8.1	cofilin 1 (non-muscle) [Homo sapiens]				
	HsFlag-VPS71_Ti_1	4.6721	0.4128	1991.18	1991.337	7052.4	1	954	56.2	7	K.KEDLVFIFWAPESAPLK.S
*	HsFLAG-FLJ20729_	4.1518	0.2757	1521.44	1520.605	7297.8	1	1599.4	81.8	1	K.HELQANCYEEVK.D
*	HsFLAG-FLJ20729_	3.1582	0.1549	1791.03	1791.881	9505.7	2	656.5	53.8	1	K.HELQANCYEEVKDR.C
*	HsFlag-VPS71_Ti_1	2.8484	0.168	1342.5	1341.591	4335.9	3	723.6	69.2	1	K.LGGSAVISLEGKPL.-
gi|5032007|re	5	18	27.00%	322	34911	6.4	purine-rich element binding protein A [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	4.3223	0.2447	3271.56	3272.511	5789.8	1	972.4	33	3	R.DYLGDFIEHYAQLGPSQPPDLAQAQDEPR.R
*	HsFLAG-ARP6_Ti_1	5.7648	0.5501	2311.75	2312.631	4748.1	1	1000	59.1	9	R.GPGLGSTQGQTIALPAQGLIEFR.D
*	HsFlag-NUFIP_Ti_1	3.9981	0.3294	2312.83	2312.631	6763.8	2	787.6	31.8	2	R.GPGLGSTQGQTIALPAQGLIEFR.D
*	HsFlag-NUFIP_Ti_1	3.3294	0.3332	2734.08	2734.928	6869.8	1	900.9	43.8	2	K.LIDDYGVEEEPAELPEGTSLTVDNK.R
*	HsFlag-NUFIP_Ti_1	2.9155	0.1773	1216.74	1217.37	6221.5	3	673.8	72.2	2	K.RFFFDVGSNK.Y
gi|5803167|re	9	30	26.90%	501	58849	5.4	splicing factor 3a, subunit 3 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.2435	0.3519	2227.4	2229.411	7021.7	1	846.2	52.8	1	R.KEELNAISGPNEFAEFYNR.L
*	HsFlag-VPS71_Ti_1	3.5167	0.2326	2641.65	2641.724	8581.1	1	1139.8	31.8	1	K.ARENPSEEAQNLVEFTDEEGYGR.Y
*	HsFLAG-Lin9_Ti_20	3.9509	0.2987	2642.5	2641.724	6284.5	1	571.3	43.2	1	K.ARENPSEEAQNLVEFTDEEGYGR.Y
*	HsFlag-VPS71_Ti_1	2.736	0.2941	1340.5	1340.485	6823.1	1	1033.6	77.8	1	R.YLDLHDCYLK.Y
*	HsFlag-VPS71_Ti_1	5.2887	0.5112	2205.18	2205.555	7996.2	1	1902.5	70.6	12	K.LDYITYLSIFDQLFDIPK.E
*	HsFLAG-p53-DNA-D	3.4371	0.1635	1516.5	1516.737	4490.9	1	589.7	66.7	8	R.VKPLQDQNELFGK.I
*	HsFlag-VPS71_Ti_1	6.4112	0.4801	3274.21	3273.54	9321.6	1	2327.7	35.8	1	K.ETSSALTHAGAHLDLSAFSSWEELASLGLDR.L
*	HsARP6-FLAG_Ti_1	3.8766	0.2629	1310.87	1311.475	6772.5	1	1294.6	81.8	1	K.SLESLDTSLFAK.N
*	HsARP6-FLAG_Ti_1	2.8243	0.2016	1134.47	1134.24	4921.5	1	620.1	81.2	4	R.HLTHENVQR.K
gi|31083035|r	1	3	26.80%	123	13664	10.3	mitochondrial ribosomal protein L52 isoform a [Homo sapiens]				
gi|31083060|r	1	3	27.00%	122	13593	10.3	mitochondrial ribosomal protein L52 isoform c [Homo sapiens]				
	HsFlag-NUFIP_Ti_1	4.6927	0.2965	3499.1	3499.923	4886.3	1	1106.2	30.5	3	R.LQQGLAANPSGYGPLTELPDWSYADGRPAPPMK.G
gi|5032161|re	2	2	26.80%	112	12473	4.8	elongin C [Homo sapiens]				
	HsFlag-VPS71_Ti_1	2.2145	0.1723	1056.48	1057.192	3922	1	353.2	72.2	1	R.EHALTSGTIK.A
*	HsFlag-VPS71_Ti_1	3.8908	0.5521	2211.93	2212.398	8745.2	1	834	47.4	1	K.AMLSGPGQFAENETNEVNFR.E
gi|18375501|r	5	12	26.70%	318	35554	8.1	APEX nuclease [Homo sapiens]				
gi|18375505|r	5	12	26.70%	318	35554	8.1	APEX nuclease [Homo sapiens]				
gi|18375503|r	5	12	26.70%	318	35554	8.1	APEX nuclease [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	3.2772	0.241	1787.29	1787.878	7504.6	1	660	50	1	K.GAVAEDGDELRTEPEAK.K
	HsFLAG-p53-DNA-D	1.9101	0.1388	1086.54	1087.261	6093.4	1	651.3	75	1	K.TSPSGKPATLK.I
	HsFLAG-FLJ20729_	4.9652	0.3489	2467.39	2467.74	7658.9	1	1133.6	35.7	1	K.LPAELQELPGLSHQYWSAPSDK.E

	HsFLAG-p53-DNA-D	3.8049	0.2968	1849.59	1849.097	6808.8	2	522.4	50	4	R.QGFGELLQAVPLADSFR.H
	HsFlag-VPS71_Ti_1(	4.0965	0.4311	2094.05	2093.394	5977.8	1	1125.2	61.8	5	R.LDYFLLSHSLLPALCDSK.I
gi|38201655|r	11	50	26.60%	418	46743	6.3	inhibitor of growth family, member 3 isoform 1 [Homo sapiens]				
	HsTIP60_Ti_105.256	5.0108	0.3715	1948.35	1949.161	9198.7	1	2393.7	76.7	5	R.EMDLQVQNAMDQLEQR.V
	HsMRGBP-FLAG_Ti_	2.4827	0.2177	1072.7	1073.252	5076.9	2	618.6	75	4	R.VSEFFMNAK.K
	HsMRGBP-FLAG_Ti_	3.0106	0.2275	1073.51	1073.252	5493.8	1	1253.1	87.5	2	R.VSEFFMNAK.K
*	HsMRGBP-FLAG_Ti_	2.6887	0.2746	1547.65	1547.751	5210.3	3	329.6	54.2	1	K.VQLANQIYDLVDR.H
*	HsH2AZ-FLAG_293_	4.9793	0.4097	1548.73	1547.751	7590.6	1	2108.6	87.5	12	K.VQLANQIYDLVDR.H
*	HsYL1-FLAG_Ti_203	2.7177	0.1597	1806.17	1805.01	10080	3	770.2	53.3	1	K.MELEADNAGITEILER.R
*	HsFLAG-TIP49b_Ti_	3.5506	0.3249	1878.41	1878.996	7335.1	1	969.1	60	7	K.YNPTSHHTTTDHIPEK.K
*	HsTIP60_Ti_103.218	2.3074	0.2857	1422.56	1423.56	7497.1	1	377.2	46.2	1	K.SEALLSTLTSDASK.E
*	HsTIP60_Ti_103.217	5.3422	0.4463	1423.55	1423.56	6697.1	1	1971.7	88.5	13	K.SEALLSTLTSDASK.E
*	HsTIP60_Ti_104.254	4.2774	0.5245	2722.71	2723.882	6778.3	1	646.2	36.5	3	R.ETVGYSSSSALMTTLTQNASSSAADSR.S
*	HsTIP60_Ti_104.254	3.7521	0.1769	2723.9	2723.882	9770.1	1	709.4	24	1	R.ETVGYSSSSALMTTLTQNASSSAADSR.S
gi|4507195|re	40	148	26.40%	2364	274630	5.6	spectrin, beta, non-erythrocytic 1 isoform 1 [Homo sapiens]				
	HsFlag-VPS71_Ti_1(	2.4092	0.2143	1127.48	1128.237	5689.4	6	523.7	68.8	1	R.IHCLENVDK.A
	HsFLAG-ARP6_Ti_1	3.9058	0.4131	1978.1	1979.162	7365.7	1	1205.9	65.6	9	K.TAGYPNVNIHNFTTSWR.D
	HsFlag-VPS71_Ti_1(	5.8347	0.4698	2485.94	2484.734	7278.9	1	2154.6	44	2	K.SNAHYNLQNAFNLAEQHLGLTK.L
	HsFLAG-UTX1_Ti_2(	2.6734	0.1132	1722.64	1722.846	5480.1	2	449.8	60.7	1	K.LLDPEDISVDHPDEK.S
	HsFLAG-ARP6_Ti_1	5.8337	0.5002	2184.87	2185.447	8103.3	1	2540	75	7	K.FANSLVGVQQQLQAFNTYR.T
	HsFLAG-ARP6_Ti_1(	4.9833	0.4833	2022.62	2023.25	5620.6	1	778.2	55.6	13	R.LVSQDNFGFDLPAVEAATK.K
	HsARP6-FLAG_Ti_1	4.3084	0.2431	1348.31	1348.628	6747.1	1	1597	88.9	12	R.LWEYLLELLR.A
	HsARP6-FLAG_Ti_1(	3.994	0.2146	1265.81	1265.495	4291.1	1	1082.5	90	4	K.HLLGVEDLLQK.H
	HsARP6-FLAG_Ti_1	4.2381	0.3312	1558.58	1558.734	9915.6	1	1638.3	75	2	R.EQWANLEQLSAIR.K
	HsFlag-VPS71_Ti_1(	3.7175	0.283	3161.41	3158.553	7243.9	1	1131.1	31.7	1	K.RLEEASLLHQFQADADDIDAWMLDILK.I
	HsFLAG-Lin9_Ti_20:	3.2087	0.2865	2050.4	2052.202	8910.3	3	545.5	41.7	1	K.IVSSSDVGHDEYSTQSLVK.K
	HsFlag-DPCD_Ti_20	3.903	0.3592	2133.04	2131.409	7473.1	1	834	52.6	1	K.VIESTQDLGNDLAGVMALQR.K
	HsFlag-VPS71_Ti_1(	3.835	0.3949	1451.38	1450.647	4887.5	1	945.8	77.3	1	R.LAEISDVWEEMK.T
	HsARP6-FLAG_Ti_1	4.7149	0.2015	1382.18	1382.472	8808.4	1	1929.5	85	3	R.DLDDFQSWLSR.T
	HsFlag-VPS71_Ti_1(	2.7367	0.1572	1096.58	1096.272	5870.3	2	738.5	81.2	3	K.LLTQHENIK.N
	HsFLAG-p53-DNA-D	3.5841	0.1503	1525.36	1525.704	8511	1	1503.5	75	3	R.LQALDTGWNELHK.M
	HsFLAG-Lin9_Ti_20!	3.7793	0.3387	1833.76	1834.045	7177.1	1	610.3	50	4	R.QNLLSQSHAYQQFLR.D
	HsFlag-VPS71_Ti_1(	5.1452	0.4389	3292.67	3291.657	6678.8	1	1245.2	31	1	K.QAEAFLNNQEYVLAHTEMPTTLEGAEAAIK.K
	HsFlag-DPCD_Ti_20	3.1456	0.2549	1888	1889.171	7209.3	4	553	46.9	1	K.EGMQLISEKPETEAVVK.E
	HsFLAG-ARP6_Ti_1	4.1616	0.4588	1876.28	1877.02	7875	1	2085.9	80	2	K.WLHGLESQIQSDDYGK.H
	HsFLAG-ARP6_Ti_1(	3.0331	0.2173	1391.23	1391.625	6010.9	4	702.7	65	1	K.FMELLEPLNER.K
	HsARP6-FLAG_Ti_1	2.9357	0.2571	1459.96	1460.583	7305.1	1	1211.4	72.7	1	R.DVEDEILWVGER.M
	HsFlag-VPS71_Ti_1(	3.1213	0.2154	2318.1	2318.697	8690.4	1	865.5	47.5	1	R.MPLATSTDHGHNLQTVQLLIK.K
	HsFlag-DPCD_Ti_20	3.8203	0.4453	1778.72	1778.914	8864.8	1	1203.3	62.5	2	R.SQNIVTDSSSLSAEAIR.Q
	HsARP6-FLAG_Ti_1	3.056	0.2169	1460.16	1459.682	6490.3	1	758.5	72.7	3	K.QLWGLLIEETEK.R
	HsFlag-VPS71_Ti_1(	6.7312	0.5129	2340.03	2339.567	8946.7	1	2686.4	47.4	5	K.HQILEQAVEDYAETVHQLSK.T
	HsFLAG-ARP6_Ti_1	3.6478	0.3483	1310.83	1311.394	6497.7	1	1131.9	77.3	8	R.ALVADSHPESER.I
	HsARP6-FLAG_Ti_1	3.8874	0.2454	1504.23	1503.609	10058.6	1	1526.7	72.7	2	R.EVDDLEQWIAER.E

	HsFlag-VPS71_Ti_1	5.4804	0.3776	1944.84	1945.136	9377.4	1	1820.8	65.6	12	K.DGLNEAWADLLELIDTR.T
	HsFLAG-ARP6_Ti_1	3.5967	0.2017	1374.74	1374.58	7304.5	2	1367.3	77.3	2	R.TQILAASYELHK.F
	HsFlag-VPS71_Ti_1	3.0277	0.1819	1243.58	1242.464	6621.9	1	1159.3	83.3	2	R.LILEVHQFSR.D
	HsFLAG-ARP6_Ti_1	4.8381	0.2564	2094.13	2093.301	6466.1	1	1364.5	61.1	8	R.DASVAEAWLLGQEPYLSSR.E
	HsFLAG-ARP6_Ti_1	3.1934	0.1898	1188.42	1187.422	7137.4	1	1364.5	94.4	1	R.LTTLELLEVR.R
	HsFLAG-FLJ20729_	3.9777	0.3773	1752.34	1752.789	8803.2	1	1491	67.9	2	K.VSEEAESQQQWDTSK.G
*	HsFlag-DPCD_Ti_20	3.5354	0.3273	1368.06	1368.576	7631	1	1032.9	69.2	4	K.TALPAQSAATLPAR.T
*	HsFLAG-FLJ20729_	3.0914	0.2277	1709.2	1709.871	6944.1	1	576.7	57.1	1	R.TQETPSAQMEGFLNR.K
*	HsFlag-VPS71_Ti_1	4.4939	0.4178	1757.57	1756.996	3519	1	533.7	62.5	11	K.TAASGIPYHSEVPVSLK.E
*	HsFLAG-FLJ20729_	4.9258	0.4618	2240.98	2241.388	8744.5	1	1810.9	63.2	4	K.DDEEMNTWIQAISSAISSDK.H
*	HsFLAG-p53-DNA-D	4.1166	0.4901	1545.4	1545.606	7109.4	1	1011.6	67.9	3	K.HEVSASTQSTPASSR.A
*	HsMRGBP-FLAG_Ti_	4.1401	0.4677	2060.93	2060.312	5964.2	1	645.2	47.4	3	R.AQTLPTSVVTITSESSPGKR.E
gi|4505763|re	8	29	26.40%	417	44615	8.1	phosphoglycerate kinase 1 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	2.1703	0.0984	1247.67	1248.462	6214	2	526.1	60	2	K.YSLEPVAVELK.S
*	HsFlag-VPS71_Ti_1	5.7238	0.3543	1770.96	1770.005	6919.7	1	2318.6	81.2	5	K.ACANPAAGSVILLENLR.F
	HsFLAG-p53-DNA-D	4.8024	0.2986	1769.7	1770.082	7796.1	1	1089	59.4	8	K.ALESPERPFLAILGGAK.V
	HsFlag-VPS71_Ti_1	4.0334	0.325	1771.18	1770.082	4605.6	1	932.2	46.9	2	K.ALESPERPFLAILGGAK.V
*	HsFlag-VPS71_Ti_1	3.512	0.1671	1967.55	1968.186	4559.9	1	508	52.9	1	K.VLNNMEIGTSLFDEEGAK.I
*	HsH2AZ-FLAG_293_	2.9574	0.2477	2022.74	2024.278	7916.5	1	854.1	52.9	1	K.ITLPVDFVTADKFDENAK.T
*	HsFlag-VPS71_Ti_1	4.6202	0.4504	2107.15	2106.391	6948.1	1	756.8	52.9	8	K.QIVWNGPVGVFEWEAFAR.G
*	HsH2AZ-FLAG_293_	3.3324	0.2919	1098.02	1098.285	6116.1	1	1274.2	80	2	K.VLPGVDALSNI.-
gi|74099697|r	9	175	26.30%	449	49264	6.3	heterogeneous nuclear ribonucleoprotein H2 [Homo sapiens]				
gi|9624998|re	9	175	26.30%	449	49264	6.3	heterogeneous nuclear ribonucleoprotein H2 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	4.61	0.2933	1685.59	1685.75	7123.9	1	2387.3	56.7	4	K.HTGPNSPDTANDGFVR.L
	HsFlag-NUFIP_Ti_1	4.405	0.4586	1685.6	1685.75	7380.1	1	1743.8	76.7	40	K.HTGPNSPDTANDGFVR.L
	HsFLAG-FLJ20309_	5.6045	0.4433	1844.33	1843	8624.1	1	2117.4	71.9	80	R.STGEAFVQFASQEIAEK.A
	HsMRGBP-FLAG_Ti_	3.4377	0.4497	2662.48	2661.629	7839.5	1	556	36	1	R.GAYGGGYGGYDDYGGYNDGYGFGSDR.F
	HsFLAG-ARP6_Ti_1	3.8358	0.4546	1603.44	1602.684	8040.3	1	1209.8	75	3	R.DLNYCFSGMSDHR.Y
	HsYL1_Ti_105.1435.	3.4682	0.4336	2084.26	2085.181	5682.9	1	836.5	52.8	1	R.YGDGGSSFQSTTGHCVHMR.G
	HsFLAG-p53-DNA-D	4.5176	0.4033	2030.45	2030.262	9785.3	1	1476.6	62.5	5	R.ATENDIYNFFSPLNPMR.V
	HsFLAG-TCF3_Ti_1	2.9392	0.214	1092.51	1093.228	6901.6	1	869.9	72.2	12	R.VHIEIGPDGR.V
	HsFLAG-ARP6_Ti_1	3.664	0.2731	1093.44	1093.228	6216	1	1638.1	88.9	29	R.VHIEIGPDGR.V
gi|4504517|re	2	3	26.30%	205	22783	6.4	heat shock 27kDa protein 1 [Homo sapiens]				
*	HsSrcap_Ti_206.302	5.7307	0.5358	4094.93	4095.606	5989.8	1	1414.3	29.7	2	A
*	HsFlag-VPS71_Ti_1	3.2368	0.3326	1784.71	1785.007	7517.9	1	536.5	46.7	1	R.VSLDVNHFAPDELTVK.T
gi|4507133|re	2	19	26.30%	76	8496	8.9	small nuclear ribonucleoprotein polypeptide G [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	2.6236	0.1793	823.45	822.986	3427.4	2	570.5	91.7	3	R.HVQGILR.G
*	HsFlag-NUFIP_Ti_1	4.1973	0.255	1446.18	1445.717	5822.2	3	667.2	70.8	16	R.GNSIIMLEALERV.-
gi|17158044|r	5	9	26.10%	249	28681	10.8	ribosomal protein S6 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.2934	0.2133	1336	1336.497	3949.1	1	707.6	77.3	2	K.LNISFPATGCQK.L
*	HsFlag-NUFIP_Ti_1	3.062	0.1452	1116.24	1117.244	7392.8	5	1090.2	87.5	1	K.LIEVDDERK.L
*	HsFLAG-ARP6_Ti_1	4.6454	0.2764	1777.38	1777.99	5931.8	1	2345	80	2	K.RMATEVAADALGEEWK.G
*	HsFlag-NUFIP_Ti_11	3.7333	0.2582	1829.11	1828.169	11608.2	1	1042.5	53.1	2	R.GCIVDANLSVLNLVIVK.K

*	HsFLAG-ARP6_Ti_1	3.6624	0.2772	1336.14	1336.487	3482.4	6	635.2	80	2	K.LFNLSKEDDVR.Q
gi|47824889|r	4	9	26.00%	154	17799	10.1	hypothetical protein LOC388272 [Homo sapiens]				
*	HsH2AZ-FLAG_293_	3.5122	0.3345	1678.17	1678.735	4634.3	2	714.1	73.1	2	K.SCPECDQQVPVACK.S
*	HsH2AZ-FLAG_293_	3.6322	0.2337	1410.22	1410.521	5158.6	1	777.8	77.3	2	K.EIDIYANLSDEK.A
*	HsH2AZ-FLAG_293_	3.62	0.2672	1437.33	1437.682	9373.9	1	1562.7	75	1	K.AFVFSVALAEINR.K
*	HsH2AZ-FLAG_293_	3.8947	0.389	1565.77	1565.856	7031.2	1	937	65.4	4	K.AFVFSVALAEINRK.I
gi|10863945|r	14	41	25.70%	732	82705	5.8	ATP-dependent DNA helicase II [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.9797	0.4033	1916.65	1916.196	4860.4	1	1287.1	76.7	5	R.HLMLPDFDLLEDIESK.I
*	HsFlag-VPS71_Ti_1	3.6878	0.2262	1268.08	1267.511	6868	2	1352	80	1	K.SQLDIIIHSLK.K
*	HsFLAG-p53-DNA-D	3.8363	0.224	1395.28	1395.685	9033.9	1	1623.3	77.3	2	K.SQLDIIIHSLKK.C
*	HsFlag-VPS71_Ti_1	4.4447	0.4853	2725.09	2725.086	6605.4	1	1407.3	50	1	R.DDEAAAVALSSLIHALDDLDMVAIVR.Y
*	HsFLAG-p53-DNA-D	7.5531	0.4602	2725.58	2725.086	10164.5	1	4151.8	45	1	R.DDEAAAVALSSLIHALDDLDMVAIVR.Y
*	HsFLAG-FLJ20729_	2.8376	0.2176	1534.43	1534.804	4507	1	534.9	61.5	1	K.RANPQVGVAFPHIK.H
*	HsFLAG-Lin9_Ti_205	3.2257	0.3327	1377.72	1378.617	5337.3	1	500.6	58.3	4	R.ANPQVGVAFPHIK.H
*	HsFLAG-p53-DNA-D	4.2216	0.2863	2450.55	2450.81	8400.1	1	1447.1	36.4	2	K.KYAPTEAQLNAVDALIDSMSLAK.K
*	HsFLAG-p53-DNA-D	5.9375	0.4284	2451.82	2450.81	10030.3	1	2613.4	61.4	3	K.KYAPTEAQLNAVDALIDSMSLAK.K
*	HsFlag-VPS71_Ti_1	4.8565	0.4331	2323.91	2322.636	6771.7	1	1008.6	52.4	8	K.YAPTEAQLNAVDALIDSMSLAK.K
*	HsFLAG-FLJ20729_	4.0297	0.2357	1381.14	1381.522	6803.1	1	1341.1	81.8	3	K.TDTLEDLFPTTK.I
*	HsFLAG-FLJ20729_	4.2353	0.3472	3318.67	3318.639	8646.5	1	874.3	26.9	2	K.ASFEEASNQLINHIEQFLDTNETPYFMK.S
*	HsFLAG-p53-DNA-D	4.844	0.3266	3633.38	3632.018	11673.8	1	1390.4	27.3	1	K.QLNHFWEIVVQDGITLITKEEASGSSVTAEEAK.K
*	HsFlag-VPS71_Ti_1	4.1493	0.3794	2512.75	2510.686	6989.4	1	690.7	39.1	7	K.DKPSGDTAAVFEEGGDVDDLLDMI.-
gi|29837655|r	7	11	25.70%	421	46089	10	DNA polymerase delta interacting protein 3 isoform 1 [Homo sapiens]				
	HsFLAG-FLJ20729_	4.7564	0.2297	2038.28	2038.398	5057.2	1	1473.2	47.4	1	K.RSSPAAFINPPIGTVTPALK.L
	HsFlag-FLJ90652_29	2.8808	0.2189	1881.67	1882.21	9471.6	1	625	44.4	1	R.SSPAAFINPPIGTVTPALK.L
*	HsFlag-FLJ90652_29	3.4816	0.2671	1136.36	1137.284	7068.3	1	1262.1	88.9	1	R.INVVNNHQAK.Q
	HsFLAG-p53-DNA-D	4.2535	0.3909	1805.4	1806.049	10098.5	1	1080.3	52.9	1	K.FAASGGFLHHMAGLSSSK.L
	HsFLAG-Lin9_Ti_204	3.5821	0.3227	2787.39	2788.211	6350.9	8	350.4	24	1	R.TLVNKEEPPKELPAAEPVLSPLEGTK.M
	HsFLAG-Lin9_Ti_205	3.4364	0.2757	1393.94	1394.7	5009.1	1	707.1	70.8	3	R.LVHPGVAEVVFVK.K
	HsFlag-DPCD_Ti_20	3.4839	0.3176	2197.69	2198.395	5636.2	1	843.2	52.5	3	R.RVNSASSSNPPAEVDPDTILK.A
gi|4507791|re	2	3	25.70%	183	20900	7.7	ubiquitin-conjugating enzyme E2M [Homo sapiens]				
*	HsFLAG-FLJ20729_	3.9203	0.2848	1887.84	1888.004	7247.1	1	1254.8	70	2	K.TCDISFSDPDDLLNFK.L
*	HsFLAG-Lin9_Ti_206	3.9967	0.1931	3660.74	3661.189	8793.6	1	637.4	23.3	1	R.EDWKPVLTINSIIYGLQYLFLEPNPEDPLNK.E
gi|21328448|r	5	21	25.60%	246	28082	4.8	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide [Homo sapiens]				
gi|4507949|re	5	21	25.60%	246	28082	4.8	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	4.7483	0.3567	1598.58	1599.654	8318.8	1	1908	80.8	5	K.AVTEQGHELSNEER.N
	HsFlag-VPS71_Ti_1	4.4063	0.2321	2390.02	2388.64	10357.1	1	892.6	44.7	6	R.EKIEAELQDICNDVLELLDK.Y
	HsFLAG-Lin9_Ti_20	5.2316	0.3819	2131.18	2131.351	6143.2	1	1245.4	64.7	6	K.IEAELQDICNDVLELLDK.Y
	HsFlag-VPS71_Ti_1	5.8257	0.4827	2160.67	2160.296	7279.1	1	1974.1	69.4	2	K.TAFDEAIAELDTLNEESYK.D
	HsFLAG-FLJ20729_	3.7624	0.1371	1189.5	1190.444	6163.6	5	1616.1	88.9	2	K.DSTLIMQLLR.D
gi|4506633|re	5	16	25.60%	125	14463	10.5	ribosomal protein L31 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	2.6329	0.1465	914.17	914.098	5762.9	1	1038.9	92.9	2	K.RIHGVGFK.K
	HsFLAG-ARP6_Ti_1	2.3237	0.1435	757.54	757.911	4178.7	2	464.4	75	2	R.IHGVGFK.K
	HsFLAG-p53-DNA-D	4.5191	0.4438	1645.94	1645.979	6059.4	1	1351.7	76.9	10	K.LYTLVTYVPVTTFK.N

*	HsFLAG-TCF3_Ti_1	2.0442	0.1341	1145.25	1146.199	7767.7	2	555.6	72.2	1	K.NLQTVNVDEN.-
*	HsVPS71-FLAG_Ti_	2.8461	0.1934	1146.29	1146.199	3807.1	1	723.4	77.8	1	K.NLQTVNVDEN.-
gi|14670350|r	18	47	25.50%	998	112416	6.4	general transcription factor II, i isoform 1 [Homo sapiens]				
gi|14670356|r	18	47	26.50%	957	108055	8.1	general transcription factor II, i isoform 4 [Homo sapiens]				
gi|14670354|r	18	47	26.00%	977	110106	7.4	general transcription factor II, i isoform 3 [Homo sapiens]				
gi|14670352|r	18	47	26.00%	978	110280	6.7	general transcription factor II, i isoform 2 [Homo sapiens]				
	HsFlag-VPS71_Ti_1	3.7876	0.2362	1749.61	1748.13	7710.9	1	1286.1	64.3	1	R.MVVTFLMSALESMCK.E
	HsFlag-VPS71_Ti_1	2.5629	0.1019	1300.46	1301.442	3600.3	1	330.9	60	1	K.HPENYDLATLK.W
	HsFlag-VPS71_Ti_1	2.7316	0.304	1272.73	1273.438	4805.7	1	403.1	58.3	2	R.SILSPGGSCGPIK.V
	HsFLAG-FLJ20729_	3.2442	0.2297	1729.58	1729.93	5519.3	1	671.2	59.4	2	K.ANELPQPPVPEPANAGK.R
	HsFLAG-p53-DNA-D	4.4885	0.3175	3471.91	3470.993	6715	1	869.3	28.3	1	K.AKGPVTIPYPLFQSHVEDLYVEGLPEGIPFR.R
	HsFLAG-FLJ20729_	3.7025	0.312	3271.31	3271.74	3730.9	1	278	25	2	K.GPVTIPYPLFQSHVEDLYVEGLPEGIPFR.R
	HsFlag-VPS71_Ti_1	5.4524	0.4714	2357.86	2358.615	6014.4	1	1169.1	60.5	3	K.FEAHPNDLYVEGLPENIPFR.S
	HsFlag-VPS71_Ti_1	4.4246	0.4166	1865.76	1866.084	5484.1	1	576.9	60	3	K.RPELLTHSTTEVTQPR.T
	HsFLAG-Lin9_Ti_20	2.9293	0.2704	1457.42	1459.602	8448.1	1	648.3	59.1	1	R.TNTPVKEDWNVR.I
	HsFlag-VPS71_Ti_1	2.8242	0.1928	1247.6	1248.465	8245.6	1	921.9	68.2	1	K.FAQALGLTEAVK.V
	HsFlag-VPS71_Ti_1	4.3223	0.1941	1248.82	1248.465	4395.6	1	1280.4	90.9	2	K.FAQALGLTEAVK.V
	HsFLAG-p53-DNA-D	5.3215	0.4301	2895.89	2897.3	7408.4	1	1222.8	47.9	12	K.VPYPVFESNPEFLYVEGLPEGIPFR.S
	HsFLAG-p53-DNA-D	3.6827	0.2493	1060.81	1061.228	6462.1	2	1228.2	93.8	3	R.SPTWFGIPR.L
	HsFlag-VPS71_Ti_1	4.5881	0.3835	1731.84	1731.103	5604.2	1	1364.1	73.3	4	K.KPELVISYLPPGMASK.I
	HsFLAG-FLJ20729_	3.6901	0.2322	2890.26	2890.264	5712.9	1	761.6	31.2	1	K.VPFALFESFPEDFYVEGLPEGVPFR.R
	HsFLAG-p53-DNA-D	4.8339	0.4677	2890.38	2890.264	5157.6	1	1104.2	54.2	6	K.VPFALFESFPEDFYVEGLPEGVPFR.R
	HsFlag-VPS71_Ti_1	3.485	0.423	1253.36	1253.502	4927.2	1	1384.5	90.9	1	K.FGEAIGMGFPVK.V
	HsFLAG-FLJ20729_	3.2775	0.2926	2088.96	2088.436	6635.2	1	526	44.7	1	K.ITINPGCVVVDGMPPGVSFK.A
gi|63029937|r	20	90	25.40%	854	98113	5.2	heat shock protein 90kDa alpha (cytosolic), class A member 1 isoform 1 [Homo sapiens]				
	HsFlag-FLJ90652_2	3.2895	0.2213	1309.47	1309.462	2906.4	8	510.1	80	1	K.IRYESLTDPSK.L
	HsFLAG-ARP6_Ti_1	2.9924	0.125	1191.24	1191.416	6634.7	1	1323.8	88.9	2	R.ELHINLIPNK.Q
	HsFlag-FLJ90652_2	4.2722	0.1492	1242.75	1243.446	5993.9	1	1316	86.4	3	K.ADLINNLGTIAK.S
	HsH2AZ-FLAG_293_	2.9898	0.2517	1312.19	1312.332	6387.6	1	888.1	83.3	1	K.EDQTEYLEER.R
	HsFLAG-Lin9_Ti_20	4.9763	0.3744	1781.46	1780.076	7077.5	1	1376.5	75	21	K.HSQFIGYPITLFVEK.E
	HsFLAG-ARP6_Ti_1	3.5608	0.2123	1781.59	1780.076	5416.1	5	1052.8	48.2	1	K.HSQFIGYPITLFVEK.E
	HsFLAG-TCF3_Ti_1	5.0498	0.4259	1834.83	1834.89	6532.8	1	1518.8	78.6	8	R.NPDDITNEEYGEFYK.S
	HsFLAG-ARP6_Ti_1	4.5448	0.3471	1528.58	1528.662	7822.8	1	1414.3	75	4	K.SLTNDWEDHLAVK.H
	HsFLAG-ARP6_Ti_1	3.5185	0.1709	1266.15	1265.414	4931.4	3	765.5	77.8	5	R.RAPFDLFENR.K
	HsFlag-VPS71_Ti_1	3.1934	0.2824	2416.72	2416.76	3515.2	3	313.6	47.2	3	R.VFIMDNCEELIPEYLNFIR.G
	HsFlag-FLJ90652_2	4.3346	0.3748	1467.49	1468.61	8763.8	1	2163.6	86.4	1	K.CLELFTELAEDK.E
	HsFLAG-Lin9_Ti_20	2.7156	0.2215	1296.7	1297.414	7186.9	3	583.6	60	1	K.LGIHEDSQNRK.K
	HsFLAG-ARP6_Ti_1	2.8757	0.3624	1224.13	1225.387	5393.2	1	637.6	66.7	2	K.HIYYITGETK.D
	HsFLAG-ARP6_Ti_1	3.4064	0.3272	1225.31	1225.387	3639.2	1	938.5	88.9	2	K.HIYYITGETK.D
	HsFlag-FLJ90652_2	4.9389	0.3888	2577.51	2578.949	7286.2	1	954.2	47.5	6	K.HGLEVIYMIEPIDEYCVQQLK.E
	HsFLAG-FLJ20729_	4.614	0.1161	2578.85	2578.949	8549.9	1	1823.8	41.2	4	K.HGLEVIYMIEPIDEYCVQQLK.E
	HsH2AZ-FLAG_293_	2.5147	0.1093	1418.23	1417.466	2950.6	7	336.9	68.2	1	K.EGLELPEDEEEK.K
	HsFlag-VPS71_Ti_1	3.4799	0.4129	2446.2	2447.697	7907.1	1	527.2	37.5	2	R.LVTSPCCIVTSTYGWTANMER.I

	HsFlag-FLJ90652_2	5.0419	0.3938	1787.05	1788.013	7875.4	1	2211.3	85.7	17	K.HLEINPDHSIIETLR.Q
	HsFLAG-FLJ20729_	4.4426	0.3544	1788.86	1788.013	10014.4	1	1501.1	46.4	5	K.HLEINPDHSIIETLR.Q
gi|4505343|re	14	51	25.40%	790	91839	6.4	nuclear cap binding protein subunit 1, 80kDa [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	5.1627	0.4349	1962.16	1963.028	6829.9	1	1645.9	68.8	2	K.TSDANETEDHLESLICK.V
*	HsFLAG-ARP6_Ti_1	5.6435	0.3706	2551.14	2551.776	8651.6	1	1628.7	54.3	11	K.SACSLESNLEGLAGVLEADLPNYK.S
*	HsFLAG-ARP6_Ti_1	3.7026	0.2162	1548.44	1548.866	7789.7	1	1335.2	73.1	2	K.LTIYTTLVGLLNAR.N
*	HsFLAG-ARP6_Ti_1	4.6851	0.4862	1647.37	1647.846	6278.2	1	1397.8	76.9	2	R.NYNFGGEFVEAMIR.Q
*	HsFlag-NUFIP_Ti_1	4.4732	0.4519	2366.69	2367.567	4935.2	1	839.2	55	3	R.MFDYTDDPEGPVMPGSHSVER.F
*	HsFLAG-ARP6_Ti_1	4.3173	0.2777	1515.76	1515.759	8396.8	1	2168.6	90.9	6	R.FVIEENLHCIIK.S
*	HsFlag-NUFIP_Ti_1	4.1506	0.241	2493.68	2491.862	4549.7	1	482.1	47.6	3	R.ILDIVPPTFSALCPANPTCIYK.Y
*	HsFLAG-ARP6_Ti_1	3.4144	0.3195	1581.98	1582.927	9997.6	1	1154.5	65.4	1	K.IEVFVQTLLHLAAK.S
*	HsFLAG-ARP6_Ti_1	2.4753	0.1591	1181.55	1182.321	6419.8	1	555.7	60	1	K.SFSHSFSALAK.F
*	HsFLAG-ARP6_Ti_1	3.1446	0.1529	1184.63	1182.321	6478	1	991.6	80	2	K.SFSHSFSALAK.F
*	HsFLAG-ARP6_Ti_1	5.0606	0.4885	2267.63	2268.497	6600.5	1	1178.8	60.5	8	R.TQIVDCAAVANWIFSSELSR.D
*	HsFlag-NUFIP_Ti_11	4.2144	0.3773	1514.72	1514.811	8265.8	1	1606.4	81.8	3	R.LFVWEILHSTIR.K
*	HsFLAG-ARP6_Ti_1	3.8345	0.2693	1149.51	1150.409	7672.4	1	1779.6	93.8	4	K.NLFLVIFQR.F
*	HsFLAG-ARP6_Ti_1	3.9549	0.3622	1372.32	1372.712	6916.5	1	1531.6	85	3	R.FIMILTEHLVR.C
gi|4504425|re	5	9	25.10%	215	24894	5.7	high-mobility group box 1 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.4373	0.1664	1465.82	1465.562	4946.6	2	794	75	2	K.HPDASVNFSEFSK.K
	HsFLAG-p53-DNA-D	2.6478	0.1858	1134.37	1134.318	3599.5	1	707	77.8	1	K.TYIPPKGETK.K
*	HsFLAG-Lin9_Ti_20	4.7417	0.2844	2004.43	2003.277	8505.1	1	1595.5	43.3	2	K.RPPSAFFLFCSEYRPK.I
	HsFlag-NUFIP_Ti_2	4.0757	0.3812	1521.49	1521.757	6102.4	1	764.5	60.7	3	K.IKGEHPGLSIGDVAK.K
	HsFLAG-Lin9_Ti_20	3.2555	0.3859	1279.61	1280.423	4393.9	1	459.4	62.5	1	K.GEHPGLSIGDVAK.K
gi|20149594|r	16	48	24.90%	724	83264	5	heat shock 90kDa protein 1, beta [Homo sapiens]				
	HsFlag-VPS71_Ti_1	2.6074	0.2479	1275.61	1276.386	3329.6	2	220.6	59.1	1	R.ELISNASDALDK.I
	HsFlag-FLJ90652_2	3.2895	0.2213	1309.47	1309.462	2906.4	8	510.1	80	1	K.IRYESLTDPSK.L
	HsFLAG-ARP6_Ti_1	4.3879	0.3501	1809.7	1810.014	3503.6	1	992.5	80	6	K.IRYESLTDPSKLDSGK.E
	HsFlag-FLJ90652_2	4.2722	0.1492	1242.75	1243.446	5993.9	1	1316	86.4	3	K.ADLINNLGTIAK.S
	HsH2AZ-FLAG_293_	2.9898	0.2517	1312.19	1312.332	6387.6	1	888.1	83.3	1	K.EDQTEYLEER.R
*	HsFlag-FLJ90652_2	3.6847	0.2775	2504.41	2502.699	7070.8	1	719.1	47.4	2	K.PIWTRNPDDITQEEYGEFYK.S
*	HsFlag-VPS71_Ti_1	5.7105	0.4133	1849.73	1848.917	6604.1	1	1652.6	78.6	10	R.NPDDITQEEYGEFYK.S
	HsFLAG-ARP6_Ti_1	4.5448	0.3471	1528.58	1528.662	7822.8	1	1414.3	75	4	K.SLTNDWEDHLAVK.H
*	HsFLAG-FLJ20729_	2.8451	0.3316	2375.49	2375.708	3737.9	2	324.4	47.2	1	R.VFIMDSCDELIPEYLNFIR.G
*	HsFlag-VPS71_Ti_1	2.6434	0.2932	1141.58	1142.214	4302.1	1	391.4	72.2	2	K.LGIHEDSTNR.R
*	HsFlag-NUFIP_Ti_2	2.6149	0.2105	1143.58	1142.214	6406.7	2	673.5	72.2	1	K.LGIHEDSTNR.R
	HsFLAG-TCF3_Ti_1	4.5031	0.29	2449.56	2449.744	4232.6	1	523.4	52.6	3	R.GFEVVYMTEPIDEYCVQQLK.E
	HsH2AZ-FLAG_293_	2.5147	0.1093	1418.23	1417.466	2950.6	7	336.9	68.2	1	K.EGLELPEDEEEK.K
*	HsFLAG-ARP6_Ti_1	4.4601	0.4332	2433.2	2433.671	7710.5	1	830.3	45	3	R.LVSSPCCIVTSTYGWTANMER.I
*	HsFLAG-FLJ20729_	4.4914	0.2935	1784.78	1784.025	5877.5	1	1724.9	85.7	8	K.HLEINPDHPIVETLR.Q
*	HsFlag-VPS71_Ti_1	4.6052	0.2568	1785.23	1784.025	5851.9	1	1353.1	51.8	1	K.HLEINPDHPIVETLR.Q
gi|20336746|r	5	18	24.90%	369	39183	9.8	H2A histone family, member Y isoform 1 [Homo sapiens]				
gi|4758496|re	5	18	24.80%	371	39489	9.8	H2A histone family, member Y isoform 2 [Homo sapiens]				
gi|20336748|r	5	18	24.70%	372	39591	9.8	H2A histone family, member Y isoform 3 [Homo sapiens]				

	HsFLAG-p53-DNA-D	5.4698	0.4284	1934.86	1934.243	7343.5	1	2142.2	78.1	8	R.HILLAVANDEELNQLLK.G
	HsFLAG-ARP6_Ti_1	4.912	0.4643	1986.65	1987.35	4303.3	1	780.4	57.9	4	K.GVTIASGGVLPNIHPELLAK.K
	HsFLAG-ARP6_Ti_1	2.8638	0.1464	1335.7	1335.63	7926.2	1	915.2	58.3	1	K.GKLEAIITPPPAK.K
	HsFLAG-p53-DNA-D	2.8306	0.1701	2127.38	2128.254	7716.2	1	544.7	40.5	1	K.AASADSTTEGTPADGFTVLSTK.S
	HsFLAG-p53-DNA-D	5.0424	0.3886	1816.47	1817.055	9113.9	1	1822.2	60.5	4	K.NGPLEVAGAAVSAGHGLPAK.F
gi|38201710|r	18	100	24.80%	729	80273	8.3	DEAD box polypeptide 17 isoform p82 [Homo sapiens]				
*	HsFLAG-FLJ20729_	3.4788	0.1701	1520.29	1520.769	9765.1	1	1044.4	68.2	2	K.KWDLSELPKFEK.N
*	HsFLAG-ARP6_Ti_1	3.4538	0.3425	1361	1361.5	7724.5	1	1335.4	80	12	K.NFYVEHPEVAR.L
*	HsFLAG-Lin9_Ti_20	2.5197	0.2557	1361.67	1361.5	4350.6	1	354.5	65	1	K.NFYVEHPEVAR.L
	HsFLAG-FLJ20729_	3.68	0.1617	1369.4	1369.57	8205	1	1337	70.8	10	R.GDGPICLVLAPTR.E
*	HsFLAG-Lin9_Ti_20	4.9557	0.4056	1692.39	1692.823	7385.6	1	2063.3	82.1	9	R.ELAQQVQQVADDYGK.C
	HsFLAG-Lin9_Ti_20	3.4493	0.2586	1173.24	1173.321	5889.8	4	1103.1	80	1	R.GVEICIATPGR.L
	HsFlag-VPS71_Ti_1	3.9446	0.3609	1338.59	1337.595	6421.6	1	1768.7	90	2	R.MLDMGFEPQIR.K
	HsFlag-VPS71_Ti_1	3.4534	0.2605	1350.45	1349.59	5704.3	1	749	80	3	R.QTLMWSATWPK.E
*	HsFLAG-p53-DNA-D	3.2248	0.2041	1677.07	1676.829	7080	1	934.6	66.7	3	K.SQPERDWVLNEFR.S
	HsFlag-DPCD_Ti_20	3.9001	0.3219	1227.45	1227.447	6409.8	1	1340.3	81.8	24	K.APILIATDVASR.G
	HsFLAG-Lin9_Ti_20	2.3447	0.1664	1227.48	1227.447	4392.5	1	224.8	54.5	1	K.APILIATDVASR.G
	HsFlag-VPS71_Ti_1	3.8816	0.4273	2082.57	2083.39	7258	1	890.5	52.6	1	K.APILIATDVASRGLDVEDVK.F
	HsH2AZ-FLAG_293_	2.0551	0.157	874.29	874.966	5857.2	2	691.2	78.6	1	R.GLDVEDVK.F
*	HsFLAG-p53-DNA-D	4.7605	0.4117	2118.84	2119.254	5229.8	1	847.9	62.5	8	K.FVINYDYPNSSEDYVHR.I
*	HsFlag-DPCD_Ti_20	4.0002	0.3646	1417.24	1417.604	7391	1	1379.4	79.2	9	K.GTAYTFFTPGNLK.Q
*	HsFLAG-FLJ20729_	3.5571	0.1539	1325.86	1326.492	6999.9	1	1914.1	86.4	5	K.VLEEANQAINPK.L
*	HsFLAG-FLJ20729_	2.8888	0.1615	1012.12	1012.215	7386.2	3	1230.6	92.9	2	K.LMQLVDHR.G
	HsFLAG-FLJ20309_	4.4208	0.3835	1456.26	1456.512	9181.5	1	1482	69.2	6	R.SSQSSSQQFSGIGR.S
gi|4757810|re	11	32	24.80%	553	59751	9.1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit precursor [Homo sapiens]				
gi|50345984|r	11	32	24.80%	553	59751	9.1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit precursor [Homo sapiens]				
gi|50345982|r	11	32	27.20%	503	54494	8.2	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit isoform b [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	2.6411	0.2203	2103.44	2105.37	5052	2	506.6	47.4	2	K.GMSLNLEPDNVGVVVFGNDK.L
	HsFLAG-ARP6_Ti_1	4.9982	0.31	1781.71	1782.05	4478.3	1	1677.7	81.2	3	K.RTGAIVDVPVGEELLGR.V
	HsFLAG-ARP6_Ti_1	4.2319	0.2911	1782.17	1782.05	5337.5	1	1480.4	50	2	K.RTGAIVDVPVGEELLGR.V
	HsFLAG-ARP6_Ti_1	3.5468	0.3156	1288.36	1288.486	6033	1	1580.3	90	2	K.HALIIYDDLSK.Q
	HsFLAG-ARP6_Ti_1	3.5257	0.4022	1555.62	1554.702	6214.3	1	934.8	70.8	3	R.EAYPGDVFYLHSR.L
	HsFLAG-TCF3_Ti_1	5.8961	0.4139	2338.78	2339.567	7053.7	1	1283.8	38.1	3	R.EVAAFAQFGSDLDAATQQLLSR.G
	HsFLAG-ARP6_Ti_1	6.6814	0.4903	2339.22	2339.567	8206.4	1	2365.4	66.7	5	R.EVAAFAQFGSDLDAATQQLLSR.G
	HsFLAG-ARP6_Ti_1	3.7713	0.3034	2310.1	2310.63	7670.1	1	729.3	45	1	K.QGQYSPMAIEEQVAVIYAGVR.G
	HsFLAG-ARP6_Ti_1	6.2558	0.4607	2367.79	2368.701	8165.5	1	2251.3	43.8	5	K.FENAFLSHVVSQHQALLGTIR.A
	HsFLAG-ARP6_Ti_1	6.0386	0.4513	2368.41	2368.701	7144.6	1	1878	65	4	K.FENAFLSHVVSQHQALLGTIR.A
	HsFLAG-ARP6_Ti_1	3.2766	0.3301	1311.13	1311.477	8047.4	1	1093.1	72.7	2	K.EIVTNFLAGFEA.-
gi|5453549|re	4	11	24.70%	271	30540	6.3	thioredoxin peroxidase [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.7768	0.2959	1293.26	1293.465	8778.8	1	1901.9	86.4	2	R.VSVADHSLHLSK.A
*	HsFLAG-ARP6_Ti_1	3.1182	0.4028	2108.36	2109.386	7762.9	1	913.9	55.6	1	K.ISKPAPYWEGTAVIDGEFK.E
*	HsFlag-NUFIP_Ti_1	3.8359	0.3869	1464.42	1465.733	8256.5	1	1263.6	70.8	7	R.IPLLSDLTHQISK.D
*	HsFLAG-FLJ20729_	3.538	0.2208	2403.52	2404.651	7352.3	1	627.4	28.4	1	K.HGEVCPAGWKPGSETIIPDPAGK.L

gi|4506773|re	2	7	24.60%	114	13242	6.1	S100 calcium-binding protein A9 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.5125	0.3453	1807.66	1808.044	8165.6	1	1249.7	67.9	4	R.NIETIINTFHQYSVK.L
*	HsFLAG-RPB5MP_2	3.4314	0.2246	1457.18	1456.598	3886.2	1	576.6	70.8	3	K.LGHPDTLNQGEFK.E
gi|30474871|r	2	3	24.50%	143	16073	6.3	serine palmitoyltransferase subunit 1 isoform b [Homo sapiens]				
gi|5454084|re	2	3	7.40%	473	52744	6	serine palmitoyltransferase subunit 1 isoform a [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.1043	0.4796	1845.6	1847.04	9328.8	1	675.3	50	1	K.DHPALNYNIVSGPPSHK.T
	HsFLAG-ARP6_Ti_1	2.8429	0.1662	2128.21	2128.358	10339.6	2	570.3	47.1	2	K.ECINFASFNFLGLLDNPR.V
gi|5031973|re	6	15	24.30%	440	48121	5.1	protein disulfide isomerase-associated 6 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.3195	0.2085	1387.68	1387.576	6235.9	1	1790.2	80.8	5	R.TGEAIVDAALSALR.Q
*	HsFLAG-ARP6_Ti_1	3.6439	0.1054	1397.43	1397.478	7227.5	1	1734.6	86.4	1	K.DVIELTDDSFDK.N
*	HsFlag-VPS71_Ti_1	4.9272	0.4328	1528.64	1528.749	8299.9	1	2391.5	82.1	2	K.LAAVDATVNQVLASR.Y
*	HsFlag-VPS71_Ti_1	3.8375	0.2366	2638.42	2638.975	2959.3	1	515.7	50	2	R.ALDLFSDNAPPPELLEIINEDIAK.R
*	HsFLAG-p53-DNA-D	3.178	0.2812	1616.69	1616.814	6811	1	817.5	59.4	1	R.GSTAPVGGGAFPTIVER.E
*	HsFLAG-ARP6_Ti_1	4.0736	0.4269	2759.13	2759.889	7254.3	1	1055.1	45.8	4	R.DGELPVEDDIDLSDVELDDLGKDEL.-
gi|4506631|re	2	7	24.30%	115	12784	9.6	ribosomal protein L30 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.0235	0.3074	1354.49	1354.602	7373.3	1	1491.9	81.8	3	K.LVILANNCPALR.K
*	HsFLAG-TCF3_Ti_1	4.4311	0.2456	1759.68	1758.976	6521.6	1	1791.9	76.7	4	R.VCTLAIIDPGDSDIIR.S
gi|29826282|r	8	13	24.20%	546	59272	4.4	protein phosphatase 1G [Homo sapiens]				
gi|4505999|re	8	13	24.20%	546	59272	4.4	protein phosphatase 1G [Homo sapiens]				
	HsH2AZ-FLAG_293_	3.0105	0.1141	1234.48	1233.45	4403.3	6	673.7	77.8	2	K.YLPDIIKDQK.A
	HsH2AZ-FLAG_293_	4.1723	0.2413	1277.19	1277.46	5337.1	1	1319.7	86.4	2	K.ALEDAFLAIDAK.L
	HsH2AZ-FLAG_293_	4.8242	0.3792	1801.38	1801.905	6349.6	1	913.9	63.3	1	K.ELAQIAGRPTEDEDEK.E
	HsH2AZ-FLAG_293_	5.2315	0.4339	2346.67	2347.328	5629.6	1	1088.2	54.2	2	K.SGGGTGEEPGSQGLNGEAGPEDSTR.E
	HsH2AZ-FLAG_293_	3.1665	0.2769	1219.23	1219.253	6044.8	1	1387.7	90	2	K.AYTGFSSNSER.G
	HsH2AZ-FLAG_293_	4.2299	0.3368	2546.64	2547.615	4846	1	631.9	46.2	2	R.GTEAGQVGEPGIPTGEAGPSCSSASDK.L
	HsH2AZ-FLAG_293_	3.5016	0.2696	1174.07	1174.253	5715.1	1	1343.8	80	1	R.NTAELQPESGK.R
	HsH2AZ-FLAG_293_	5.4073	0.3757	2205.55	2206.328	7939	1	1365.9	57.9	1	K.RKLEEVLSTEGAEENGNSDK.K
gi|8923059|re	10	22	24.10%	410	46717	7.1	mbt domain containing 1 [Homo sapiens]				
*	HsMRGBP-FLAG_Ti_	3.3524	0.3333	1460.66	1460.59	3685.4	3	484.4	70.8	1	R.VEVPNTDCSLPTK.V
*	HsMRGBP-FLAG_Ti_	2.7827	0.1135	1033.97	1033.302	3921.2	1	827	87.5	1	K.VFWIAGIVK.L
*	HsH2AZ-FLAG_293_	3.1825	0.2448	992	991.178	4053	1	918.2	93.8	3	K.LAGYNALLR.Y
*	HsMRGBP-FLAG_Ti_	2.9058	0.299	1762.66	1761.03	4226.6	7	274.6	46.2	1	K.VSESMQYPFKPCMR.V
*	HsMRGBP-FLAG_Ti_	1.9212	0.3668	1085.66	1086.277	5118.8	1	469.4	70	1	R.VAVVESVIGGR.L
*	HsMRGBP-FLAG_Ti_	4.2509	0.3411	1086.76	1086.277	8310.7	1	2296.3	95	2	R.VAVVESVIGGR.L
*	HsFLAG-TIP49b_Ti_	4.3609	0.4007	1739.31	1738.943	7148	1	1310.7	71.4	5	K.KQDGHFDTPPHLFAK.V
*	HsMRGBP-FLAG_Ti_	2.4745	0.3116	1224.47	1225.3	3467.2	9	179.5	55.6	3	K.EVDQSGEWFK.E
*	HsMRGBP-FLAG_Ti_	2.7747	0.1457	1225.55	1225.3	6303.6	2	663.2	72.2	2	K.EVDQSGEWFK.E
*	HsMRGBP-FLAG_Ti_	5.3918	0.4586	2001	2000.309	6180.8	1	1776.7	76.5	3	K.LEAIDPLNLSTICVATIR.K
gi|4758158|re	5	11	24.10%	361	41487	6.6	septin 2 [Homo sapiens]				
gi|56549640|r	5	11	24.10%	361	41487	6.6	septin 2 [Homo sapiens]				
gi|56549638|r	5	11	24.10%	361	41487	6.6	septin 2 [Homo sapiens]				
gi|56549636|r	5	11	24.10%	361	41487	6.6	septin 2 [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.6171	0.3824	1883.56	1883.152	8237.9	1	1360.2	66.7	2	K.STLINSLFLTDLYPER.V

	HsFLAG-p53-DNA-D	3.6835	0.3976	1513.59	1514.675	7347.9	1	1353.4	77.3	1	K.TIISYIDEQFER.Y
	HsFLAG-p53-DNA-D	3.5983	0.2949	1760.48	1761.028	6089.6	1	575.3	50	3	K.ASIPFSVVGSNQLIEAK.G
	HsFlag-VPS71_Ti_1(	3.851	0.1818	2286.61	2286.549	5373.7	1	821.7	58.3	2	R.LYPWGVVEVENPEHNDFLK.L
	HsFLAG-p53-DNA-D	6.0023	0.3672	2864.98	2864.22	9449.3	1	1558.6	37.5	3	R.TMLITHMQDLQEVTQDLHYENFR.S
gi|46430642|r	16	29	24.00%	1028	117949	9.4	myosin IC [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.1087	0.4112	2612.72	2612.942	10038.2	1	1436	52.3	1	R.VGVQDFVLLENFTSEAAFIENLR.R
*	HsFLAG-ARP6_Ti_1	3.5309	0.3214	2211.89	2211.566	7702.1	1	666.2	47.2	1	R.ENLIYTYIGPVLVSVNPYR.D
	HsFLAG-ARP6_Ti_1	3.4338	0.2414	1600.58	1601.843	6182.3	1	627.1	60.7	1	R.LLQSNPVLEAFGNAK.T
*	HsFLAG-ARP6_Ti_1	4.2079	0.3696	1554.69	1554.83	5576.7	1	1133.7	75	4	K.GAPVGGHILSYLLEK.S
*	HsFLAG-ARP6_Ti_1	3.1522	0.2482	1226.27	1225.43	8031.7	1	884.8	77.8	2	R.NPQSYLYLVK.G
*	HsFLAG-ARP6_Ti_1	3.6297	0.363	1876.2	1875.089	5228.1	1	638.5	56.2	1	K.GEELLSPLNLEQAAYAR.D
*	HsFLAG-ARP6_Ti_1	3.5927	0.4341	2012.91	2014.285	8478.5	1	954	55.9	3	R.LLHYAGEVTYSVTGFLDK.N
*	HsFLAG-Lin9_Ti_20	3.3574	0.1687	1305.23	1305.52	8635.5	1	1090.9	75	1	K.KRPETVATQFK.M
*	HsFLAG-ARP6_Ti_1	5.0649	0.2948	1502.21	1502.853	8967.6	1	2348.2	83.3	2	K.MSLLQLVEILQSK.E
*	HsFLAG-Lin9_Ti_20	4.0679	0.3409	1504.66	1505.639	10023.2	1	1415.2	77.3	1	R.CPENAFFLDHVR.T
*	HsFLAG-ARP6_Ti_1	3.6864	0.4525	1664.66	1664.902	3932.4	1	708.9	67.9	2	R.NVLDTSWPTPPPALR.E
*	HsScrap_Ti_102.271	2.9671	0.2518	1913.12	1912.28	4823.6	2	556	55.9	2	R.VLQALGSEPIQYAVPVVK.Y
*	HsFLAG-ARP6_Ti_1	3.114	0.2632	1723.64	1724.051	4295.8	1	731.4	66.7	2	R.QLLLTPNAVVIVEDAK.V
*	HsFLAG-Lin9_Ti_20	2.9557	0.2384	1756.96	1754.978	9035	1	825.7	53.3	2	K.GDVVLQSDHVIETLTK.T
*	HsFLAG-ARP6_Ti_1	4.3313	0.437	1901.9	1903.105	7859.8	1	1199.6	58.3	3	R.VNSININQGSITFAGGPGR.D
*	HsFLAG-ARP6_Ti_1	3.2562	0.3719	1034.24	1034.206	6830.3	1	1224.9	83.3	1	K.NGHLAVVAPR.L
gi|5174409|re	4	7	23.80%	341	37646	4.6	CD2 antigen (cytoplasmic tail) binding protein 2 [Homo sapiens]				
*	HsFlag-ZnF-HIT2_Ti_	4.3882	0.4143	2121.53	2120.274	6116.7	1	1126.2	61.1	1	K.VTFQGVGDEEDEDEIIVPK.K
*	HsARP6-FLAG_Ti_1	3.3296	0.2587	1392.23	1391.523	6363.1	1	1094	80	1	R.DSWLDNIDWVK.I
*	HsFlag-ZnF-HIT2_Ti_	5.0069	0.3406	4161.55	4162.537	9183.7	1	1111.7	25.7	3	K.GLGCQTLGPHNPTPPPSLDMFAEELAEEELETPTPTQR.G
*	HsFlag-ZnF-HIT2_Ti_	3.3079	0.2828	1450.74	1451.622	2675.5	1	533.2	79.2	2	R.KLDPPGGQFYNSK.R
gi|55956919|r	8	44	23.80%	332	35968	6.9	heterogeneous nuclear ribonucleoprotein AB isoform a [Homo sapiens]				
gi|55956921|r	8	44	27.70%	285	30588	7.9	heterogeneous nuclear ribonucleoprotein AB isoform b [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.445	0.3497	1456.46	1456.7	6618.3	2	712.4	62.5	2	K.MFVGGLSWDTSKK.D
	HsFLAG-p53-DNA-D	2.7107	0.1482	929.11	929.15	2788	4	617.9	85.7	1	R.GFGFILFK.D
	HsFLAG-p53-DNA-D	5.2679	0.2949	1633.72	1632.854	5829.7	1	1586.1	82.1	12	K.KIFVGGLNPEATEEK.I
	HsFLAG-p53-DNA-D	3.742	0.2361	1505.67	1504.68	8395	1	1575.3	76.9	1	K.IFVGGLNPEATEEK.I
	HsFLAG-p53-DNA-D	5.0639	0.1738	2214.7	2215.479	7729.9	1	1927.1	66.7	8	R.EYFGEFGEIEAIELPMDPK.L
	HsFLAG-ARP6_Ti_1	4.6326	0.3549	1670.23	1670.946	8906.9	1	1682.2	73.1	15	R.GFVFITFKEEEPVK.K
	HsFLAG-p53-DNA-D	4.7012	0.3907	1798.33	1799.12	9146.6	1	1798.3	71.4	2	R.GFVFITFKEEEPVKK.V
	HsFLAG-p53-DNA-D	3.3662	0.3027	990.51	991.135	4333.3	1	601.2	81.2	3	K.KFHTVSGSK.C
gi|12707570|r	4	7	23.80%	290	31371	8.1	mitochondrial short-chain enoyl-coenzyme A hydratase 1 precursor [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.0923	0.2532	1467.01	1467.712	6965.6	1	760	62.5	1	K.NNTVGLIQLNRPK.A
*	HsFLAG-ARP6_Ti_1	4.4688	0.4569	1971.47	1972.212	7085.7	1	2175.4	73.5	3	K.ALNALCDGLIDELNQALK.I
*	HsFLAG-p53-DNA-D	4.1623	0.305	2127.69	2126.42	5882.3	1	569.6	45	1	K.AQFAQPEILIGTIPGAGGTQR.L
*	HsFLAG-p53-DNA-D	4.6246	0.4892	1991.26	1990.19	8596.5	1	1606.2	65.6	2	K.ICPVETLVEEAIQCAEK.I
gi|33946324|r	7	20	23.70%	354	40361	6	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.3939	0.2836	1566.37	1565.643	5934.3	1	1364.4	83.3	1	K.IIHEAGYSEEECK.Q

	HsFLAG-ARP6_Ti_1	2.6401	0.3146	2062.5	2064.172	12844.4	1	1031.7	50	1	R.EYQLNDSAAYYLNDLDR.I
	HsFLAG-ARP6_Ti_1	3.3505	0.2431	1381.35	1381.571	5505.5	1	661.5	68.2	5	K.TTGIVETHFTFK.D
	HsFLAG-ARP6_Ti_1	3.8486	0.2132	1599.42	1598.882	7907.5	1	1179.4	70.8	2	K.WFTDTSIILFLNK.K
	HsFLAG-ARP6_Ti_1	3.3093	0.3202	1727.16	1727.056	5833.3	1	574.2	53.8	3	K.WFTDTSIILFLNKK.D
	HsFLAG-ARP6_Ti_1	3.3771	0.3264	1587.44	1587.692	7621.9	1	909.3	66.7	2	K.EIYTHFTCATDTK.N
	HsFLAG-ARP6_Ti_1	3.2254	0.2473	1708.53	1708.995	6149.4	1	791.4	57.1	6	K.NVQFVFDAVTDVIIK.N
gi|57863301|r	28	118	23.60%	1506	164886	8.2	CLIP-associating protein 2 [Homo sapiens]				
*	HsFlag-FLJ20643_Ti	4.2089	0.3234	2216.82	2217.267	5771.8	1	810.6	52.5	2	K.SFDDEESVDGNRPSSAASAFK.V
*	HsH2AZ-FLAG_293_	3.5178	0.2748	1424.41	1423.476	4544.3	1	879.4	76.9	3	K.EGGAGAVDEDDFIK.A
*	HsH2AZ-FLAG_293_	4.1429	0.4213	1585.97	1584.769	3228.7	1	570.7	73.1	4	K.AFTDVPSIQIYSSR.E
*	HsFLAG-ARP6_Ti_1	5.4668	0.5053	2096.36	2097.347	7918.3	1	1795.6	67.6	18	R.SLLVAGAAQYDCFFQHLR.L
*	HsFLAG-ARP6_Ti_1	4.2194	0.4541	1713.83	1713.938	6434.3	1	846.8	60	2	R.EACITVAHLSTVLGNK.F
*	HsFLAG-ARP6_Ti_1	2.7792	0.1724	2241.09	2241.552	4561	2	452.1	42.5	1	K.FDHGAEAIVPTLFNLVPNSAK.V
*	HsFlag-NUFIP_Ti_1	4.7624	0.2619	2241.49	2241.552	5972.7	1	1764.8	46.2	2	K.FDHGAEAIVPTLFNLVPNSAK.V
*	HsFLAG-ARP6_Ti_1	5.9791	0.4658	2392.03	2392.673	9453.5	1	1949.3	63.9	10	R.SFEFLDLLLQEWQTHSLER.H
*	HsFLAG-UTX1_Ti_2	3.5429	0.1599	2393.62	2392.673	6215.9	3	782.8	34.7	1	R.SFEFLDLLLQEWQTHSLER.H
*	HsH2AZ-FLAG_293_	2.2243	0.1094	1080.39	1081.301	4257.4	2	614.9	72.2	3	R.HAAVLVETIK.K
*	HsFlag-DPCD_Ti_20	3.3008	0.3023	1081.02	1081.301	8550.3	1	1404.9	83.3	2	R.HAAVLVETIK.K
*	HsH2AZ-FLAG_293_	4.3817	0.3979	1210.97	1209.475	5905.6	1	1462.5	90	12	R.HAAVLVETIKK.G
*	HsFlag-NUFIP_Ti_2	3.9997	0.3202	2324.26	2325.496	6686.5	1	993.5	39.5	4	R.NHFPGEAETLYNSLEPSYQK.S
*	HsFlag-NUFIP_Ti_1	4.9427	0.3258	2325.65	2325.496	5351.4	1	1158.1	63.2	7	R.NHFPGEAETLYNSLEPSYQK.S
*	HsH2AZ-FLAG_293_	4.0806	0.1482	1728.2	1728.813	6019.1	1	1011.1	63.3	8	R.SSSSSQESLNRPFSSK.W
*	HsFlag-FLJ20643_Ti	4.3331	0.3043	1376.51	1375.481	7248.7	1	1473.2	76.9	2	R.SRSDIDVNAAAGAK.A
*	HsFLAG-TCF3_Ti_1	2.5409	0.21	1033.49	1034.123	5802.2	2	476	72.2	2	K.AHHAAGQSVR.S
*	HsFlag-NUFIP_Ti_2	3.0105	0.3263	1620.74	1620.844	10402.4	1	926.4	53.3	1	R.VLTTTALSTVSSGVQR.V
*	HsH2AZ-FLAG_293_	2.6223	0.2099	1017.66	1017.17	4163.6	9	533.6	77.8	1	R.VLVNSASAQK.R
*	HsH2AZ-FLAG_293_	3.8171	0.4328	1681.34	1681.845	5376.6	1	1130	76.7	5	R.SFQPLGPGYGISQSSR.L
*	HsH2AZ-FLAG_293_	4.6897	0.467	1731.76	1731.897	8033.7	1	2014.3	71.9	4	R.VLNTGSDVEEAVADALK.K
*	HsH2AZ-FLAG_293_	4.7754	0.4052	1551.23	1551.564	9639.9	1	2155.9	73.3	5	R.AGGDATDSSQTALDNK.A
*	HsH2AZ-FLAG_293_	3.4856	0.2878	1924.37	1925.018	6850.2	1	985.9	60	1	R.DYNPYNYSDSISPFNK.S
	HsFlag-FLJ90652_2	5.0632	0.4171	1442.97	1442.78	10047	1	2191	83.3	10	K.TILLLLLETLGDK.E
*	HsFLAG-ARP5_Ti_1	3.3754	0.2498	2039.67	2039.464	8863.7	2	648.7	44.1	2	K.TILLLLLETLGDKEPTIR.A
*	HsFLAG-ARP5_Ti_1	3.3745	0.2438	1660.51	1659.886	5241.6	1	743	69.2	2	K.TLEAHKDPHKEVVR.S
	HsH2AZ-FLAG_293_	5.2582	0.4941	2114.01	2114.499	7264.5	1	1341.9	61.1	3	K.VLCPIIQTADYPINLAAIK.M
*	HsFlag-FLJ90652_2	2.5684	0.33	1792.58	1792.814	10002.9	1	497	41.7	1	K.RAQTGSGGADPTTDVSGQS.-
gi|4502891|re	3	12	23.60%	237	26215	4.1	chloride channel, nucleotide-sensitive, 1A [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	6.3018	0.4722	2721.01	2721.085	9282.8	1	2159.3	39.6	8	R.LSWLDGSGLGFSLEYPTISLHALSR.D
*	HsFLAG-TCF3_Ti_1	2.937	0.4185	2721.16	2721.085	6900.6	1	296.5	31.2	3	R.LSWLDGSGLGFSLEYPTISLHALSR.D
*	HsFlag-FLJ20643_Ti	5.656	0.4436	3460.72	3459.543	6075.4	1	1207.4	34.2	1	R.TEDSIRDYEDGMEVDTTPTVAGQFEDADVDH.-
gi|55770900|r	4	14	23.50%	353	41401	9.9	BRIX [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.2541	0.3073	1525.95	1526.819	8265.9	1	2580.8	91.7	8	K.FLVQNIHTLAELK.M
*	HsFLAG-ARP6_Ti_1	5.0567	0.3247	2487.75	2487.861	6468.5	1	1241.8	40.5	2	K.GSRPLLSFDPAFDELPHYALLK.E
*	HsFLAG-ARP6_Ti_1	3.1118	0.3424	2037.83	2037.282	5377.4	1	411.7	46.9	1	K.SQPFVDHVFTFTILDNR.I

*	HsFLAG-p53-DNA-D	5.5482	0.4413	3525.79	3527.055	7139.3	1	1409.5	32.5	3	K.TLLPHDPTADVFVTPAEEKPIEIQWVKPEPK.V
gi|33383233|r	11	21	23.40%	796	90251	5.7	arsenate resistance protein ARS2 isoform b [Homo sapiens]				
gi|58331218|r	11	21	21.20%	876	100667	6	arsenate resistance protein ARS2 isoform a [Homo sapiens]				
	HsFLAG-FLJ20729_	4.9702	0.3022	2727.45	2727.899	9049.8	2	1226.8	33.7	1	R.ILEQEEEEEQAGKPGEPSKKEEGR.A
	HsFLAG-p53-DNA-D	3.5979	0.2262	1557.61	1557.744	6701.8	2	787.3	72.7	1	K.EKPKEEEWEKPK.D
	HsFLAG-Lin9_Ti_20	2.7285	0.2284	1593.42	1592.805	8568.3	3	512.4	53.8	1	K.DAAGLECKPRPLHK.T
	HsFlag-NUFIP_Ti_2	4.172	0.3132	1430.44	1430.57	9815.5	1	1608.8	77.3	5	R.LRECELSPGVNR.D
	HsFLAG-p53-DNA-D	2.3799	0.0838	1024.61	1025.153	4130	3	351	75	1	R.NINGITQHK.Q
	HsFLAG-p53-DNA-D	4.1823	0.3992	2672.59	2674.069	5469.7	1	538	41.7	3	R.TQLWASEPGTPPLPTSLPSQNPILK.N
	HsFLAG-Lin9_Ti_20	3.6025	0.3081	4510.48	4510.82	6215.1	1	555.9	20.1	1	R.D
	HsARP6-FLAG_Ti_1	3.2034	0.2009	1326.86	1326.495	7466.7	1	1315.4	85	1	R.ISHGEVLEWQK.T
	HsFLAG-p53-DNA-D	3.2904	0.2397	1467.24	1467.619	6924.6	1	775.4	66.7	1	K.FVTSNTQELGKDK.W
	HsARP6-FLAG_Ti_1	4.4664	0.4243	1519.22	1516.693	6056.9	1	1367	87.5	5	K.EVAFFNNFLTDAK.R
	HsFlag-VPS71_Ti_1	1.8593	0.1525	1268.49	1269.307	4698	9	390.4	60	1	R.DLDAPDDVDFF.-
gi|42657272|r	3	7	23.40%	124	13614	10.1	PREDICTED: similar to 40S ribosomal protein S25 [Homo sapiens]				
gi|88988836|r	3	7	23.40%	124	13615	10	PREDICTED: similar to 40S ribosomal protein S25 [Homo sapiens]				
gi|4506707|re	3	7	23.20%	125	13742	10.1	ribosomal protein S25 [Homo sapiens]				
	HsFlag-NUFIP_Ti_1	3.7256	0.2251	1076.38	1076.281	6297.2	7	1060	87.5	5	K.LNNLVLFDK.A
	HsFLAG-ARP8_Ti_2	3.2755	0.1862	973.33	973.158	6103.8	1	1253.5	93.8	1	R.AALQELLSK.G
	HsFLAG-p53-DNA-D	1.8649	0.2027	930.34	930.904	4773.4	6	347.7	50	1	K.GGDAPAAGEDA.-
gi|22208967|r	2	16	23.40%	107	11676	10.3	high mobility group AT-hook 1 isoform a [Homo sapiens]				
gi|22208977|r	2	16	23.40%	107	11676	10.3	high mobility group AT-hook 1 isoform a [Homo sapiens]				
gi|22208971|r	2	16	23.40%	107	11676	10.3	high mobility group AT-hook 1 isoform a [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.4573	0.3357	1594.94	1594.852	3413.2	1	567.3	73.3	14	R.KQPPVSPGTALVGSQK.E
	HsFLAG-p53-DNA-D	3.8524	0.2649	2559.05	2559.922	5036.6	1	282.6	37.5	2	R.KQPPVSPGTALVGSQKEPSEVPTPK.R
gi|4758030|re	16	34	23.30%	1224	138331	7.7	coatomer protein complex, subunit alpha [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	3.5137	0.297	1593.18	1593.817	6436.3	1	712	60	1	R.GITGVDLFGTTDAVVK.H
*	HsSrcap_Ti_204.323	4.1993	0.369	2254.69	2255.556	8651.4	1	1125.6	36.2	4	R.GVNWAAFHPTMPLIVSGADDR.Q
*	HsSrcap_Ti_204.322	4.2859	0.3631	2257.8	2255.556	4829.2	1	556.2	50	2	R.GVNWAAFHPTMPLIVSGADDR.Q
*	HsFLAG-Lin9_Ti_20	4.4415	0.3817	1829.58	1830.001	8320.2	1	1526.1	66.7	2	R.ASNLENSTYDLYTIPK.D
*	HsSrcap_Ti_204.304	4.2461	0.3784	2409.22	2408.726	4504.6	1	685.3	52.5	1	K.KVQVPNCDEIFYAGTGNLLLR.D
*	HsSrcap_Ti_202.019	2.2179	0.2881	1479.56	1480.615	5897.6	1	564.1	62.5	1	R.DADSITLFDVQQK.R
*	HsSrcap_Ti_205.192	3.5661	0.144	1597.76	1596.793	9542.4	1	1078.6	66.7	2	R.KLDALCNIHENIR.V
*	HsSrcap_Ti_203.160	2.0707	0.1925	1302.63	1303.461	4712.4	3	297.3	50	1	K.YAVTTGDHGIIR.T
*	HsSrcap_Ti_203.288	3.8403	0.2878	1334.42	1333.614	6739.7	1	1563.9	86.4	2	K.LVGQSIIAYLQK.K
*	HsSrcap_Ti_206.241	3.7404	0.2195	1761.8	1761.031	6630.1	1	879.9	67.9	1	K.KGYPEVALHFVKDEK.T
*	HsSrcap_Ti_203.386	4.1851	0.3325	4161.47	4161.52	9917.8	1	755.3	21.6	1	K.SLAYLTAATHGLDEEAESLKETFDPEKETIPDIDPNAK.L
*	HsFlag-VPS71_Ti_1	2.8243	0.2387	2444.72	2445.966	3989.5	2	241.8	40.5	1	K.LLQPPAPIMPLDTNWPLLTVSK.G
*	HsSrcap_Ti_205.250	4.6977	0.4372	1714.5	1715.005	5632.3	1	1311.3	75	10	R.LLHDQVGVIQFGPYK.Q
*	HsSrcap_Ti_204.459	2.5546	0.0882	3165.19	3165.708	7842.8	2	327.3	27.8	1	R.SILLSVPLLVVDNKQEIAEAQQLITICR.E
*	HsFlag-VPS71_Ti_1	3.5339	0.4028	1679.85	1679.957	4443.6	1	768.1	71.4	3	R.LLELGPKPEVAQQTR.K
*	HsSrcap_Ti_204.307	3.8907	0.3599	3406.48	3407.707	9772.8	1	759.3	24.1	1	K.NPTDAYQLNYDMHNPFDICAASYRPIYR.G
gi|4507879|re	4	9	23.30%	283	30773	8.5	voltage-dependent anion channel 1 [Homo sapiens]				

*	HsFLAG-ARP6_Ti_1	3.739	0.4251	1960.84	1961.003	6045.9	1	877.2	55.6	2	K.SENGLEFTSSGSANTETTK.V
*	HsFLAG-ARP6_Ti_1	3.2695	0.3758	1528.35	1529.69	8495.5	1	1167.3	65.4	2	K.LTFDSSFSPNTGKK.N
*	HsFLAG-ARP6_Ti_1	3.2206	0.2895	1458.19	1457.629	7277.7	1	1100.3	75	1	K.SRVTQSNFAVGYK.T
*	HsFLAG-ARP6_Ti_1	4.1017	0.3766	2103.7	2104.455	5099.5	1	532.2	47.4	4	K.VNNSSLIGLGYTQTLKPGIK.L
gi|14150124|r	3	11	23.30%	129	15225	10.4	hypothetical protein LOC84298 [Homo sapiens]				
gi|88959164|r	3	11	23.30%	129	15441	10.1	PREDICTED: hypothetical protein XP_943746 [Homo sapiens]				
gi|88953955|r	3	11	23.30%	129	15441	10.1	PREDICTED: hypothetical protein XP_934680 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.9978	0.3959	1523.34	1523.813	5935.7	1	1236.7	73.1	2	K.DVQEIATVVVPKPK.H
	HsFlag-NUFIP_Ti_1	4.9091	0.4628	2000.67	2001.27	7398.6	1	1262.1	66.7	7	K.TLLDQHGQYPIWMNQR.Q
	HsFlag-NUFIP_Ti_1	4.4023	0.1295	2002.22	2001.27	5816	5	978.4	45	2	K.TLLDQHGQYPIWMNQR.Q
gi|4557641|re	7	21	23.20%	488	55325	5.8	histone deacetylase 2 [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.2556	0.3406	1608.84	1608.899	9133.6	1	1844.7	79.2	3	R.MTHNLLLNYGLYR.K
	HsH2AZ-FLAG_293_	3.9749	0.1887	1428.75	1427.572	6906	1	1117.8	72.7	3	R.SIRPDNMSEYSK.Q
*	HsH2AZ-FLAG_293_	3.0291	0.3309	1863.28	1865.076	7357.4	1	852	53.1	4	R.QQTDMAVNWAGGLHHAK.K
	HsARP6-FLAG_Ti_1	2.7103	0.2598	1375.1	1375.48	4614.8	1	500.1	68.2	1	K.YGEYFPGTGDLR.D
*	HsFlag-VPS71_Ti_1	4.5171	0.4227	2513.79	2514.794	5256.9	1	996	52.3	2	K.VMEMYQPSAVVLQCGADSLSGDR.L
*	HsFLAG-p53-DNA-D	4.8037	0.3953	1824.05	1824.191	7391.9	1	1467.1	71.9	3	K.TFNLPLLMLGGGGYTIR.N
*	HsFlag-VPS71_Ti_1	5.9957	0.4438	2235.2	2235.491	6953.5	1	1881.6	72.2	5	K.LHISPSNMTNQNTPEYMEK.I
gi|4758394|re	6	16	23.20%	379	41685	5.3	flotillin 2 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.0645	0.3115	1380.33	1379.602	8423.6	1	2179.7	86.4	4	K.NVVLQTLEGHLR.S
*	HsFLAG-ARP6_Ti_1	3.415	0.1022	1738.33	1736.963	10851.3	1	1055.7	57.1	1	R.SILGTLTVEQIYQDR.D
*	HsFLAG-ARP6_Ti_1	4.802	0.3652	1521.2	1521.67	8176.9	1	2262.1	80.8	2	K.TAEAQLAYELQGAR.E
*	HsFLAG-ARP6_Ti_1	4.0853	0.3537	1388.83	1389.607	7945.4	1	1770.7	73.1	2	K.IGEAEAAVIEAMGK.A
*	HsFLAG-ARP6_Ti_1	4.6754	0.2933	1468.88	1468.838	5913.8	1	1759.9	80.8	3	K.MALVLEALPQIAAK.I
*	HsFLAG-ARP6_Ti_1	5.5499	0.5431	1934.46	1935.271	3874.3	1	835.4	63.9	4	R.LLAELPASVHALTGVDLSK.I
gi|38045913|r	3	6	23.20%	177	19654	5.6	non-metastatic cells 1, protein (NM23A) expressed in isoform a [Homo sapiens]				
gi|4557797|re	3	6	27.00%	152	17149	6.2	non-metastatic cells 1, protein (NM23A) expressed in isoform b [Homo sapiens]				
	HsFLAG-p53-DNA-D	2.7564	0.1325	1151.25	1150.366	8005	2	1179.8	83.3	1	K.DRPFFAGLVK.Y
	HsFLAG-ARP6_Ti_1	4.4463	0.3575	1787.15	1787.041	6441.4	1	868.6	59.4	3	R.VMLGETNPADSKPGTIR.G
	HsFlag-FLJ90652_2	3.4402	0.3263	1486.14	1486.579	5218.9	1	794.1	73.1	2	R.NIIHGSDSVESAEK.E
gi|21359867|r	9	28	23.10%	325	35390	9	cytochrome c-1 [Homo sapiens]				
*	HsSrcap_Ti_204.210	2.8328	0.3596	1298.6	1299.47	5065.7	1	325.3	54.5	2	R.GLLSSLDHTSIR.R
*	HsSrcap_Ti_204.210	3.421	0.3621	1300.57	1299.47	8634.2	1	1216.9	68.2	5	R.GLLSSLDHTSIR.R
*	HsSrcap_Ti_203.160	3.2245	0.3542	1520.53	1521.633	7006.1	1	981	62.5	2	R.HLVGVCYTEDEAK.E
*	HsSrcap_Ti_203.161	3.8653	0.2576	1521.36	1521.633	4746.8	1	1106.4	83.3	2	R.HLVGVCYTEDEAK.E
*	HsScrap_Ti_105.231	3.3517	0.3422	1915.48	1916.143	3876.5	1	568.4	60	2	K.LFDYFPKPYPNSEAAR.A
*	HsSrcap_Ti_203.228	3.7137	0.2931	1916.5	1916.143	4832.9	1	707.6	40	1	K.LFDYFPKPYPNSEAAR.A
*	HsSrcap_Ti_204.369	5.7456	0.2571	2655.38	2655.89	8689.2	1	1766.5	38	3	R.HGGEDYVFSLLTGYCEPPTGVSLR.E
*	HsSrcap_Ti_204.369	5.8755	0.485	2655.88	2655.89	7766.9	1	1655.1	54.3	9	R.HGGEDYVFSLLTGYCEPPTGVSLR.E
*	HsSrcap_Ti_203.122	2.7344	0.3054	1264.5	1264.299	5888.8	1	876.6	83.3	2	R.WASEPEHDHR.K
gi|4506723|re	5	39	23.10%	264	29945	9.7	ribosomal protein S3a [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	2.6958	0.2261	919.73	920.117	4582	1	882	92.9	2	K.APAMFNIR.N
	HsFLAG-ARP6_Ti_1	5.3162	0.3754	1954.19	1953.159	9005.6	1	1457.3	65.6	9	R.VFEVSLADLQNDEVAFR.K

	HsFLAG-ARP6_Ti_1	2.4371	0.2371	1002.2	1003.141	6614.1	8	656.9	75	2	K.LITEDVQGK.N
	HsFlag-NUFIP_Ti_1	4.526	0.2731	1579.68	1579.737	7557	1	2218.3	87.5	10	K.NCLTNFHGMDLTR.D
	HsFLAG-ARP6_Ti_1	4.4478	0.4012	1705.36	1705.92	4182.9	1	949.7	76.9	16	K.ACQSIYPLHDVFVR.K
gi|72534660|r	5	54	23.10%	238	27367	11.8	splicing factor, arginine/serine-rich 7, 35kDa [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.2533	0.3437	1719.73	1720.923	7166.5	1	994.3	59.4	15	K.VYVGNLGTGAGKGELER.A
*	HsFLAG-ARP6_Ti_2	2.961	0.2818	1074.47	1074.224	5976.7	1	958.2	87.5	1	R.AFSYYGPLR.T
	HsFLAG-ARP6_Ti_2	3.9808	0.2277	1621.89	1622.777	5591.6	1	1081.1	76.9	35	R.NPPGFAFVEFEDPR.D
*	HsFlag-NUFIP_Ti_1	3.7728	0.3106	2378.86	2379.547	4898.2	4	317.5	42.5	2	R.NPPGFAFVEFEDPRDAEDAVR.G
*	HsFLAG-UTX1_Ti_2	2.6091	0.1545	1017.15	1017.089	3366.7	9	648.3	100	1	R.RPFDPNDR.C
gi|5729875|re	2	6	23.10%	195	21671	4.7	progesterone receptor membrane component 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.2895	0.4454	1518.99	1517.684	5745.1	1	1703.2	88.5	4	K.FYGPEGPYGVFAGR.D
*	HsFLAG-ARP6_Ti_1	5.7667	0.4	3627.04	3625.835	8959.5	1	1418.9	29.2	2	K.EALKDEYDDLSDLTAAQQETLSDWESQFTFK.Y
gi|15431306|r	5	28	23.00%	257	28025	11	ribosomal protein L8 [Homo sapiens]				
gi|4506663|re	5	28	23.00%	257	28025	11	ribosomal protein L8 [Homo sapiens]				
	HsFLAG-TCF3_Ti_1	3.8273	0.2217	3396.71	3397.844	11958.2	1	888.7	24.2	1	K.KAQLNIGNVLPVGTMPEGTIVCCLEEKPGDR.G
	HsFLAG-ARP6_Ti_1	4.3435	0.3177	1691.74	1689.822	7282.8	1	1170.8	63.3	14	R.ASGNYATVISHNPETK.K
	HsFLAG-ARP6_Ti_1	4.1795	0.359	1816.92	1817.996	8121.4	1	1098.4	59.4	4	R.ASGNYATVISHNPETKK.T
	HsFLAG-p53-DNA-D	3.1319	0.3564	941.43	942.106	6967	4	621.6	70	3	R.AVVGVVAGGGR.I
	HsFlag-Ies6_293_Ti_	3.6954	0.3255	942.39	942.106	6292.5	1	1732.4	85	6	R.AVVGVVAGGGR.I
gi|15431290|r	4	18	23.00%	178	20252	9.6	ribosomal protein L11 [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	3.2025	0.4065	1546.59	1547.792	4409.8	1	379	61.5	1	K.VLEQLTGQTPVFSK.A
*	HsFlag-NUFIP_Ti_1	4.1573	0.3317	1547.93	1547.792	8832.2	1	1468	69.2	4	K.VLEQLTGQTPVFSK.A
*	HsFLAG-ARP6_Ti_1	4.036	0.4568	2047.2	2048.346	7344.2	1	1384	64.7	11	K.YDPSIGIYGLDFYVVLGR.P
*	HsFlag-Ies6_293_Ti_	3.0966	0.1225	976.2	976.161	4106.8	1	874.9	87.5	2	K.YDGIILPGK.-
gi|4507793|re	2	3	23.00%	152	17138	6.6	ubiquitin-conjugating enzyme E2N [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.1595	0.2133	2197.99	2197.455	7031.5	1	912.4	52.6	1	R.YFHVVIAGPQDSPFEGGTFK.L
*	HsFLAG-FLJ20729_	3.3242	0.2429	1748.34	1749.075	3808	1	582.4	60.7	2	K.LELFLPEEYPMAAPK.V
gi|4507955|re	9	38	22.90%	414	44713	6.3	YY1 transcription factor [Homo sapiens]				
*	HsFLAG-ARP5_Ti_1	4.1224	0.4295	1919.43	1921.077	7414.4	1	1228.5	39.3	1	K.KSYLSGGAGAAGGGGADPGNKK.W
*	Hs293Flag-Ies2_Ti_1	5.919	0.484	1664.15	1664.729	5467.2	1	1319.7	68.4	14	K.SYLSGGAGAAGGGGADPGNK.K
*	HsFLAG-ARP5_Ti_1	3.6711	0.2141	1793.21	1792.903	5006.9	1	376.5	42.5	2	K.SYLSGGAGAAGGGGADPGNKK.W
*	HsFlag-FLJ90652_2	2.5824	0.3777	3195.85	3197.408	7687.1	1	366.5	29.6	1	K.DIDHETVVEEQIIGENSPPDYSEYMTGK.K
	HsFLAG-ARP5_Ti_1	4.0803	0.427	2360.62	2361.551	7768	1	480.6	42.1	1	R.HQLVHTGEKPFQCTFEGCGK.R
	HsFLAG-ARP8_Ti_2	3.0856	0.2641	1331.33	1331.4	10549.1	1	1172.6	75	1	K.PFQCTFEGCGK.R
*	HsFlag-FLJ90652_2	3.7893	0.3898	2036.67	2037.171	5707.4	1	626.1	56.2	5	R.IHTGDRPYVCPFDGCNK.K
*	HsFlag-FLJ90652_2	2.6186	0.0828	907.13	907.06	4683	8	724.6	85.7	1	K.SHILTHAK.A
*	HsFLAG-Lin9_Ti_20	2.5003	0.2271	907.28	907.06	4643.9	3	392.7	71.4	12	K.SHILTHAK.A
gi|18426915|r	8	10	22.80%	649	71439	4.5	drebrin 1 isoform a [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.9254	0.3819	3678.99	3679.97	12164.2	1	882.9	22.6	1	R.LELLAAYEEVIREESAADWALYTYEDGSDDLK.L
*	HsFLAG-ARP6_Ti_1	2.5715	0.2161	2277.7	2279.332	7744.4	1	517.2	42.1	1	R.EESAADWALYTYEDGSDDLK.L
	HsFLAG-Lin9_Ti_20	5.4035	0.4495	2072.7	2073.227	9162.1	1	1441.1	57.9	2	K.LAASGEGGLQELSGHFENQK.V
	HsFLAG-Lin9_Ti_20	4.0594	0.2873	1748.3	1746.96	8676.9	1	1442.3	71.4	1	K.YVLINWVGEDVPDAR.K
	HsFLAG-Lin9_Ti_20	2.7391	0.2196	909.18	909.076	6081.7	1	726.4	85.7	1	R.LSSPVLHR.L

	HsFLAG-ARP6_Ti_1	5.5983	0.4576	1851.55	1850.98	5489.5	1	1794.9	83.3	2	R.LREDENAEPVGTTYQK.T
	HsFLAG-Lin9_Ti_20	3.87	0.3008	2311.37	2311.514	5718.4	2	484.4	30	1	K.KSESEVEEAAAIIAQRPDNPR.E
	HsFLAG-Lin9_Ti_20	3.5437	0.2159	3848.99	3849.197	5874.6	1	411.2	22.1	1	R.ALDEVTSSQPPPLPPPPPPAQETQEPSPILDSEETR.A
gi|23397427|r	10	35	22.60%	623	69633	8.6	synaptotagmin binding, cytoplasmic RNA interacting protein [Homo sapiens]				
*	HsFLAG-p53-DNA-D	5.3904	0.4517	2334.86	2335.662	8267.2	1	1740.4	60	2	R.AIEALKEFNEDGALAVLQQFK.D
*	HsFLAG-FLJ20729_	5.5711	0.3737	1710.51	1709.896	8411.2	1	1763.7	71.4	6	K.EFNEDGALAVLQQFK.D
*	HsFLAG-p53-DNA-D	3.0339	0.1662	1143.54	1143.199	9676.1	5	899.3	72.2	2	K.DSDLSHVQNK.S
*	HsFlag-VPS71_Ti_1	4.7602	0.457	2570.01	2567.814	6623.4	1	820.1	45.8	2	K.YGGPPPDSVYSGQQPSVGTEIFVGK.I
*	HsARP6-FLAG_Ti_1	4.4061	0.1713	1595.65	1594.802	4095	3	975.8	79.2	8	R.DLFEDELVPLFEK.A
*	HsFLAG-p53-DNA-D	3.3671	0.134	1059.18	1059.17	6865	2	880.6	85.7	2	K.LYNNHEIR.S
*	HsFLAG-Lin9_Ti_20	3.094	0.2787	1943.18	1944.149	11374.5	2	640.8	43.8	1	K.VTEGLTDVILYHQPDDK.K
*	HsFlag-VPS71_Ti_1	4.2859	0.3313	2654.91	2655.939	6821.7	1	833.5	43.5	1	K.VWGNVGTVEWADPIEDPDPEVMAK.V
*	HsFlag-VPS71_Ti_1	4.6721	0.3759	1474.69	1474.651	6224.2	1	1631.3	87.5	10	R.NLANTVTEEILEK.A
*	HsFLAG-p53-DNA-D	2.8463	0.2839	1183.25	1183.352	8178.9	3	939.5	72.2	1	K.AFSQFGKLER.V
gi|4504733|re	18	52	22.50%	1257	133767	8.4	insulin receptor substrate 4 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.8938	0.4472	2038.16	2039.034	4073.7	1	865.7	64.7	2	R.SDSESEEEDLPVGEEVCK.R
*	HsFLAG-ARP6_Ti_1	2.9469	0.2228	1982.7	1983.145	5172.6	8	363.5	50	1	K.LETADAPARLEYYENAR.K
*	HsFLAG-ARP6_Ti_1	5.26	0.3896	2056.53	2056.419	7968.8	1	1033.9	47.7	2	R.AAAAAAAAAASGAAIPPLIPPRR.V
*	HsFLAG-TCF3_Ti_1	3.1528	0.4038	2644.77	2645.895	7602.3	1	525.4	36.5	1	R.CGTLGAQPDGEPAALAAAAAAEPPFYK.D
*	HsFLAG-ARP6_Ti_1	3.1777	0.1439	1240.31	1240.491	6385.4	2	1115.3	83.3	2	K.DVWQVIVKPR.G
*	HsFLAG-ARP6_Ti_1	3.5484	0.3692	1742.22	1742.069	7988.3	1	791.5	56.7	2	R.LNTEVASVVVQLLSIR.R
*	HsFLAG-ARP6_Ti_1	4.257	0.4259	1802.66	1803.112	5387.4	1	917	65.6	1	R.SYSISIGAHLLTLLSAR.R
*	HsFLAG-ARP6_Ti_1	3.5254	0.2234	1544.66	1544.84	3967.9	2	613.1	65.4	3	R.HLGLVPLEPGGWLR.R
*	HsFLAG-ARP6_Ti_1	3.1682	0.2748	1327.27	1327.483	5278.3	1	645.6	72.7	4	R.FVTPSEPVAHSR.R
*	HsFLAG-ARP6_Ti_1	3.9748	0.3689	1588.36	1588.762	5362.9	1	998.4	79.2	4	K.SWSSYFSLPNPFR.S
*	HsFLAG-ARP6_Ti_1	3.7712	0.4471	1710.37	1709.779	5715.9	1	825.1	64.3	4	R.EADSSSDYVNMDFTK.R
*	HsFLAG-ARP6_Ti_1	3.7816	0.1866	2578.82	2580.817	11166.7	1	1286	32.6	2	K.RESNTPAPSTQGLPDSWGIIAEPR.Q
*	HsFLAG-TCF3_Ti_1	4.0337	0.3298	2424.05	2424.629	5768.7	1	617.4	47.7	1	R.ESNTPAPSTQGLPDSWGIIAEPR.Q
*	HsFLAG-ARP6_Ti_1	4.4056	0.4837	2376.28	2376.616	6836.8	1	1013.4	57.9	2	R.IYVVDPFSECCMDISLSPSR.C
*	HsFLAG-ARP6_Ti_1	4.1661	0.3578	1646.56	1645.815	4095.4	1	1117.6	78.6	1	R.WFQPVANAADAEAVR.G
*	HsFLAG-ARP6_Ti_1	4.1491	0.245	2060.97	2062.166	4137	1	962.2	38.1	2	R.GAQDVAGGSNPGAHNPSANLAR.G
*	HsFLAG-ARP6_Ti_1	5.2227	0.4013	2061.72	2062.166	6777.7	1	1460.6	61.9	14	R.GAQDVAGGSNPGAHNPSANLAR.G
*	HsFLAG-ARP6_Ti_1	4.8476	0.5153	1789.45	1789.902	8042.3	1	1484.5	60.5	4	R.GDNQAGGAAAAAAAPEPPPR.S
gi|89038911|r	4	30	22.50%	218	24802	8.9	PREDICTED: similar to ribosomal protein S3a isoform 1 [Homo sapiens]				
gi|89038917|r	4	30	22.50%	218	24802	8.9	PREDICTED: similar to ribosomal protein S3a isoform 7 [Homo sapiens]				
gi|89038915|r	4	30	22.50%	218	24802	8.9	PREDICTED: similar to ribosomal protein S3a isoform 6 [Homo sapiens]				
gi|89038913|r	4	30	22.50%	218	24802	8.9	PREDICTED: similar to ribosomal protein S3a isoform 5 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	2.4371	0.2371	1002.2	1003.141	6614.1	8	656.9	75	2	K.LITEDVQGK.N
	HsFlag-NUFIP_Ti_1	4.526	0.2731	1579.68	1579.737	7557	1	2218.3	87.5	10	K.NCLTNFHGMDLTR.D
	HsFLAG-ARP6_Ti_1	4.4478	0.4012	1705.36	1705.92	4182.9	1	949.7	76.9	16	K.ACQSIYPLHDVFVR.K
	HsFLAG-ARP6_Ti_1	2.9563	0.3967	1331.22	1332.471	5365.6	1	472.9	58.3	2	R.LMELHGEGSSSGK.A
gi|5031877|re	10	19	22.40%	586	66408	5.2	lamin B1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.0778	0.187	1415.47	1415.589	7362.7	1	1405.9	77.3	2	K.AEHDQLLLNYAK.K

*	HsFLAG-ARP6_Ti_1	3.8174	0.136	1294.55	1294.45	7215.2	1	1406.6	85	1	K.LREYEAALNSK.D
*	HsFLAG-ARP6_Ti_1	5.6843	0.3429	2529.82	2529.804	8234.2	1	1915.1	56.5	4	K.SLEGDLEDLKDQIAQLEASLAAAK.K
*	HsFLAG-ARP6_Ti_1	4.0677	0.2912	1429.26	1429.613	7682.4	1	2204	84.6	1	K.DQIAQLEASLAAAK.K
*	HsFLAG-p53-DNA-D	3.3569	0.3535	1069.06	1069.267	6225.9	1	1190.3	93.8	1	K.LAQALHEMR.E
*	HsFLAG-p53-DNA-D	4.6649	0.3001	1652.52	1652.844	8196.9	1	1713.3	79.2	1	R.LYKEELEQTYHAK.L
*	HsFLAG-ARP6_Ti_1	4.7391	0.3935	1734.55	1735.009	8111.6	1	1857.5	75	3	R.MRIESLSSQLSNLQK.E
*	HsFLAG-ARP6_Ti_1	4.508	0.3365	1447.28	1447.629	10185.3	1	1909.4	79.2	1	R.IESLSSQLSNLQK.E
*	HsFLAG-p53-DNA-D	5.9542	0.3442	2110.14	2109.315	8716.9	1	3021.1	81.2	3	R.DQMQQQLNDYEQLLDVK.L
*	HsFLAG-p53-DNA-D	4.0376	0.1858	3415.38	3413.587	4325.5	1	489.8	26.7	2	K.TTIPEEEEEEEEAAGVVVEEELFHQQGTPR.A
gi|29789090|r	7	19	22.40%	522	56085	8.8	RCC1-like [Homo sapiens]				
*	HsMRGBP-FLAG_Ti_	3.8156	0.2148	1480.95	1480.661	6523	2	963	64.3	3	K.AGGAAVVITEPEHTK.E
*	HsFLAG-p53-DNA-D	4.7126	0.4255	1931.92	1932.147	9236.4	1	1614.9	58.3	3	R.TVVSGSCAAHSLLITTEGK.L
*	HsFlag-VPS71_Ti_1(	5.0936	0.4645	1811.8	1812.042	8892.7	1	2062.1	68.8	4	R.LIEGLSHEVIVSAACGR.N
*	HsFLAG-p53-DNA-D	3.0652	0.2194	2300.86	2301.4	6329.4	4	272.4	35	2	K.GNLYSFGCPEYGQLGHNSDGK.F
*	HsFLAG-p53-DNA-D	2.8416	0.1225	1636.61	1635.947	5391.7	4	473.1	50	2	K.TKDGQILPVPNVVVR.D
*	HsFLAG-p53-DNA-D	3.2246	0.3009	1884.81	1885.053	6904.1	1	679.7	53.1	1	R.DVACGANHTLVLDSQKR.V
*	HsFlag-VPS71_Ti_1(	4.3211	0.4074	1510.58	1510.708	8996.7	1	2030.9	79.2	4	R.LGHAEQKDEMVPR.L
gi|4826734|re	9	27	22.40%	526	53426	9.4	fusion (involved in t(12;16) in malignant liposarcoma) isoform a [Homo sapiens]				
*	HsFLAG-p53-DNA-D	6.6134	0.344	3586.29	3587.748	7755.9	1	1595.5	33.1	13	R.HDSEQDNSDNNTIFVQGLGENVTIESVADYFK.Q
*	HsFLAG-p53-DNA-D	3.9878	0.3135	1537.23	1537.774	4844.8	1	892	79.2	1	K.KTGQPMINLYTDR.E
*	HsFLAG-p53-DNA-D	3.5914	0.2673	1952.5	1953.221	6692.3	1	930.5	62.5	2	K.KTGQPMINLYTDRETGK.L
	HsFlag-VPS71_Ti_1(	4.1712	0.4305	1421.9	1421.503	4776.8	1	1058.8	76.9	3	K.GEATVSFDDPPSAK.A
	HsFlag-VPS71_Ti_1(	2.5337	0.1023	1022.72	1023.133	6069	2	567.1	68.8	1	K.AAIDWFDGK.E
*	HsFlag-VPS71_Ti_1(	2.0633	0.208	891.59	891.999	3281.8	1	288.9	78.6	2	K.EFSGNPIK.V
*	HsFlag-VPS71_Ti_1(	4.1462	0.3835	1814.79	1813.914	5646.5	1	907.4	73.1	2	K.CPNPTCENMNFSWR.N
*	HsFLAG-p53-DNA-D	4.1091	0.4325	2253.84	2254.355	7114.1	1	941.5	52.2	2	K.APKPDGPGGGPGGSHMGGNYGDDR.R
*	HsFlag-NUFIP_Ti_2(	4.0827	0.3326	2254.04	2254.355	6174	1	782.1	33.7	1	K.APKPDGPGGGPGGSHMGGNYGDDR.R
gi|56676335|r	34	111	22.30%	2472	274464	5.5	RAP1 interacting factor 1 [Homo sapiens]				
*	HsFLAG-UTX1_Ti_2(	3.8311	0.3246	3327.11	3327.629	4441.2	1	355.6	25.8	1	R.GQSPLAPLLETLEDPSASHGGQTDAYLTLTSR.M
*	HsFlag-DPCD_Ti_20	3.6129	0.2922	1720.66	1718.942	6807.9	1	699	56.7	3	K.ITSELSEANALELLSK.L
*	HsFlag-DPCD_Ti_20	3.7101	0.3024	1686.11	1684.948	4898.5	1	1135.7	78.6	1	R.LIEQAPIQMGEEAVR.W
*	HsFlag-DPCD_Ti_20	3.6096	0.2996	1304.07	1304.619	4916.4	1	810.4	77.3	11	K.LVIPLVVHSAQK.V
*	HsARP6-FLAG_Ti_1	5.2159	0.3509	1909.98	1911.165	8975.5	1	2388.4	75	16	R.SGSFINSLLQLEELGFR.S
*	HsFLAG-p53-DNA-D	4.82	0.2544	1892.14	1892.125	7056.8	1	1144.1	62.5	1	K.SLIDNFALNPDILCSAK.R
*	HsFLAG-UTX1_Ti_2(	4.7101	0.4232	2340.49	2341.753	5395.8	1	773.8	52.5	11	K.LVLSLEPLEHPLISSPSFFSK.H
*	HsFLAG-Lin9_Ti_20	3.7618	0.3366	2341.48	2341.753	5171	1	667.1	35	2	K.LVLSLEPLEHPLISSPSFFSK.H
*	HsARP6-FLAG_Ti_1	3.9055	0.3421	1880	1881.142	8356.5	1	1240.7	58.8	2	K.HANTLITAVHDSFVAVGK.D
*	HsFlag-NUFIP_Ti_2(	2.6425	0.1709	1187.95	1188.285	5057.9	1	670.6	77.8	1	K.SPQRPSDWSK.K
*	HsFlag-NUFIP_Ti_2(	3.4105	0.1497	1984.54	1985.334	10716.9	2	816.2	46.9	1	K.IFATLTRPLALFYENSK.L
*	HsYL1_Ti_101.1334.	2.8305	0.2658	1412.23	1411.431	5897.2	1	701	66.7	1	K.SSLSNNECGSLDK.T
*	HsFlag-DPCD_Ti_20	5.2795	0.3773	2593.6	2594.841	9004.8	1	1217.7	33.7	4	K.FDGSENRPFSPSPLNNISSTVTVK.N
*	HsFlag-NUFIP_Ti_2(	3.7816	0.269	1362.5	1362.612	5802.3	1	967.1	72.7	7	K.SPLHIKDDVLPK.Q
*	HsFlag-DPCD_Ti_20	4.3175	0.3206	1643.05	1642.89	9166	1	1737.4	73.1	4	K.LIAEQTLQENLIEK.G

*	HsFlag-VPS71_Ti_1	4.8699	0.4866	1593.8	1593.645	8089.9	1	1500.1	71.4	4	K.TLGETSANAETEQNK.K
*	HsFLAG-ARP5_Ti_1	3.6882	0.4011	2590.62	2591.745	5478	1	405	28.3	1	K.KADPENIKSEGDGTQDIVDKSSEK.L
*	HsYL1_Ti_101.1312.	2.8869	0.293	1263.98	1264.288	4577.1	1	837.4	81.8	2	K.SEGDGTQDIVDK.S
*	HsYL1_Ti_101.1427.	3.5563	0.2429	1521.02	1521.535	4469.5	1	860.6	75	2	K.SNESVDIQDQEEK.V
*	HsH2AZ-FLAG_293_	3.0364	0.2943	1973.51	1974.177	4061.3	1	261.7	43.8	4	K.YAEYSFTSLPVPESNLR.T
*	HsFLAG-ARP6_Ti_2	3.1089	0.2394	1248.7	1249.404	5463.4	1	964	77.3	1	K.IGISDISSLSEK.T
*	HsFLAG-FLJ20309_	2.8869	0.1873	1292.31	1292.4	7969.8	2	848.2	72.2	1	K.TFQTLECQHK.R
*	HsFlag-VPS71_Ti_1	2.6217	0.1788	1495.83	1493.524	7718.8	2	612.8	62.5	2	K.NTENNDVEISETK.K
*	HsTIP60_Ti_102.195	3.3616	0.3929	1793.48	1793.879	7203.4	1	718	56.7	3	K.EDNDTINDSLIVSETK.S
*	HsFlag-DPCD_Ti_20	4.1796	0.3249	1391.12	1391.475	7718.2	1	1788.6	83.3	2	K.TGISEEAAIEENK.R
*	HsFLAG-Lin9_Ti_20	3.5345	0.3245	2296.11	2297.434	9330.1	1	687.6	45	2	K.EVATEEFNSDISLSDNTTPVK.L
*	HsFlag-DPCD_Ti_20	4.6817	0.3637	3561.16	3562.65	9548.4	1	1026.6	24.2	1	K.LNAQTEISEQTAAGELDGGNDVSDLHSSEETNTK.M
*	HsARP6-FLAG_Ti_1	3.4665	0.1571	1647.31	1646.89	5981	1	1109.4	64.3	2	R.CVWSPLASPSTSILK.R
*	HsFlag-VPS71_Ti_1	3.5779	0.2328	1490.4	1489.582	7995.8	3	933.5	66.7	1	K.RSQEDEISSPVNK.V
*	HsH2AZ-FLAG_293_	4.6681	0.4029	1967.43	1967.142	5936.3	1	1865	73.5	5	R.VSFADPIYQAGLADDIDR.R
*	HsTIP60_Ti_106.348	4.3021	0.3097	3967.55	3969.517	6445.8	1	396.6	20.6	1	K.ESIPCPTESVYPPLVNCVAPVDIILPQITSNMWAR.G
*	HsARP6-FLAG_Ti_1	3.9062	0.3869	1449.22	1449.641	6360.3	1	1155.9	73.1	3	K.TIGDLSTLTASEIK.T
*	HsFLAG-ARP6_Ti_2	2.944	0.1703	1477.18	1476.667	2733.7	3	397.5	66.7	2	R.GLEEIPVFDISEK.T
*	HsH2AZ-FLAG_293_	5.8854	0.4286	1823.36	1823.18	5868.6	1	1697.7	75	6	R.LVSDIIDPVALEIPLSK.N
gi|40254861|r	15	72	22.30%	1087	114543	7.1	ubiquitin associated protein 2-like [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.174	0.2116	1837.3	1837.906	3911	2	292	53.6	2	R.GNWEQPQNQNQTQHK.Q
*	HsFLAG-ARP6_Ti_1	2.8249	0.1416	1298.05	1298.445	4624.4	2	482	70	1	K.QRPQATAEQIR.L
*	HsFLAG-ARP6_Ti_1	5.5412	0.4255	2210.32	2211.497	5372.2	1	1277.1	63.2	5	R.AINVLLEGNPDTHSWEMVGK.K
*	HsYL1_Ti_101.2372.	4.3068	0.4272	2242.94	2242.271	4970.4	1	732.2	58.3	10	R.TATEEWGTEDWNEDLSETK.I
*	HsFLAG-ARP6_Ti_1	4.7121	0.3581	2473.14	2473.789	4168.9	1	412.5	43.5	2	K.IFTASNVSSVPLPAENVTITAGQR.I
*	HsARP6-FLAG_Ti_1	3.0649	0.2397	1487.15	1487.609	7445.7	1	761.5	57.7	2	K.GGSTTGSQFLEQFK.T
*	HsFLAG-ARP6_Ti_1	4.5521	0.3908	1387.44	1387.492	9341.6	1	2006.5	83.3	7	K.NPSDSAVHSPFTK.R
*	HsFLAG-ARP6_Ti_1	4.5013	0.371	2131.22	2131.469	8963.8	1	1556.5	64.7	3	K.RQAFTPSSTMMEVFLQEK.S
*	HsFLAG-ARP6_Ti_1	4.2069	0.4339	1974.67	1975.282	5627.1	1	544.4	53.1	2	R.QAFTPSSTMMEVFLQEK.S
*	HsFLAG-ARP6_Ti_1	4.4813	0.3983	1961.62	1961.222	3238.4	1	654.1	65	16	K.SPAVATSTAAPPPPSSPLPSK.S
*	HsFLAG-ARP6_Ti_1	3.9135	0.2078	1337.15	1337.475	5847.3	1	886.2	77.3	4	R.RYPSSISSSPQK.D
*	HsFLAG-ARP6_Ti_1	4.8601	0.361	2597.05	2597.798	9003.5	1	1562.4	48	2	K.NGFSSVQATQLQTTQSVEGATGSAVK.S
*	HsYL1_Ti_103.3086.	3.9362	0.3678	2283.99	2284.616	2737.6	1	315	50	8	R.FPLDYYSIPFPTPTTPLTGR.D
*	HsYL1_Ti_101.1939.	3.9772	0.3521	1527.62	1525.612	4257.8	3	734.5	67.9	5	R.DGSLASNPYSGDLTK.F
*	HsFLAG-FLJ20309_	3.1694	0.2549	1544.64	1544.705	4032.3	1	389.8	61.5	3	R.SQTSSIPQKPQTNK.S
gi|32189394|r	6	11	22.30%	529	56560	5.4	ATP synthase, H+ transporting, mitochondrial F1 complex, beta subunit precursor [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.6994	0.4105	1651.59	1651.903	8318.4	1	1133.9	64.3	4	R.LVLEVAQHLGESTVR.T
*	HsFLAG-ARP6_Ti_1	3.539	0.2492	1457.87	1458.8	10428.5	2	1281.2	66.7	1	K.TVLIMELINNVAK.A
*	HsFLAG-TCF3_Ti_1	5.09	0.4724	1923.6	1923.133	7762.3	1	1746	73.3	2	R.DQEGQDVLLFIDNIFR.F
*	HsFLAG-p53-DNA-D	4.9228	0.3061	3846	3845.298	10886.3	1	828.6	22.9	1	K.KGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR.A
*	HsFLAG-TCF3_Ti_1	4.327	0.2819	1988.58	1989.233	4316.6	1	559.1	50	2	R.AIAELGIYPAVDPLDSTSR.I
*	HsFLAG-ARP6_Ti_1	3.1146	0.2579	2023.85	2024.345	7154.6	1	539.5	47.1	1	R.FLSQPFQVAEVFTGHMGK.L
gi|4507231|re	2	4	22.30%	148	17260	9.6	single-stranded DNA binding protein 1 [Homo sapiens]				

*	HsFLAG-ARP6_Ti_1	2.5296	0.3072	1780.39	1780.051	7215	3	552.9	53.6	1	K.NPVTIFSLATNEMWR.S
*	HsFLAG-ARP6_Ti_1	4.1756	0.3894	1993	1993.265	7305.3	1	900.1	55.9	3	R.QATTIIADNIIFLSDQTK.E
gi|7705425|re	1	5	22.30%	130	14502	9.8	mitochondrial ribosomal protein S17 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	6.4883	0.3867	3083.24	3081.41	7932.6	1	1301.6	31.2	5	K.VIDPVTGKPCAGTTYLESPLSSETTQLSK.N
gi|5031863|re	9	40	22.20%	585	65331	5.3	galectin 3 binding protein [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	6.0169	0.4795	2453.77	2453.603	8087.8	1	2121.4	62.5	7	R.GQWGTVCDNLWDLTDASVVCR.A
*	HsFLAG-ARP6_Ti_1	4.768	0.3465	1593.35	1593.734	6836.1	1	1449.8	76.9	2	R.ELSEALGQIFDSQR.G
*	HsFLAG-ARP6_Ti_1	3.4387	0.2773	1132.28	1132.346	6753.5	1	1366.1	88.9	2	R.RIDITLSSVK.C
*	HsFLAG-ARP6_Ti_1	3.5542	0.3404	1327.4	1327.434	6589.8	1	1282.1	81.8	2	R.ASHEEVEGLVEK.I
*	HsFLAG-ARP6_Ti_1	5.2755	0.3369	1985.21	1985.337	6381.5	1	1188	62.5	17	K.TLQALEFHTVPFQLLAR.Y
*	HsFLAG-ARP6_Ti_1	4.8758	0.286	1985.74	1985.337	5096.9	1	1154.5	50	3	K.TLQALEFHTVPFQLLAR.Y
*	HsSrcap_Ti_204.280	3.1459	0.2445	2522.96	2522.778	8177.6	1	364.7	36.8	1	R.YYPYQSFQTPQHPSFLFQDK.R
*	HsFLAG-ARP6_Ti_1	3.6634	0.4312	2301.76	2302.613	9169.5	1	1393.5	55.3	1	K.ALMLCEGLFVADVTDFEGWK.A
*	HsFLAG-ARP6_Ti_1	3.0025	0.3887	1769.21	1769.88	4055	1	542.8	60	5	K.STSSFPCPAGHFNGFR.T
gi|51492636|r	15	82	22.10%	1085	124025	8.6	PREDICTED: U2-associated SR140 protein [Homo sapiens]				
gi|88971174|r	15	82	22.10%	1085	124025	8.6	PREDICTED: similar to U2-associated SR140 protein [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	4.0055	0.3022	2238.84	2238.428	10251.6	1	910.9	47.2	4	R.ESLCDSPHQNLSRPLLENK.L
	HsFLAG-FLJ20729_	4.3735	0.3939	2132.96	2133.276	9471.8	1	1765.7	57.9	5	K.AAAEIYEEFLAAFEGSDGNK.V
	HsFlag-VPS71_Ti_1	4.1013	0.4352	1713.68	1713.798	8987.2	1	1203.3	60	4	R.GGVVNAAKEEHETDEK.R
	HsFLAG-Lin9_Ti_20	3.9826	0.2027	2220.63	2221.475	9177.7	1	859.2	50	4	K.NPPNQSSNERPPSLLVIETK.K
	HsFLAG-Lin9_Ti_20	2.9917	0.1366	1350.56	1350.555	12274.3	6	999	70	1	K.SNLELFKEELK.Q
	HsFlag-NUFIP_Ti_11	3.0478	0.134	950.49	950.172	5702	6	1117.3	92.9	6	R.NLLALIHR.M
	HsFlag-NUFIP_Ti_1	4.8325	0.4681	1785.8	1785.999	5429.2	1	969.5	73.1	16	R.FLFENQTPAHVYYR.W
	HsFlag-VPS71_Ti_1	5.9202	0.4005	3686.32	3685.067	8671.4	1	1148.1	26.6	3	R.KNDIGDAMVFCLNNAEAAEEIVDCITESLSILK.T
	HsFLAG-Lin9_Ti_20	4.7387	0.4325	1571.53	1572.798	6700.1	1	1544.4	76.9	4	R.LYLVSDVLYNSSAK.V
	HsFLAG-Lin9_Ti_20	4.6977	0.3946	1600.22	1601.766	8022.7	1	1809.6	83.3	3	K.LCQIFSDLNATYR.T
	HsFLAG-Lin9_Ti_20	4.1032	0.261	1402.42	1402.55	7544.8	1	1394.8	77.3	12	R.TIQGHLQSENFK.Q
	HsFLAG-p53-DNA-D	3.1841	0.2465	1878.69	1879.165	6164	1	731.7	60.7	2	R.AWEDWAIYPEPFLIK.L
	HsFLAG-Lin9_Ti_20	4.7698	0.3392	1744.37	1744.084	5878.6	1	1216.1	71.4	12	K.LQNIFLGLVNIIEEK.E
	HsFlag-DPCD_Ti_20	3.9656	0.4299	1905.86	1905.964	3426.9	1	290.3	50	5	K.SLDDDLDGVPLDATEDSK.K
	HsFLAG-ARP5_Ti_1	3.3951	0.1256	1434.29	1434.592	10093.8	1	1270.7	72.7	1	K.FQDELESGKRPK.K
gi|32483374|r	11	47	22.10%	594	66050	9.2	nucleolar protein 5A [Homo sapiens]				
*	HsH2AZ-FLAG_293_	3.7142	0.2401	2354.5	2354.66	4291	1	418.9	47.5	1	K.EVEEISLLQPQVEESVLNLGK.F
*	HsFLAG-p53-DNA-D	3.6075	0.2499	1151.47	1151.392	7616.8	1	1474.2	88.9	3	R.LLLETHLPSK.K
*	HsFLAG-Lin9_Ti_20	3.2553	0.2803	1189.16	1189.316	7331	1	1269.1	85	3	K.AQLGLGHSYSR.A
*	HsFLAG-p53-DNA-D	5.595	0.4394	1859.64	1858.163	5249.6	1	1020.9	63.9	9	K.MSQVAPSLSALIGEAVGAR.L
*	HsFLAG-Lin9_Ti_20	3.8246	0.388	1308.56	1309.552	5909.6	1	987.2	75	3	R.LIAHAGSLTNLAK.Y
*	HsFlag-NUFIP_Ti_11	3.9592	0.3684	1309.48	1309.552	5722.1	1	1583	87.5	12	R.LIAHAGSLTNLAK.Y
*	HsFLAG-Lin9_Ti_20	4.0049	0.3378	1376.98	1377.58	8805.2	1	2385.4	87.5	3	K.YPASTVQILGAEK.A
*	HsH2AZ-FLAG_293_	3.7181	0.245	1716.26	1715.863	3033.6	1	703.3	75	6	R.IDCFSEVPTSVFGEK.L
*	HsFLAG-Lin9_Ti_20	3.6252	0.2928	1313.87	1312.465	10881.9	1	1697.3	80	1	R.LSFYETGEIPR.K
*	HsFLAG-p53-DNA-D	5.1113	0.4174	1905.7	1906.1	5885.3	1	1007.6	64.7	2	R.KFSKEEPVSSGPEEAVGK.S
*	HsFLAG-ARP6_Ti_1	4.7179	0.5277	1777.22	1777.926	4674	1	1081.6	71.9	4	K.FSKEEPVSSGPEEAVGK.S

gi|4506621|re	3	5	22.10%	145	17258	10.6	ribosomal protein L26 [Homo sapiens]				
	HsFlag-NUFIP_Ti_1	2.7663	0.2103	1082.53	1083.189	4620.4	7	658.6	87.5	1	K.FNPFVTSDR.S
	HsFlag-NUFIP_Ti_11	2.6981	0.1226	1079.25	1079.206	4593.7	1	882.4	81.2	2	R.HFNAPSHIR.R
	HsFlag-NUFIP_Ti_11	4.0513	0.2987	1418.38	1418.596	7793.3	1	787.4	57.7	2	K.ANGTTVHVGIHPSK.V
gi|31543164|r	5	15	22.00%	341	37535	7.4	WD repeat domain 58 [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	4.0326	0.1975	2038.48	2038.398	8477	1	1604.4	44.4	2	R.AVPLAVPLGQTEVFQALQR.L
*	HsFLAG-ARP6_Ti_1	4.3836	0.3229	2038.89	2038.398	4377.5	1	1201.5	72.2	9	R.AVPLAVPLGQTEVFQALQR.L
*	HsARP6-FLAG_Ti_1	3.6178	0.2825	3035.48	3034.35	7331	1	726.8	26.8	1	K.FLAAGNNYGQIAIFSLSSALSSEAKEESK.K
*	HsFLAG-Lin9_Ti_20	2.7878	0.2185	1126.26	1126.255	5746.2	2	675.8	70	1	R.HLLSAGDGEVK.A
*	HsFLAG-p53-DNA-D	3.1747	0.2657	1736.97	1737.09	4282.9	7	389.2	53.3	2	R.TSLEVPEINALLLVPK.E
gi|21361657|r	7	14	21.80%	505	56782	6.4	protein disulfide isomerase-associated 3 precursor [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.087	0.4509	1348.83	1348.502	9054.2	1	1432.9	72.7	3	K.RLAPEYEAAATR.L
*	HsFLAG-p53-DNA-D	4.6298	0.4737	2350.7	2349.515	8396.5	1	993.5	50	2	K.DASIVGFFDDSFSEAHSEFLK.A
*	HsFlag-VPS71_Ti_1	5.7073	0.4393	2577.91	2576.866	9004.6	1	1662	52.2	1	K.TFSHELSDFGLESTAGEIPVVAIR.T
*	HsFLAG-Lin9_Ti_20	3.8879	0.2372	1834.86	1833.993	9326.8	1	1228	60	1	K.VVVAENFDEIVNNENK.D
*	HsFLAG-p53-DNA-D	3.3929	0.253	1342.39	1342.537	4877	1	868.8	72.7	2	R.GFPTIYFSPANK.K
*	HsFlag-VPS71_Ti_1	3.8715	0.3411	1372.55	1371.533	5559.1	1	1096.1	85	4	R.ELSDFISYLQR.E
*	HsFlag-VPS71_Ti_1	2.9907	0.1341	1580.51	1580.778	4690.2	1	519.9	65.4	1	R.EATNPPVIQEEKPK.K
gi|13128860|r	8	16	21.80%	482	55103	5.5	histone deacetylase 1 [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.2556	0.3406	1608.84	1608.899	9133.6	1	1844.7	79.2	3	R.MTHNLLLNYGLYR.K
	HsH2AZ-FLAG_293_	3.9749	0.1887	1428.75	1427.572	6906	1	1117.8	72.7	3	R.SIRPDNMSEYSK.Q
*	HsFLAG-Lin9_Ti_20	4.3572	0.341	2482.73	2483.874	10169.2	1	1233.8	47.6	1	K.KSEASGFCYVNDIVLAILELLK.Y
*	HsFLAG-Lin9_Ti_20	4.4237	0.4228	2355.85	2355.7	8361.2	1	1264.5	55	2	K.SEASGFCYVNDIVLAILELLK.Y
	HsARP6-FLAG_Ti_1	2.7103	0.2598	1375.1	1375.48	4614.8	1	500.1	68.2	1	K.YGEYFPGTGDLR.D
*	HsFlag-VPS71_Ti_1	2.9281	0.3941	2045.38	2045.268	11005.9	1	984.5	52.9	2	R.DGIDDESYEAIFKPVMSK.V
*	HsFlag-VPS71_Ti_1	5.8983	0.1142	2233.19	2234.445	5847.4	1	1862.4	75	3	K.LHISPSNMTNQNTNEYLEK.I
*	HsH2AZ-FLAG_293_	3.0063	0.2607	1067.57	1066.166	5546.8	1	788.1	87.5	1	K.RISICSSDK.R
gi|4506185|re	3	6	21.80%	261	29484	7.7	proteasome alpha 4 subunit [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.4955	0.3535	2593.9	2594.819	7347.5	1	534	39.1	2	K.LNEDMACSVAGITSDANVLTNELR.L
*	HsFLAG-FLJ20729_	3.5064	0.3351	1650.71	1651.949	6887.1	1	537.3	53.8	2	K.RPFGVSLLYIGWDK.H
*	HsFlag-FLJ90652_2	3.4955	0.3173	2206.55	2205.35	5890.5	1	746.3	61.1	2	K.HYGFQLYQSDPSGNYGGWK.A
gi|55770864|r	4	15	21.80%	257	26888	11.2	THO complex 4 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	5.287	0.4102	2843.16	2843.203	5484.8	1	993.6	48	7	K.LLVSNLDFGVSDADIQELFAEFGTLK.K
*	HsFLAG-p53-DNA-D	3.6885	0.2149	2970.86	2971.377	5995.5	1	672.4	26.9	2	K.LLVSNLDFGVSDADIQELFAEFGTLKK.A
*	HsFLAG-Lin9_Ti_20	3.6094	0.3232	1232.08	1232.338	7744	1	1356.4	85	1	R.SLGTADVHFER.K
*	HsFLAG-p53-DNA-D	4.9006	0.4163	2035.75	2036.163	9307.1	1	1224.2	58.8	5	K.QQLSAEELDAQLDAYNAR.M
gi|29570791|r	7	18	21.70%	391	45144	7.7	casein kinase II alpha 1 subunit isoform a [Homo sapiens]				
gi|4503095|re	7	18	21.70%	391	45144	7.7	casein kinase II alpha 1 subunit isoform a [Homo sapiens]				
	HsFlag-FLJ90652_2	2.9355	0.2391	1310.88	1311.564	5798.8	1	663.8	62.5	1	R.GGPNIITLADIVK.D
	HsFLAG-p53-DNA-D	5.275	0.4383	1865.6	1866.168	7781.5	1	1539.1	61.8	3	R.GGPNIITLADIVKDPVSR.T
	HsFLAG-p53-DNA-D	5.2552	0.3252	1732.51	1732.933	8768.9	1	2475.4	82.1	4	R.TPALVFEHVNNTDFK.Q
	HsFlag-FLJ90652_2	4.1255	0.424	2307.93	2308.558	6527.1	1	790.2	55.6	4	R.LIDWGLAEFYHPGQEYNVR.V
	HsFlag-FLJ90652_2	4.3431	0.4082	1543.69	1544.698	5678.7	1	1220.4	79.2	2	K.VLGTEDLYDYIDK.Y

	HsFlag-FLJ90652_2	5.0431	0.4646	2325.43	2326.571	9077.7	1	1733.2	60.5	2	R.FVHSENQHLVSPEALDFLDK.L
	HsFLAG-p53-DNA-D	4.5539	0.3756	2329.04	2326.571	7712.5	1	1905.7	44.7	2	R.FVHSENQHLVSPEALDFLDK.L
gi|5454024|re	3	3	21.60%	268	29321	8.9	ribonuclease P (30kD) [Homo sapiens]				
*	HsSrcap_Ti_204.319	2.9913	0.2258	2558.35	2556.018	8241.8	1	523.5	38.6	1	K.KQEIEKPVAVSELFTTLPIVQGK.S
*	HsFlag-VPS71_Ti_1	3.5737	0.2708	1669.13	1668.934	5547.6	1	717.9	64.3	1	K.NVIISSAAERPLEIR.G
*	HsYL1_Ti_102.3386.	2.9703	0.3155	2068.15	2067.303	6934.5	1	578	44.7	1	R.GPYDVANLGLLFGLSESDAK.A
gi|27436929|r	14	487	21.50%	641	70405	6	heat shock 70kDa protein 1-like [Homo sapiens]				
	HsFlag-FLJ90652_2	3.6517	0.3726	1487.89	1488.594	3812.9	1	610.4	75	34	R.TTPSYVAFTDTER.L
	Hs293Flag-Ies2_Ti_1	3.2174	0.4318	1488.58	1488.594	3710.2	1	167.1	54.2	6	R.TTPSYVAFTDTER.L
	HsFLAG-FLJ20729_	4.0267	0.3494	1616.65	1615.882	4580.3	1	846.5	76.9	19	K.AFYPEEISSMVLTK.L
	HsFlag-FLJ20643_Ti	2.8122	0.287	1197.73	1198.408	3228.1	7	262.1	59.1	5	K.DAGVIAGLNVLR.I
	HsFLAG-ARP6_Ti_1	4.5976	0.2685	1198.23	1198.408	6316.9	1	2167	95.5	46	K.DAGVIAGLNVLR.I
	HsFLAG-Lin9_Ti_20	5.2508	0.4465	1660.49	1660.908	5331.5	1	1768.4	80	50	R.IINEPTAAAIAYGLDK.G
	HsFlag-ZnF-HIT2_Ti_	4.6766	0.4075	1675.9	1676.696	6824.2	1	1767	76.7	48	K.ATAGDTHLGGEDFDNR.L
	HsFLAG-ARP6_Ti_1	6.6812	0.5227	2303.95	2305.608	7222.4	1	2114.5	63.6	124	K.SINPDEAVAYGAAVQAAILMGDK.S
	HsFLAG-ARP6_Ti_1	6.7971	0.4665	2304.11	2305.608	8353	1	2965.1	46.6	47	K.SINPDEAVAYGAAVQAAILMGDK.S
	HsFLAG-FLJ20309_	5.4572	0.4673	2788.6	2788.043	9884.1	1	1776.8	37	8	K.QTQIFTTYSDNQPGVLIQVYEGER.A
	HsFlag-ZnF-HIT2_Ti_	4.6245	0.4536	2788.77	2788.043	6989.1	1	643	41.3	55	K.QTQIFTTYSDNQPGVLIQVYEGER.A
	HsFLAG-TCF3_Ti_1	3.0245	0.244	1138.56	1138.222	3708.8	1	704.6	93.8	3	K.YKAEDEVQR.E
	HsFlag-FLJ90652_2	4.362	0.2456	1288.02	1288.461	6806.6	1	1526.8	90	24	K.NALESYAFNMK.S
	HsFLAG-ARP6_Ti_1	3.1355	0.2732	1289.43	1288.461	4692.1	1	433.4	70	18	K.NALESYAFNMK.S
gi|7662502|re	2	4	21.50%	181	20555	8.8	malignant T cell amplified sequence 1 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.0141	0.1481	2396.35	2396.81	5545.7	1	404.8	42.1	2	K.NQLIEQFPGIEPWLNQIMPK.K
*	HsFlag-VPS71_Ti_1	3.305	0.354	1921.85	1921.228	5927.9	1	516.9	47.2	2	K.FVLSGANIMCPGLTSPGAK.L
gi|88942850|r	5	23	21.40%	294	32601	4.8	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma lamini				
gi|88951517|r	5	23	21.40%	294	32601	4.8	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma lamini				
gi|88951515|r	5	23	21.40%	294	32601	4.8	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma lamini				
gi|88951513|r	5	23	21.40%	294	32601	4.8	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma lamini				
gi|88951511|r	5	23	21.40%	294	32601	4.8	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma lamini				
gi|88951507|r	5	23	21.40%	294	32601	4.8	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma lamini				
gi|88951505|r	5	23	21.40%	294	32601	4.8	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma lamini				
gi|88942860|r	5	23	21.40%	294	32601	4.8	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma lamini				
gi|88942858|r	5	23	21.40%	294	32601	4.8	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma lamini				
gi|88942856|r	5	23	21.40%	294	32601	4.8	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma lamini				
gi|88942854|r	5	23	21.40%	294	32601	4.8	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma lamini				
	HsFlag-NUFIP_Ti_1	3.5193	0.3235	2616.14	2618.967	9326.7	1	632.1	36.4	3	K.FLAAGTHLGGTNLDFQMEQYIYK.R
	HsFlag-NUFIP_Ti_1	4.6361	0.1686	2617.8	2618.967	11645.9	1	1168.9	31.8	1	K.FLAAGTHLGGTNLDFQMEQYIYK.R
	HsFlag-NUFIP_Ti_1	3.2111	0.1384	1136.52	1136.334	3726.7	3	871.1	83.3	9	K.SDGIYIINLK.R
	HsFLAG-TCF3_Ti_1	3.9474	0.3587	1742.78	1741.982	7911.5	1	1408.1	65.6	3	R.AIVAIENPADVSVISSR.N
	HsFlag-NUFIP_Ti_1	4.2588	0.3692	1204.09	1204.371	8028.8	1	1826.1	83.3	7	K.FAAATGATPIAGR.F
gi|9506651|re	3	7	21.40%	234	26093	6.2	potassium channel tetramerisation domain containing 5 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.1738	0.3362	1659.34	1659.849	8648.1	2	1227.3	59.4	1	R.CSAGLGALAQRPGSVSK.W
*	HsFLAG-Lin9_Ti_20	3.0599	0.2432	1343.72	1342.538	9104	1	995.8	68.2	1	R.LNVGGTYFLTTR.Q

*	HsFLAG-FLJ20729_	5.4786	0.4185	2385.61	2384.642	9155	1	1739.8	57.5	5	K.DLAEEGVLEEAEFYNITSLIK.L
gi|4507191|re	38	156	21.30%	2472	284281	5.3	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) [Homo sapiens]				
*	HsFLAG-p53-DNA-D	2.9142	0.2463	1870.09	1869.015	7925.9	1	552.2	53.6	1	K.KFEEFQTDMAAHEER.V
*	HsFLAG-ARP6_Ti_1	4.1049	0.2671	1606.28	1606.816	5769.7	2	1143.9	79.2	3	K.LIQEQHPEEELIK.T
*	HsFLAG-FLJ20729_	4.5952	0.2414	2565.6	2565.855	7780.9	1	1338.3	36.4	2	K.ALCAEADRLQQSHPLSATQIQVK.R
*	HsFLAG-ARP6_Ti_1	4.6341	0.2447	1678.28	1678.929	4843.4	1	872.4	71.4	4	R.LQQSHPLSATQIQVK.R
*	HsFLAG-ARP6_Ti_1	3.8995	0.3009	1679	1678.929	5396.2	1	1394.5	55.4	2	R.LQQSHPLSATQIQVK.R
*	HsARP6-FLAG_Ti_1	5.0792	0.2772	2127.29	2128.344	7209.9	1	1789.9	42.5	3	K.ALINADELASDVAGAEALLDR.H
*	HsFLAG-p53-DNA-D	6.1288	0.4757	2127.68	2128.344	10239.4	1	2738.1	65	9	K.ALINADELASDVAGAEALLDR.H
*	HsARP6-FLAG_Ti_1	3.693	0.1037	1214.28	1214.45	7335	1	1125.2	77.8	3	R.AALLELWELR.R
*	HsFLAG-p53-DNA-D	4.9757	0.3897	1708.84	1708.917	8842.4	1	1935.8	76.9	4	R.AQLADSFHLQQFFR.D
*	HsFlag-VPS71_Ti_1	3.9852	0.3281	1531.23	1532.659	8118.7	1	1401.9	81.8	1	K.LREANQQQFNR.N
*	HsFlag-VPS71_Ti_1	4.0659	0.3289	2696.62	2695.899	7549.5	1	1010	47.7	2	R.NVEDIELWLYEVEGHLASDDYGK.D
*	HsFLAG-ARP6_Ti_1	3.5502	0.2097	1556.46	1557.709	5875.5	1	1082.1	50	1	K.HQALQAEIAGHEPR.I
*	HsARP6-FLAG_Ti_1	3.5917	0.2527	1484.57	1484.689	7061.4	1	1023.3	72.7	5	K.ELVLALYDYQEK.S
*	HsFLAG-ARP6_Ti_1	4.6436	0.3105	1417.42	1417.646	7949.6	1	1811.1	79.2	5	K.KGDILTLLNSTNK.D
*	HsFLAG-FLJ20729_	3.915	0.2444	1324.88	1325.467	6529.6	1	1188	77.3	17	R.SQLLGSAHEVQR.F
*	HsARP6-FLAG_Ti_1	2.8629	0.1877	1041.26	1041.109	8444.2	4	1126.2	81.2	3	K.LGDSHDLQR.F
*	HsFlag-NUFIP_Ti_11	5.0216	0.2791	2877.43	2877.188	7145.6	1	1639	37	11	R.AGTFQAFEQFGQQLLAHGHYASPEIK.Q
*	HsFLAG-p53-DNA-D	5.3361	0.3718	1972.32	1973.282	5625.4	1	1424.3	47.2	13	K.IAALQAFADQLIAAGHYAK.G
*	HsFlag-VPS71_Ti_1	5.4127	0.3991	1972.94	1973.282	7017.1	1	1926.4	66.7	18	K.IAALQAFADQLIAAGHYAK.G
*	HsARP6-FLAG_Ti_1	3.8595	0.3349	1435.99	1434.543	6876.4	1	1635.2	86.4	1	R.DVDEIEAWISEK.L
*	HsFLAG-ARP6_Ti_1	4.7021	0.3276	1633.39	1631.915	7722.8	1	2092.3	80.8	3	R.LAALADQWQFLVQK.S
*	HsFLAG-ARP6_Ti_1	3.7236	0.4137	2245.69	2246.408	10052.4	1	832.7	45	1	K.DLNSQADSLMTSSAFDTSQVK.D
*	HsFLAG-ARP6_Ti_1	3.6753	0.1952	1268.52	1268.337	4364.9	4	841.8	83.3	3	R.DMDDEESWIK.E
*	HsFlag-FLJ90652_2	2.8862	0.3465	2221.98	2219.503	3183.8	1	185.2	47.5	1	K.RLEAELAAHEPAIQGVLDTGK.K
*	HsFlag-FLJ90652_2	2.6923	0.1918	1876.5	1875.046	8795.8	2	686.5	56.7	1	K.KLSDDNTIGKEEIQQR.L
*	HsFLAG-ARP6_Ti_1	3.1776	0.0915	1158.25	1158.345	5974.3	1	1117.9	87.5	3	R.LAQFVEHWK.E
*	HsMRGBP-FLAG_Ti_	4.4062	0.4705	2212.3	2210.548	8456.3	1	1516.9	60	4	K.MTLVASEDYGDTLAAIQGLLK.K
*	HsARP6-FLAG_Ti_1	4.6427	0.3698	2495.38	2494.764	7303.2	1	1503.8	38.6	2	K.QETFDAGLQAFQQEGIANITALK.D
*	HsFLAG-p53-DNA-D	5.1793	0.4641	3234.51	3234.634	7586.8	1	701.5	25.9	2	K.QETFDAGLQAFQQEGIANITALKDQLLAAK.H
*	HsARP6-FLAG_Ti_1	3.4416	0.3239	1373.29	1373.558	6464.6	1	933.5	72.7	2	K.RWSQLLANSAAR.K
*	HsFlag-VPS71_Ti_1	5.6268	0.4826	2300.35	2299.415	6786.8	1	1653	63.2	8	K.ASAFNSWFENAEEDLTDPVR.C
*	HsFlag-VPS71_Ti_1	4.769	0.2408	1953.16	1953.073	7003.2	1	1976.7	70.6	5	R.SSLSSAQADFNQLAELDR.Q
*	HsFlag-VPS71_Ti_1	4.5776	0.4923	2333.87	2332.592	7814.2	1	939.8	52.8	4	R.VASNPYTWFTMEALEETWR.N
*	HsFLAG-FLJ20729_	5.8314	0.3679	2512.85	2511.765	8909.1	1	1753.7	40.8	2	K.LRQEFAQHANAFHQWIQETR.T
*	HsFLAG-FLJ20729_	3.9106	0.1991	1495.83	1496.684	8254.6	1	1523.9	81.8	2	R.MQHNLEQQIQAR.N
*	HsARP6-FLAG_Ti_1	2.9771	0.1694	1280.4	1280.464	6693.1	1	963.8	72.7	2	R.ALSSEGKPYVTK.E
*	HsFLAG-p53-DNA-D	4.4544	0.3079	2427.81	2427.717	8126.7	1	1336.9	36.2	2	R.ALSSEGKPYVTKEELYQNLTR.E
*	HsFlag-DPCD_Ti_20	3.4629	0.3948	1800.87	1801.996	7430.6	1	1177.4	67.9	1	K.GRELPTAFDYVEFTR.S
gi|5031755|re	11	41	21.30%	633	70943	8.1	heterogeneous nuclear ribonucleoprotein R [Homo sapiens]				
*	HsFLAG-p53-DNA-D	2.8861	0.1519	1157.57	1157.225	7170.7	1	717.6	72.2	2	K.ESDLSHVQNK.S
*	HsFLAG-p53-DNA-D	4.9671	0.3538	2636.47	2636.964	5383.5	1	793.7	34	2	R.KYGGPPPDSVYSGVQPGIGTEVFVGK.I

*	HsFLAG-p53-DNA-D	4.9364	0.2451	3002.78	3003.428	9472.8	1	1245.1	31.2	1	R.KYGGPPPDSVYSGVQPGIGTEVFVGKIPR.D
*	HsFLAG-Lin9_Ti_20	4.6609	0.4565	2506.89	2508.79	5769	1	1029.2	52.1	6	K.YGGPPPDSVYSGVQPGIGTEVFVGK.I
*	HsFLAG-FLJ20729_	4.0194	0.3263	1610.12	1610.801	4113.9	1	1350.3	83.3	4	R.DLYEDELVPLFEK.A
*	HsFlag-VPS71_Ti_1	3.5731	0.2527	1338.84	1338.469	6782.9	2	1118.4	75	1	K.LCDSYEIRPGK.H
*	HsFLAG-p53-DNA-D	3.1692	0.2731	1940.64	1942.176	10980.5	2	823.7	46.9	1	K.VTEGLVDVILYHQPDDK.K
*	HsFLAG-p53-DNA-D	3.3551	0.1443	1445.06	1445.537	9198	1	1625.8	85	3	R.GFCFLEYEDHK.S
*	HsFLAG-p53-DNA-D	4.6446	0.3541	1461.55	1461.653	7736.2	1	1930.8	83.3	13	R.NLATTVTEEILEK.S
*	HsFLAG-Lin9_Ti_20	5.0708	0.3153	1909.5	1910.172	7905.6	1	1142.7	59.4	5	K.EIEGEEIEIVLAKPPDK.K
*	HsFLAG-p53-DNA-D	3.814	0.4035	1759.59	1759.872	5515.7	1	675.7	57.7	3	R.STAYEDYYYHPPPR.M
gi|6912494|re	3	7	21.30%	268	29999	5.1	microtubule-associated protein, RP/EB family, member 1 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	2.9071	0.3173	2020.39	2020.337	4747.7	1	468	50	2	R.QGQETAVAPSLVAPALNKPK.K
*	HsFLAG-p53-DNA-D	3.9308	0.2763	1925.86	1926.183	9480.4	1	1000.1	52.9	4	K.KPLTSSSAAPQRPISTQR.T
*	HsFlag-VPS71_Ti_1	3.5032	0.38	2270.69	2271.412	6239.3	1	625.9	50	1	R.NIELICQENEGENDPVLQR.I
gi|14589953|r	3	5	21.30%	150	17143	4.7	PolII_Rpb8 {RNA polymerase II, polypeptide H} [Homo sapiens]				
*	HsFlag-FLJ20643_Ti	4.4042	0.2777	1800.04	1798.904	6764.6	1	1585.7	70	2	K.VYRIEGDETSTEAATR.L
*	HsFlag-FLJ20643_Ti	3.4803	0.309	1381.28	1380.408	5507.7	1	950.5	75	1	R.IEGDETSTEAATR.L
*	HsFlag-NUFIP_Ti_1	4.7919	0.488	1772.28	1772.872	6850.6	1	1274	66.7	2	R.LQGDANNLHGFEVDSR.V
gi|21536320|r	9	28	21.20%	756	84794	8.8	E1B-55kDa-associated protein 5 isoform d [Homo sapiens]				
gi|21536326|r	9	28	18.70%	856	95739	6.9	E1B-55kDa-associated protein 5 isoform a [Homo sapiens]				
gi|21536322|r	9	28	19.90%	804	90292	6.9	E1B-55kDa-associated protein 5 isoform b [Homo sapiens]				
	HsFlag-NUFIP_Ti_1	2.6735	0.2141	2039.68	2040.283	4667.1	3	251.3	41.7	1	K.QGAPTSFLPPEASQLKPDR.Q
	HsFLAG-ARP6_Ti_1	4.3225	0.4554	2077.07	2076.316	8893.9	1	989.5	50	8	R.SSGYPLTIEGFAYLWSGAR.A
	HsFlag-NUFIP_Ti_1	2.7949	0.1676	1484.52	1484.655	3848.9	2	478.7	66.7	2	K.HLPSTEPDPHVVR.I
	HsFLAG-Lin9_Ti_20	3.1794	0.3315	2798	2797.958	6826.5	1	399.2	34	1	R.IGWSLDSCSTQLGEEPFSYGYGGTGK.K
	HsFlag-NUFIP_Ti_1	4.395	0.389	1596.64	1595.882	7400.5	1	1299.3	71.4	10	K.EALGGQALYPHVLVK.N
	HsFLAG-Lin9_Ti_20	2.581	0.1253	2561.85	2562.894	4948.5	3	235.9	33.3	1	R.AEPYCSVLPGFTFIQHLPLSER.I
	HsFLAG-ARP6_Ti_1	4.0166	0.4265	1742.29	1742.886	7779.1	1	1332.9	71.4	2	R.NYILDQTNVYGSAQR.R
	HsFlag-NUFIP_Ti_11	2.7858	0.2086	1168.57	1168.359	4874.2	4	529.1	75	1	K.MRPFEGFQR.K
	HsFLAG-Lin9_Ti_20	4.3236	0.3737	2555.43	2552.886	10312.9	1	891.1	42.9	2	K.ANFTLPDVGDFLDEVLFIELQR.E
gi|12056468|r	11	31	21.20%	745	81745	6.1	junction plakoglobin [Homo sapiens]				
gi|4504811|re	11	31	21.20%	745	81745	6.1	junction plakoglobin [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.946	0.3141	1412.7	1412.734	5349.5	1	1214.8	76.9	2	R.ALMGSPQLVAAVVR.T
	HsFLAG-ARP6_Ti_1	4.2396	0.3354	1808.87	1808.236	9688.3	1	770.8	50	3	K.LIILANGGPQALVQIMR.N
	HsFLAG-ARP6_Ti_1	4.1129	0.2985	2328.55	2327.711	5526.2	1	864	34.1	1	K.VLSVCPSNKPAIVEAGGMQALGK.H
	HsFLAG-ARP6_Ti_1	3.463	0.25	1303.54	1303.513	7930	1	1399.4	88.9	2	R.LVQNCLWTLR.N
	HsFLAG-ARP6_Ti_1	4.1109	0.4276	1831.56	1832.061	8870.6	1	1457	65.6	2	R.NLSDVATKQEGLESVLK.I
	HsFLAG-ARP6_Ti_1	4.5405	0.465	1935.73	1936.262	9628.6	1	1290.2	58.8	3	K.TLVTQNSGVEALIHAILR.A
	HsFLAG-ARP6_Ti_1	3.1636	0.2769	1450.39	1450.724	4451.4	1	788	81.8	1	K.LLNQPNQWPLVK.A
	HsFLAG-ARP6_Ti_1	4.666	0.378	2154.63	2156.459	6690.3	1	841.5	52.6	4	R.NLALCPANHAPLQEAAVIPR.L
	HsFLAG-ARP6_Ti_1	5.6947	0.4347	2156.55	2156.459	7322.6	1	1385.4	42.1	6	R.NLALCPANHAPLQEAAVIPR.L
	HsFLAG-ARP6_Ti_1	5.2619	0.4428	1599.86	1600.731	5023.8	1	1390.5	82.1	2	R.HVAAGTQQPYTDGVR.M
	HsFLAG-ARP6_Ti_1	3.502	0.3672	1392.67	1393.626	7202.6	1	975.4	72.7	5	K.RVSVELTNSLFK.H
gi|40217790|r	9	19	21.20%	567	64682	9.8	zinc finger protein 512 [Homo sapiens]				

*	HsFLAG-ARP6_Ti_1	3.7281	0.1767	2147.3	2147.315	6042.5	1	815	37.5	1	R.SEHGPISFFPESGQPECLK.E
*	HsFLAG-ARP6_Ti_1	4.0258	0.4153	2149.91	2147.315	6482.9	1	810.4	58.3	2	R.SEHGPISFFPESGQPECLK.E
*	HsFLAG-Lin9_Ti_204	4.7171	0.3386	1756.63	1757.04	8556.6	1	1765.1	70	6	K.IAVYHLQELASAELAK.E
*	HsFLAG-ARP6_Ti_1	3.5689	0.313	1873.74	1874.15	5901.6	1	425.7	50	1	K.YTRPGLPTFSQEVLHK.W
*	HsFLAG-ARP6_Ti_1	4.6606	0.4451	2098.26	2098.25	6556.1	1	1207	63.9	2	R.IQCPNQGCEAVYSSVSGLK.A
*	HsFLAG-Lin9_Ti_205	2.9003	0.2827	1531.77	1532.706	5946.9	1	535.2	53.6	1	K.AHLGSCTLGNFVAGK.Y
*	HsFLAG-Lin9_Ti_205	4.072	0.4736	1532.06	1532.706	6848.7	1	1746.6	78.6	4	K.AHLGSCTLGNFVAGK.Y
*	HsFLAG-Lin9_Ti_205	4.3305	0.4374	2361.28	2359.603	9555.1	1	1103.7	50	1	K.YHINSVHAEDWFVVNPTTTK.S
*	HsFLAG-Lin9_Ti_202	2.6932	0.1498	1711.62	1710.925	7042.6	2	472.6	50	1	R.QQPGIELPETELSLR.V
gi|4504511|re	5	30	21.20%	397	44868	7.1	DnaJ (Hsp40) homolog, subfamily A, member 1 [Homo sapiens]				
*	HsFLAG-ARP8_Ti_2	3.6878	0.4721	2325.25	2324.547	8268.2	1	542.7	37	3	K.EGGAGGGFGSPMDIFDMFFGGGGR.M
*	HsFlag-NUFIP_Ti_20	4.0869	0.2328	2720.97	2722.024	7721	1	1590.4	34.4	3	K.ITFHGEGDQEPGLEPGDIIIVLDQK.D
*	HsSrcap_Ti_205.181	2.9398	0.261	1392.62	1393.67	6160.8	1	524.4	58.3	4	R.TIVITSHPGQIVK.H
*	HsFlag-NUFIP_Ti_20	3.8172	0.2649	1393.39	1393.67	7602.2	1	1243.8	75	17	R.TIVITSHPGQIVK.H
*	HsFLAG-ARP6_Ti_1	4.0696	0.3483	2666.18	2667.771	5849.2	1	795.4	47.6	3	K.EVEETDEMDQVELVDFDPNQER.R
gi|4504983|re	4	9	21.20%	250	26188	8.5	galectin 3 [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	3.461	0.1409	1642.66	1642.013	6691.7	1	1036.7	64.3	3	R.MLITILGTVKPNANR.I
*	HsMRGBP-FLAG_Ti	2.9811	0.2675	1275.95	1274.381	6036.8	1	948.7	70	2	R.GNDVAFHFNPR.F
*	HsFlag-VPS71_Ti_10	3.5237	0.2553	1499.82	1498.722	4895.4	2	578.8	70.8	3	R.QSVFPFESGKPFK.I
*	HsFLAG-Lin9_Ti_205	2.9456	0.2105	1650.78	1650.837	9160.1	1	916.8	57.7	1	K.VAVNDAHLLQYNHR.V
gi|4503531|re	7	19	21.10%	407	46394	5.5	eukaryotic translation initiation factor 4A, isoform 2 [Homo sapiens]				
	HsFLAG-Lin9_Ti_201	2.3621	0.254	1047.39	1048.183	9240.5	1	837.8	75	2	R.GIYAYGFEK.P
	HsFLAG-ARP6_Ti_1	4.6012	0.3935	1829.59	1829.065	4460.2	1	954.3	73.3	7	R.GIYAYGFEKPSAIQQR.A
*	HsFLAG-Lin9_Ti_204	2.8501	0.2821	1546.3	1545.782	10094.2	1	976.6	60.7	1	K.LQAEAPHIVVGTPGR.V
	HsFlag-VPS71_Ti_10	4.883	0.3827	1556.72	1556.789	7213.7	1	2553.4	91.7	2	K.MFVLDEADEMLSR.G
	HsFLAG-Lin9_Ti_201	3.6979	0.2526	1115.19	1115.359	6528.4	1	1517.9	94.4	2	R.VLITTDLLAR.G
	HsFLAG-Lin9_Ti_205	5.0028	0.364	2144.5	2145.42	8462.8	1	1564.8	58.3	3	R.GIDVQQVSLVINYDLPTNR.E
*	HsFLAG-Lin9_Ti_203	3.6037	0.2739	1479.45	1478.645	7904.6	1	893.8	66.7	2	K.GVAINFVTEEDKR.I
gi|24308261|r	8	15	20.90%	536	60654	4.5	mesoderm induction early response 1 [Homo sapiens]				
*	HsH2AZ-FLAG_293_	5.2252	0.4603	3477.38	3478.492	6647.2	1	957.5	28.2	1	K.DSSGQEDETQSSNDDPSQSVASQDAQEIIRPR.R
*	HsH2AZ-FLAG_293_	5.3396	0.3698	2382.25	2382.542	6620.2	1	1229.1	58.3	3	K.VYENDDQLLWDPEYLPEDK.V
*	HsH2AZ-FLAG_293_	2.4859	0.224	1236.39	1237.398	4877.4	8	423.7	59.1	1	K.GVEAIPEGSHIK.D
*	HsH2AZ-FLAG_293_	3.8778	0.1472	1322.21	1322.458	6242.3	1	1669.7	85	2	K.DNEQALYELVK.C
*	HsH2AZ-FLAG_293_	5.1138	0.3119	1865.32	1865.96	7236.6	1	1935.1	82.1	4	K.AAREELSVWTEEECR.N
*	HsH2AZ-FLAG_293_	2.9008	0.2561	1085.23	1086.236	6003.9	1	864.8	75	2	K.DFHLIQANK.V
*	HsH2AZ-FLAG_293_	2.9176	0.106	1088.16	1086.236	6409.7	5	1047.6	81.2	1	K.DFHLIQANK.V
*	HsH2AZ-FLAG_293_	4.0661	0.2715	1393.31	1393.542	6190.6	1	1143.8	73.1	1	K.VEGLHINGPTGGNK.K
gi|5031573|re	3	12	20.80%	418	47371	5.9	ARP3 actin-related protein 3 homolog [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.0823	0.2946	2193.16	2193.514	4185.3	1	865.3	60.5	5	K.LGYAGNTEPQFIIPSCIAIK.E
*	HsFLAG-Lin9_Ti_203	6.5406	0.4366	3060.52	3060.438	7570.3	1	2052.8	37.9	3	R.TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK.H
*	HsFLAG-Lin9_Ti_204	4.5798	0.3345	4317.93	4318.795	9845.5	1	1158.3	23.6	4	R.FLGPEIFFHPEFANPDFTQPISEVVDEVIQNCPIDVR.R
gi|5453842|re	4	9	20.80%	394	43813	6.6	proliferation-associated 2G4, 38kDa [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.1323	0.3596	2348.57	2349.624	7920.6	1	904.9	50	1	K.GIAFPTSISVNNCVCHFSPLK.S

*	HsFLAG-Lin9_Ti_20	3.6711	0.3643	3239.76	3237.643	10497.3	1	1105.8	25.8	1	K.IDLGVHVDGFIANVAHTFVVDVAQGTQVTGR.K
*	HsFLAG-Lin9_Ti_20	3.5101	0.356	1927.85	1928.155	6049.1	1	770.9	56.2	2	R.LVKPGNQNTQVTEAWNK.V
*	HsFLAG-p53-DNA-D	4.4101	0.2686	1630.99	1630.884	5271.7	1	1227.9	83.3	5	K.HELLQPFNVLYEK.E
gi|14702171|r	3	9	20.70%	275	31441	4.9	PolII_Rpb3 {DNA directed RNA polymerase II polypeptide C; polymerase (RNA) II (DNA directed) polypeptide				
gi|14702173|r	3	9	20.70%	275	31441	4.9	PolII_Rpb3 {DNA directed RNA polymerase II polypeptide C; polymerase (RNA) II (DNA directed) polypeptide				
	HsFlag-NUFIP_Ti_1	3.6888	0.2507	1511.58	1511.799	2757.5	1	577.4	76.9	4	R.LGLIPLISDDIVDK.L
	HsFLAG-p53-DNA-D	2.6792	0.2839	2038.84	2037.196	9328.4	1	684.8	47.1	1	K.WNPTAGVAFEYDPDNALR.H
	HsSrcap_Ti_204.422	4.9448	0.2903	2804.65	2805.166	7512.4	1	1314	33.3	4	R.FYYNVESCGSLRPETIVLSALSGLK.K
gi|38488718|r	14	39	20.60%	878	98172	8.2	hypothetical protein LOC54891 [Homo sapiens]				
*	HsFLAG-ARP5_Ti_1	3.8602	0.3035	2158.45	2159.372	7441.5	1	528	44.1	2	K.HIHFSEVDNKPLCSYSPK.L
*	Hs293Flag-Ies2_Ti_1	4.0867	0.3439	1676.83	1676.922	5301	1	931	69.2	1	R.YCNSHLQVLGFIPK.K
*	HsFLAG-ARP5_Ti_1	4.6532	0.2797	3007.95	3008.265	9318.4	1	1288.8	32.3	3	R.VPLHYLETELEDPFAFNEEDDDLKK.G
*	HsFLAG-FLJ20309_	6.6047	0.3514	2632.49	2632.954	5992.6	1	1224.3	38.5	4	K.SPQPQNTSLPMQGVAPTTHTIAQAR.Q
*	Hs293Flag-Ies2_Ti_1	3.5053	0.3054	1136.16	1136.383	4150.3	1	912.2	94.4	5	K.RPLPLLPSSR.A
*	HsFLAG-ARP8_Ti_2	3.7844	0.3156	1483.26	1481.617	5278.8	1	629.1	66.7	7	K.ATAFSPHFSCISR.L
*	HsFLAG-ARP5_Ti_1	4.0309	0.2997	2484.86	2484.822	9850.2	1	1072.2	33.3	1	R.KALLQAASKEPECTGQLIQELR.R
*	HsFLAG-FLJ20309_	4.4145	0.3691	2354.58	2356.648	12141.7	1	1626.6	36.2	2	K.ALLQAASKEPECTGQLIQELR.R
*	HsFLAG-FLJ20309_	4.0495	0.3242	2355.76	2356.648	5244	1	327.6	42.5	1	K.ALLQAASKEPECTGQLIQELR.R
*	HsFLAG-FLJ20309_	3.5915	0.1157	1575.41	1573.709	6544	2	902.4	70.8	1	K.EPECTGQLIQELR.R
*	HsFLAG-FLJ20309_	4.5015	0.3045	1517.17	1517.689	5412.3	1	1236.4	76.9	6	K.LREVEPAACSGTVK.G
*	HsFLAG-FLJ20309_	3.0964	0.215	1248.41	1248.342	5216.6	4	535	63.6	1	R.EVEPAACSGTVK.G
*	HsFLAG-FLJ20309_	4.3856	0.2249	3016.04	3016.226	7859.4	1	762	29	2	K.FADGQQCSVPVFDITHQTPLCEEHAK.K
*	HsFLAG-ARP5_Ti_1	3.7649	0.387	1685.98	1686.815	7917	1	1303.5	73.1	3	R.LPDDLQDFDFFEGK.N
gi|4505895|re	6	16	20.60%	514	57194	9.2	pleiotropic regulator 1 (PRL1 homolog, Arabidopsis) [Homo sapiens]				
*	HsFlag-NUFIP_Ti_2	3.5707	0.2244	2525	2523.783	8117.6	1	948.8	33.3	1	K.RTHDMFVADNGKPVPLDEESHK.R
*	HsFlag-NUFIP_Ti_2	3.6807	0.237	1473.96	1473.687	7506.5	1	858.4	62.5	2	R.NEYGPVLHMPTSK.E
*	HsFlag-VPS71_Ti_1	3.343	0.23	1317.26	1317.401	7145.3	1	912	68.2	3	K.GPQNATDSYVHK.Q
*	HsFLAG-ARP6_Ti_1	3.8371	0.4074	1942.65	1943.266	10000.5	1	1467.6	58.3	3	R.MPSESAAQSLAVALPLQTK.A
*	HsFLAG-p53-DNA-D	3.8604	0.3599	1436.85	1437.552	5475.8	1	1127.8	79.2	5	R.HYTFASGSPDNIK.Q
*	HsFlag-NUFIP_Ti_2	5.3795	0.4265	2866.38	2867.024	9658.7	1	1102.1	28.8	2	R.VHAAVQPGSLDSESGIFACAFDQSESR.L
gi|7706322|re	3	6	20.50%	244	28068	6.7	chromosome 14 open reading frame 166 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.1266	0.2368	1813.76	1814.005	8958.1	1	720.8	53.3	2	K.NAEPLINLDVNNPDFK.A
*	HsFLAG-p53-DNA-D	4.2964	0.242	1498.53	1498.827	6441.6	1	1515.8	73.1	2	K.AGVMALANLLQIQR.H
*	HsFLAG-FLJ20729_	3.4462	0.3064	2153.97	2154.431	8325	1	773.7	47.4	2	K.HILGFDTGDAVLNEAAQILR.L
gi|4506713|re	2	13	20.50%	156	17965	9.6	ubiquitin and ribosomal protein S27a precursor [Homo sapiens]				
gi|88952640|r	2	13	20.50%	156	17967	9.5	PREDICTED: similar to ubiquitin and ribosomal protein S27a precursor [Homo sapiens]				
gi|88943644|r	2	13	20.50%	156	17967	9.5	PREDICTED: similar to ubiquitin and ribosomal protein S27a precursor [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.7329	0.5119	2171.87	2173.25	8988.6	1	1026.7	52.8	9	R.ECPSDECGAGVFMASHFDR.H
	HsFlag-NUFIP_Ti_1	4.3192	0.3503	1736.56	1735.829	8161.8	1	1281.1	70.8	4	K.CCLTYCFNKPEDK.-
gi|24430155|r	4	7	20.40%	387	43508	5.3	proteasome 26S ATPase subunit 4 isoform 2 [Homo sapiens]				
gi|5729991|re	4	7	18.90%	418	47366	5.2	proteasome 26S ATPase subunit 4 isoform 1 [Homo sapiens]				
	HsFlag-VPS71_Ti_1	5.0933	0.3298	3632.48	3631.975	4176	1	406.1	25	3	K.AQDEIPALSVSRPQTGLSFLGPEPEDLEDLYSR.Y
	HsFlag-FLJ90652_2	3.2742	0.1407	937.48	937.087	7372.2	1	1426	93.8	1	K.PNASVALHK.H

	HsFLAG-ARP6_Ti_1	3.2119	0.259	1944.94	1945.22	6809.3	1	567	52.9	2	K.ENAPAIIFIDEIDAIATK.R
	HsFLAG-ARP6_Ti_1	3.2781	0.26	2204.73	2204.546	9235.4	1	655.1	44.4	1	R.ILLELLNQMDGFDQNVNVK.V
gi|38569503|r	6	16	20.20%	491	55217	9.7	ATP-dependent RNA helicase ROK1 isoform b [Homo sapiens]				
gi|38569505|r	6	16	16.50%	599	67498	9.7	ATP-dependent RNA helicase ROK1 isoform a [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	5.9566	0.4572	2656.77	2657.94	9957.7	1	1853.6	37.5	2	K.IHVQGTDLPDPIATFQQLDQEYK.I
	HsARP6-FLAG_Ti_1	3.0485	0.1279	1474.47	1475.873	4974.9	1	772.8	66.7	2	K.TLAFSIPILMQLK.Q
	HsFLAG-Lin9_Ti_20	3.4674	0.2361	1304.5	1304.532	6748.3	5	1107	75	2	K.KFDILVTTPNR.L
	HsFLAG-FLJ20309_	3.4778	0.374	2137.59	2138.336	8599.5	1	622.1	44.7	1	R.NSAVETVEQELLFVGSETGK.L
	HsFLAG-p53-DNA-D	4.1982	0.4386	1666.71	1666.915	8405.4	1	1182.5	65.4	6	K.AITFFTEDDKPLLR.S
	HsFLAG-Lin9_Ti_20	4.6278	0.4202	1972.88	1974.23	7097.1	1	1319.2	64.7	3	R.SVANVIQQAGCPVPEYIK.G
gi|31543831|r	5	7	20.20%	451	51170	6.1	tubulin, gamma 1 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	3.2054	0.2966	1341.54	1342.581	6542.8	1	626.6	63.6	2	R.VIHSILNSPYAK.L
	HsFLAG-ARP6_Ti_1	3.305	0.2505	1343.14	1342.581	7834	3	944.7	68.2	2	R.VIHSILNSPYAK.L
	HsFLAG-Lin9_Ti_20	4.7909	0.4138	3256.62	3256.473	9755.1	1	1039.3	25.8	1	R.EADGSDSLEGFVLCHSIAGGTGSGLGSYLLER.L
	HsSrcap_Ti_205.297	5.1965	0.4868	2338.53	2338.684	6263.4	1	1314	55	1	R.LHFLMTGYTPLTTDQSVASVR.K
	HsFLAG-Lin9_Ti_20	4.0816	0.233	3093.1	3092.348	9244	6	629.7	25	1	R.EIVQQLIDEYHAATRPDYISWGTQEQ.-
gi|15147219|r	2	3	20.20%	312	33241	5.4	purine-rich element binding protein B [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	5.2958	0.3298	3257.48	3257.454	9290	1	1821.7	31.5	1	R.DSLGDFIEHYAQLGPSSPEQLAAGAEEGGGPR.R
*	HsFlag-NUFIP_Ti_1	3.5189	0.2767	2869.08	2869.209	6110.5	1	473.2	33.3	2	R.GGGGFGAGPGPGGLQSGQTIALPAQGLIEFR.D
gi|4506697|re	7	32	20.20%	119	13373	9.9	ribosomal protein S20 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	2.2873	0.1463	1247.65	1248.425	3431.7	2	263.3	60	2	K.TPVEPEVAIHR.I
*	HsFlag-NUFIP_Ti_1	3.7125	0.2652	1248.28	1248.425	5086.8	1	1353.4	90	8	K.TPVEPEVAIHR.I
*	HsFlag-NUFIP_Ti_1	4.336	0.234	1248.75	1248.425	7182.7	1	2541.2	67.5	1	K.TPVEPEVAIHR.I
*	HsFlag-NUFIP_Ti_11	3.1041	0.2467	1507.75	1507.773	4287.3	1	410.9	62.5	2	K.RLIDLHSPSEIVK.Q
*	HsFlag-NUFIP_Ti_11	3.9451	0.3339	1507.86	1507.773	7838	1	1154.9	75	10	K.RLIDLHSPSEIVK.Q
*	HsFlag-NUFIP_Ti_1	3.9537	0.2723	1351.31	1351.586	7015.9	1	1088.4	77.3	4	R.LIDLHSPSEIVK.Q
*	HsFlag-NUFIP_Ti_1	3.0778	0.2821	1351.57	1351.586	6212.5	1	620.4	59.1	5	R.LIDLHSPSEIVK.Q
gi|4504431|re	1	4	20.20%	109	11832	10.6	high mobility group AT-hook 2 isoform a [Homo sapiens]				
gi|62912484|r	1	4	23.90%	92	10063	11.9	high mobility group AT-hook 2 isoform c [Homo sapiens]				
gi|62912482|r	1	4	20.80%	106	11456	12	high mobility group AT-hook 2 isoform b [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	4.7545	0.3628	2036.58	2036.166	6046.6	1	1085.5	57.1	4	R.GEGAGQPSTSAQGQPAAPAPQK.R
gi|54112121|r	15	82	20.10%	1217	135577	5.3	splicing factor 3b, subunit 3 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	2.5683	0.1839	959.34	960.078	6034	1	501.2	71.4	4	K.IHQETFGK.S
*	HsARP6-FLAG_Ti_1	2.9235	0.2375	1196.54	1196.389	6632.5	2	719.2	70	2	R.LTISSPLEAHK.A
*	HsFLAG-ARP6_Ti_2	4.2724	0.1837	1304.38	1304.532	5511.5	1	1569.9	86.4	13	R.FLAVGLVDNTVR.I
*	HsARP6-FLAG_Ti_1	3.6245	0.3358	1489.09	1489.623	5319.4	1	1118.9	76.9	2	R.TVLDPVTGDLSDTR.T
*	HsFLAG-Lin9_Ti_20	4.6583	0.2577	3886.67	3888.289	8002.9	1	623.5	22.1	1	R.FHLTPLSYETLEFASGFASEQCPEGIVAISTNTLR.I
*	HsFlag-NUFIP_Ti_1	4.8307	0.4397	1921.74	1922.237	6168.2	1	955	59.4	17	K.LGAVFNQVAFPLQYTPR.K
*	HsFLAG-p53-DNA-D	4.7603	0.2803	2998.18	2999.35	5802.8	1	932.4	34	1	R.KFVIHPESNNLIIIETDHNAYTEATK.A
*	HsFlag-VPS71_Ti_1	5.9777	0.3355	2871.56	2871.176	4722.4	1	1148.7	38.5	6	K.FVIHPESNNLIIIETDHNAYTEATK.A
*	HsFlag-VPS71_Ti_1	5.9559	0.4701	2535.09	2534.887	6087.6	1	1179.8	52.2	9	R.ELAAEMAAAFLNENLPESIFGAPK.A
*	HsFLAG-FLJ20729_	3.767	0.4333	1786.27	1785.994	10366.2	1	1130	56.7	2	R.FSNTGEDWYVLVGVAK.D
*	HsFLAG-UTX1_Ti_2	4.6572	0.4099	1683.65	1682.917	3625.5	1	949.5	76.7	18	K.TPVEEVPAAIAPFQGR.V

*	HsFlag-NUFIP_Ti_11	5.2998	0.4298	1680.51	1680.907	6166.9	1	2609.2	92.9	1	K.HIANYISGIQTIGHR.V
*	HsFlag-VPS71_Ti_1	3.7027	0.33	1927.02	1927.118	5889.1	1	987.2	58.8	1	R.WVTTASLLDYDTVAGADK.F
*	HsFLAG-ARP6_Ti_1	3.2	0.3271	2110.14	2111.254	9813.8	1	531.1	47.1	1	K.NVIDGDLCEQFNSMEPNK.Q
*	HsFLAG-UTX1_Ti_2	4.0555	0.2707	1700.22	1700.843	8037	1	1613.4	71.4	4	K.NVSEELDRTPPEVSK.K
gi|31881687|r	4	11	20.10%	363	39682	8	replication factor C 4 [Homo sapiens]				
gi|4506491|re	4	11	20.10%	363	39682	8	replication factor C 4 [Homo sapiens]				
	HsFlag-DPCD_Ti_20	3.0867	0.1338	1229.83	1230.447	7354.2	1	1108.5	72.7	2	K.GTSISTKPPLTK.D
	HsFlag-VPS71_Ti_1	4.8002	0.3743	2047.86	2047.315	4999.8	1	852.4	55.3	4	K.SLEGADLPNLLFYGPPGTGK.T
	HsFLAG-Lin9_Ti_20	3.6369	0.297	1326.36	1326.576	6153.7	2	1252	75	1	K.VITDIAGVIPAEK.I
	HsFLAG-p53-DNA-D	5.2275	0.4047	3088.32	3088.358	8734.5	1	1252.6	31.5	4	K.DLIDEGHAATQLVNQLHDVVVENNLSDK.Q
gi|4557032|re	5	6	20.10%	334	36639	6.1	lactate dehydrogenase B [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.3674	0.4121	1631.21	1630.833	7588.4	1	1534.4	71.4	1	K.SLADELALVDVLEDK.L
	HsFlag-VPS71_Ti_1	3.4513	0.3412	1249.89	1249.332	4382.8	1	752.9	77.3	2	R.VIGSGCNLDSAR.F
*	HsFLAG-ARP6_Ti_1	1.8333	0.2619	1012.23	1012.255	3583.5	1	392.7	68.8	1	R.IHPVSTMVK.G
*	HsFLAG-ARP6_Ti_1	3.0858	0.1392	2298.16	2297.64	8875.9	1	653.3	42.1	1	K.GMYGIENEVFLSLPCILNAR.G
*	HsFLAG-Lin9_Ti_20	2.9677	0.1146	1287.42	1287.499	8547.9	3	1137.7	80	1	K.LKDDEVAQLKK.S
gi|20149643|r	8	25	20.00%	470	53846	5.9	hypothetical protein LOC54680 [Homo sapiens]				
*	HsFLAG-TIP49a_Ti_	3.6345	0.281	1226.62	1226.335	5667.8	1	1153.9	79.2	3	K.SGGGLHSVAEGVR.L
*	HsFLAG-TIP49a_Ti_	3.1253	0.2384	2012.72	2013.214	6182.3	1	473.8	50	1	R.LAGQWVEQEVEDRPEVK.D
*	HsFLAG-TIP49a_Ti_	5.2489	0.3088	3068.07	3068.367	7085.5	9	619.4	26	3	R.LAGQWVEQEVEDRPEVKDENAGVLEVK.Q
*	HsFLAG-TIP49a_Ti_	3.8375	0.3091	1605.52	1604.813	4108.4	1	818.9	76.9	5	K.VKEEPPINHPVGCK.R
*	HsFLAG-TIP49a_Ti_	3.6575	0.2552	1581.76	1581.766	4638.4	1	1167.4	83.3	1	K.LQFPQSQAEYIEK.R
*	HsFlag-NUFIP_Ti_2	3.606	0.2622	1674.47	1673.947	5897.3	1	1108.7	73.1	7	K.TINEILKPYIDPEK.S
*	HsFLAG-TIP49a_Ti_	2.7575	0.1632	1524.47	1524.887	5222.2	2	528.1	54.2	3	K.VIIEYPTLHVVLK.G
*	HsFLAG-TIP49a_Ti_	3.2453	0.2331	1524.64	1524.887	4240.4	1	964.5	79.2	2	K.VIIEYPTLHVVLK.G
gi|4557491|re	3	6	20.00%	431	48358	6.6	cleavage stimulation factor subunit 1 [Homo sapiens]				
gi|75709220|r	3	6	20.00%	431	48358	6.6	cleavage stimulation factor subunit 1 [Homo sapiens]				
gi|75709217|r	3	6	20.00%	431	48358	6.6	cleavage stimulation factor subunit 1 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	5.0614	0.4014	4366.41	4367.095	8348.7	1	838.9	23	2	K.LIISQLLYDGYISIANGLINEIKPQSVCAPSEQLLHLIK.L
	HsFlag-VPS71_Ti_1	4.7282	0.3282	2961.31	2961.224	5669.8	1	931.7	32	2	R.TLYDHVDEVTCLAFHPTEQILASGSR.D
	HsFLAG-p53-DNA-D	5.2043	0.473	2310.03	2310.618	6630.7	1	1520.7	62.5	2	R.SISFHPSGDFILVGTQHPTLR.L
gi|21704261|r	2	3	20.00%	160	18275	6.3	MAX protein isoform a [Homo sapiens]				
gi|21704263|r	2	3	21.20%	151	17202	6.5	MAX protein isoform b [Homo sapiens]				
	HsFlag-NUFIP_Ti_2	3.7095	0.1937	1357.01	1355.54	7836.6	1	1319.4	80	2	K.RQNALLEQQVR.A
	HsFLAG-Lin9_Ti_20	2.9508	0.3098	2289.99	2290.405	6338.9	1	420.6	40	1	R.SSAQLQTNYPSSDNSLYTNAK.G
gi|16117794|r	3	5	20.00%	105	12254	11.6	ribosomal protein L36 [Homo sapiens]				
gi|16117796|r	3	5	20.00%	105	12254	11.6	ribosomal protein L36 [Homo sapiens]				
	HsVPS71-FLAG_Ti_	2.0229	0.1047	992.53	993.209	3768.5	3	375.4	68.8	2	R.YPMAVGLNK.G
	HsFLAG-ARP6_Ti_1	3.8143	0.3767	1389.88	1389.613	6002.7	1	811	72.7	2	K.REELSNVLAAMR.K
	HsFLAG-ARP6_Ti_1	2.7247	0.1941	1233.48	1233.425	6213	1	806.1	75	1	R.EELSNVLAAMR.K
gi|16753225|r	5	32	19.90%	216	23503	10.9	ribosomal protein L14 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	2.7312	0.2694	1232.42	1233.412	5953.7	1	613.7	63.6	4	R.VAYVSFGPHAGK.L
	HsFLAG-ARP6_Ti_1	3.5293	0.3627	1233.18	1233.412	5200.2	1	903.9	77.3	4	R.VAYVSFGPHAGK.L

	HsFLAG-ARP6_Ti_1	4.7851	0.2923	1355.35	1355.577	8307.7	1	2317.2	86.4	21	K.LVAIVDVIDQNR.A
	HsFLAG-Lin9_Ti_20	3.2918	0.3123	1217.15	1216.346	6769.9	1	936	75	2	R.ALVDGPCTQVR.R
*	HsFLAG-p53-DNA-D	1.8314	0.0896	951.48	952.06	3864.9	4	355.6	64.3	1	K.FPHSAHQK.Y
gi|31542319|r	4	8	19.80%	308	34482	5.1	epsilon subunit of coatomer protein complex isoform a [Homo sapiens]				
gi|40805825|r	4	8	23.70%	257	28797	5.3	epsilon subunit of coatomer protein complex isoform b [Homo sapiens]				
	HsSrcap_Ti_203.253	4.3121	0.1862	2155.65	2156.487	4024.6	1	466.6	47.4	2	K.FGVVLDEIKPSSAPELQAVR.M
	HsSrcap_Ti_203.253	5.913	0.3301	2156.85	2156.487	7373.6	1	1820.5	44.7	4	K.FGVVLDEIKPSSAPELQAVR.M
	HsFlag-VPS71_Ti_1	3.679	0.2498	1574.19	1573.743	6253.7	2	835.2	65.4	1	R.WEAAEGLLQEALDK.D
	HsSrcap_Ti_204.404	3.5584	0.2792	2980.12	2978.375	3222.7	8	229.4	26.9	1	K.DSGYPETLVNLIVLSQHLGKPPEVTNR.Y
gi|5174745|re	2	16	19.80%	91	10755	4.4	ubiquinol-cytochrome c reductase hinge protein [Homo sapiens]				
*	HsSrcap_Ti_204.306	5.3125	0.3864	2236.88	2237.31	6994.1	1	1285.5	45.6	8	R.SHTEEDCTEELFDFLHAR.D
*	HsSrcap_Ti_206.282	6.3792	0.4489	2238.37	2237.31	9828.9	1	2550.7	70.6	8	R.SHTEEDCTEELFDFLHAR.D
gi|19913406|r	20	67	19.70%	1531	174384	8.7	DNA topoisomerase II, alpha isozyme [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	3.9805	0.1768	1462.4	1462.643	8120.4	1	1780.5	79.2	3	K.IFDEILVNAADNK.Q
*	HsFLAG-Lin9_Ti_20	4.6434	0.3723	1927.47	1928.152	6897	1	1066.2	62.5	9	R.VTIDPENNLISIWNNGK.G
	HsFLAG-FLJ20729_	2.6641	0.3413	1234.61	1235.469	4339	5	421.9	70	1	K.GIPVVEHKVEK.M
*	HsFLAG-p53-DNA-D	5.8809	0.454	2519.43	2520.813	9032.2	1	1630.3	54.8	7	K.MYVPALIFGQLLTSSNYDDDEK.K
*	HsFLAG-FLJ20729_	4.6343	0.3758	2519.72	2520.813	9413.1	1	1721.5	38.1	1	K.MYVPALIFGQLLTSSNYDDDEK.K
*	HsFLAG-p53-DNA-D	3.9644	0.3189	1082.41	1082.202	7747.9	1	1528	88.9	2	R.RAYDIAGSTK.D
*	HsFLAG-FLJ20309_	2.6583	0.1129	1132.31	1132.267	4889.7	1	679.5	81.2	1	K.VIHEQVNHR.W
*	HsFLAG-Lin9_Ti_20	4.1093	0.4761	1627.54	1627.838	5708.5	1	1051.3	67.9	2	K.GFQQISFVNSIATSK.G
*	HsFLAG-Lin9_Ti_20	5.2859	0.4513	1730.12	1731.011	8014.9	1	1508.1	66.7	12	K.AAIGCGIVESILNWVK.F
	HsFLAG-p53-DNA-D	3.7293	0.2984	1336.52	1336.614	7630.8	1	1623.8	85	2	R.FLEEFITPIVK.V
*	HsFLAG-p53-DNA-D	3.5972	0.3503	2176.38	2177.436	8428.3	1	862	53.1	1	K.NKQEMAFYSLPEFEEWK.S
*	HsFLAG-FLJ20729_	3.6398	0.3669	1672.42	1671.801	8452.5	1	1345.1	63.3	2	K.YSGPEDDAAISLAFSK.K
*	HsFLAG-Lin9_Ti_20	3.683	0.3138	2956.41	2957.306	6943.5	1	624	35.4	2	K.LLGLPEDYLYGQTTTYLTYNDFINK.E
*	HsFLAG-p53-DNA-D	3.8889	0.4031	1301.47	1302.574	7336	1	1543.7	85	1	R.YIFTMLSSLAR.L
*	HsFLAG-FLJ20729_	3.8677	0.3385	2764.73	2765.107	8593.3	1	837.4	39.1	4	K.SDSVTDSGPTFNYLLDMPLWYLTK.E
*	HsFLAG-p53-DNA-D	4.9227	0.3837	2620.83	2621.901	8951	1	1098	45.5	5	K.SPSDLWKEDLATFIEELEAVEAK.E
*	HsFLAG-FLJ20309_	4.021	0.3073	1807.69	1807.992	9769.3	1	1945.4	70	2	K.EDLATFIEELEAVEAK.E
*	HsFLAG-Lin9_Ti_20	4.4745	0.4195	2044.79	2046.109	5318.2	1	888.4	61.1	1	K.NENTEGSPQEDGVELEGLK.Q
*	HsFLAG-p53-DNA-D	3.2949	0.4441	2704.62	2705.981	9352.6	1	509.2	34	1	K.GSVPLSSSPPATHFPDETEITNPVPK.K
*	HsFLAG-p53-DNA-D	4.2004	0.3499	1780.63	1780.979	5936.8	1	956.8	65.6	8	K.RDPALNSGVSQKPDPAK.T
gi|4507677|re	13	43	19.70%	803	92469	4.8	tumor rejection antigen (gp96) 1 [Homo sapiens]				
	HsFlag-VPS71_Ti_1	2.6074	0.2479	1275.61	1276.386	3329.6	2	220.6	59.1	1	R.ELISNASDALDK.I
*	HsFLAG-FLJ20729_	3.5658	0.2661	2046.46	2047.267	8170.2	1	624.8	44.4	1	R.LISLTDENALSGNEELTVK.I
*	HsFLAG-p53-DNA-D	3.4944	0.3046	1513.89	1514.74	6958.1	4	561.8	53.8	2	K.NLLHVTDTGVGMTR.E
*	HsFlag-VPS71_Ti_1	3.8423	0.1142	2115.88	2113.437	6284.4	1	913.7	38.9	1	K.NLLHVTDTGVGMTREELVK.N
*	HsFLAG-p53-DNA-D	4.3139	0.3291	2006.8	2008.327	6914.8	1	1796.1	73.3	2	K.KYSQFINFPIYVWSSK.T
*	HsFLAG-p53-DNA-D	4.839	0.3617	1879.47	1880.153	5945.1	1	1431.6	75	16	K.YSQFINFPIYVWSSK.T
*	HsFLAG-ARP6_Ti_1	3.3014	0.3266	1866.91	1867.782	6626.6	1	730.1	56.7	2	K.EESDDEAAVEEEEEEK.K
*	HsFLAG-FLJ20729_	4.3079	0.273	1485.92	1486.622	5137.7	1	1227.4	73.1	2	K.GVVDSDDLPLNVSR.E
*	HsFLAG-ARP6_Ti_1	5.3248	0.3087	2260.43	2261.412	9582.1	1	2102.3	45.8	6	R.FQSSHHPTDITSLDQYVER.M

*	HsFLAG-ARP6_Ti_1	4.1683	0.3744	2260.63	2261.412	5242.4	1	597.3	52.8	6	R.FQSSHHPTDITSLDQYVER.M
*	HsFLAG-Lin9_Ti_20	3.7747	0.2621	3077.59	3078.408	5737.3	1	849.1	32	2	K.KGYEVIYLTEPVDEYCIQALPEFDGK.R
*	HsFLAG-p53-DNA-D	4.5311	0.2731	3234.68	3234.596	9819.8	1	860.5	26.9	1	K.KGYEVIYLTEPVDEYCIQALPEFDGKR.F
*	HsFLAG-FLJ20729_	3.5806	0.3674	1762.5	1762.1	10963.1	1	1126	56.7	1	K.TVLDLAVVLFETATLR.S
gi|17298690|r	6	18	19.70%	542	58172	5.3	fuse-binding protein-interacting repressor isoform b [Homo sapiens]				
gi|17978512|r	6	18	19.10%	559	59876	5.3	fuse-binding protein-interacting repressor isoform a [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.1578	0.3027	1763.59	1763.044	4523	1	545.8	60	2	K.LGLPPLTPEQQEALQK.A
	HsFlag-VPS71_Ti_1	4.2901	0.3964	2363.05	2363.636	3738.5	1	496.1	50	3	K.VGRPSNIGQAQPIIDQLAEEAR.A
	HsFlag-VPS71_Ti_1	5.3917	0.375	2364.43	2363.636	6732.2	1	1260.2	36.9	4	K.VGRPSNIGQAQPIIDQLAEEAR.A
	HsFlag-VPS71_Ti_1	4.6394	0.4738	2387.88	2388.614	5301	1	1114	57.1	3	K.AQSSQDAVSSMNLFDLGGQYLR.V
	HsFLAG-FLJ20729_	4.6017	0.2193	2796.35	2796.341	6431.5	1	912.6	30	2	K.AVTPPMPLLTPATPGGLPPAAAVAAAAATAK.I
	HsFlag-DPCD_Ti_20	4.9181	0.4994	1824.29	1824.813	7453.9	1	2092.2	76.7	4	K.DIDDDLEGEVTEECGK.F
gi|9910244|re	4	9	19.70%	360	41280	7.9	mitochondrial ribosomal protein S22 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	3.7527	0.2315	1385.51	1385.646	6701.8	1	1069.7	72.7	4	K.PAIQELKPPTYK.L
*	HsFlag-NUFIP_Ti_1	4.7674	0.3782	2164.61	2165.51	11219.6	1	1545.3	58.3	1	K.MPPVLEERVPINDVLAEDK.I
*	HsFlag-NUFIP_Ti_1	3.6605	0.3077	1588.08	1586.915	8442.8	1	972.4	66.7	2	K.ILTPIIFKEENLR.T
*	HsFlag-NUFIP_Ti_1	5.0816	0.3623	2920.04	2920.208	7304.9	1	838.2	29.8	2	R.DLIDDATNLVQLYHVLHPDGQSAQGAK.D
gi|41148736|r	5	17	19.70%	295	32707	4.8	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma lamini				
gi|89028699|r	5	17	19.70%	295	32707	4.8	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma lamini				
gi|89028697|r	5	17	19.70%	295	32707	4.8	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma lamini				
gi|89028693|r	5	17	21.70%	267	29710	5.5	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma lamini				
gi|89028091|r	5	17	19.70%	295	32707	4.8	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma lamini				
gi|89028089|r	5	17	19.70%	295	32707	4.8	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma lamini				
gi|89028084|r	5	17	21.70%	267	29710	5.5	PREDICTED: similar to 40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon carcinoma lamini				
	HsFlag-NUFIP_Ti_1	3.5193	0.3235	2616.14	2618.967	9326.7	1	632.1	36.4	3	K.FLAAGTHLGGTNLDFQMEQYIYK.R
	HsFlag-NUFIP_Ti_1	4.6361	0.1686	2617.8	2618.967	11645.9	1	1168.9	31.8	1	K.FLAAGTHLGGTNLDFQMEQYIYK.R
	HsFlag-NUFIP_Ti_1	3.2111	0.1384	1136.52	1136.334	3726.7	3	871.1	83.3	9	K.SDGIYIINLK.R
	HsFLAG-TCF3_Ti_1	3.9474	0.3587	1742.78	1741.982	7911.5	1	1408.1	65.6	3	R.AIVAIENPADVSVISSR.N
	HsFlag-NUFIP_Ti_1	3.0509	0.2708	913.3	913.105	4232	2	978	92.9	1	R.LLVVTDPR.A
gi|57242798|r	5	12	19.60%	455	50814	5.6	acid sphingomyelinase-like phosphodiesterase 3B isoform 1 [Homo sapiens]				
gi|57242800|r	5	12	23.90%	373	41689	6.2	acid sphingomyelinase-like phosphodiesterase 3B isoform 2 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.7254	0.4057	1470.2	1469.643	7517.6	1	1140.5	70.8	2	K.VYAALGNHDFHPK.N
	HsFLAG-ARP6_Ti_1	3.8833	0.4186	2207.25	2208.438	6498.7	1	858	55.6	3	K.NQFPAGSNNIYNQIAELWK.P
	HsFLAG-ARP6_Ti_1	4.6514	0.4335	1963.3	1964.289	4932.2	1	1475.1	76.5	3	K.AGDMVYIVGHVPPGFFEK.T
	HsFLAG-ARP6_Ti_1	4.2575	0.4262	2509.1	2510.969	2994.5	1	507.2	52.3	2	R.MLYDDAGVPISAMFITPGVTPWK.T
	HsFLAG-ARP6_Ti_1	3.438	0.3269	1594.61	1594.811	5878.8	1	603.9	53.3	2	K.TTLPGVVNGANNPAIR.V
gi|31742498|r	10	20	19.50%	717	80311	6.7	unc-84 homolog B [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.8711	0.1928	1302.03	1302.346	6962.5	1	924.8	75	1	R.DSSPHFQAEQR.V
*	HsFLAG-ARP6_Ti_1	4.0541	0.4996	1750.32	1750.952	7646.7	1	837.5	60.7	2	R.RLEALAAEFSSNWQK.E
*	HsFLAG-ARP6_Ti_1	4.7236	0.2893	2081.19	2081.42	8412.6	1	1482.9	58.3	4	R.RLEDQLAGLQQELAALALK.Q
*	HsFLAG-TCF3_Ti_1	5.0036	0.387	2010.76	2010.213	4451.5	1	1032.5	68.8	1	R.DDVESQFPAWISQFLAR.G
*	HsFLAG-TCF3_Ti_1	2.9328	0.2506	1226.41	1227.464	6401.7	1	748.1	65	1	K.ILTHVAEMQGK.S
*	HsFLAG-TCF3_Ti_1	3.1103	0.3414	1226.48	1227.464	5881	1	1231	85	3	K.ILTHVAEMQGK.S

*	HsFLAG-ARP6_Ti_1	3.8956	0.3805	2186.96	2187.549	3873.9	1	454.4	50	3	K.TALLSLFGIPLWYHSQSPR.V
*	Hs293Flag-Ies2_Ti_1	2.9832	0.222	1462.58	1461.748	4364.1	3	573.4	66.7	1	R.IRPTAVTLEHVPK.A
*	HsFLAG-ARP6_Ti_1	4.896	0.5047	2244.65	2244.463	8138.9	1	1501.9	60.5	1	K.DFAIFGFDEDLQQEGTLLGK.F
*	HsFLAG-ARP6_Ti_1	4.2956	0.3072	1922.96	1924.132	4281.5	1	651.3	64.3	3	R.ILTNWGHPEYTCIYR.F
gi|4503249|re	7	18	19.50%	375	42674	8.6	DEK oncogene (DNA binding) [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	5.2357	0.3482	2134.85	2135.486	7150.1	1	1714.6	63.9	5	R.LTMQVSSLQREPFTIAQGK.G
*	HsFLAG-p53-DNA-D	4.0401	0.2236	1448.57	1448.706	9381.5	4	1159.1	66.7	1	K.LLYNRPGTVSSLK.K
*	HsFLAG-p53-DNA-D	2.9421	0.1057	1577.7	1576.88	6396.9	1	692.7	61.5	1	K.LLYNRPGTVSSLKK.N
*	HsFLAG-Lin9_Ti_20	3.7392	0.3541	1358.53	1357.508	6794.6	1	1113.5	77.3	6	K.NVGQFSGFPFEK.G
*	HsFLAG-p53-DNA-D	3.5812	0.2915	1527.79	1528.743	4975.8	1	782.2	79.2	2	K.KPPTDEELKETIK.K
*	HsFLAG-p53-DNA-D	3.2607	0.1983	1656.6	1656.917	5881.9	1	869.3	73.1	2	K.KPPTDEELKETIKK.L
*	HsFLAG-p53-DNA-D	3.6226	0.2529	1791.66	1791.955	5601	1	1257.4	73.1	1	K.KVYENYPTYDLTER.K
gi|89031528|r	5	30	19.50%	261	29663	9.5	PREDICTED: similar to ribosomal protein S3a isoform 2 [Homo sapiens]				
gi|89033501|r	5	30	19.50%	261	29663	9.5	PREDICTED: similar to ribosomal protein S3a isoform 4 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	5.3162	0.3754	1954.19	1953.159	9005.6	1	1457.3	65.6	9	R.VFEVSLADLQNDEVAFR.K
	HsFLAG-ARP6_Ti_1	2.4371	0.2371	1002.2	1003.141	6614.1	8	656.9	75	2	K.LITEDVQGK.N
	HsFLAG-TCF3_Ti_1	2.225	0.0948	1345.67	1346.489	4817.4	8	250.3	60	1	R.KTSYAQHQQVR.Q
	HsFLAG-TCF3_Ti_1	3.5192	0.389	1346.3	1346.489	8913.7	1	1196.9	75	2	R.KTSYAQHQQVR.Q
	HsFLAG-ARP6_Ti_1	4.4478	0.4012	1705.36	1705.92	4182.9	1	949.7	76.9	16	K.ACQSIYPLHDVFVR.K
gi|5803111|re	5	11	19.30%	306	34820	10.1	EBNA1 binding protein 2 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.3451	0.3034	1536.24	1534.883	2417.5	1	496.7	75	2	R.GLLKPGLNVVLEGPK.K
*	HsFLAG-ARP6_Ti_1	3.4897	0.2749	1662.95	1663.057	2714.2	1	485.3	66.7	2	R.GLLKPGLNVVLEGPKK.A
*	HsFLAG-ARP6_Ti_1	4.2629	0.3455	2189.74	2190.458	4924.3	1	480.8	45.2	4	R.LDVTLGPVPEIGGSEAPAPQNK.D
*	HsFLAG-ARP6_Ti_1	2.8466	0.3083	1237.6	1237.488	7382.1	3	1026.5	77.3	1	R.QAQAAVLAVLPR.L
*	HsFLAG-ARP6_Ti_1	2.7016	0.1134	1073.36	1073.278	5881.8	4	851.7	87.5	2	K.KVQTEVLQK.R
gi|21735621|r	5	17	19.20%	338	35503	8.7	mitochondrial malate dehydrogenase precursor [Homo sapiens]				
*	HsFLAG-p53-DNA-D	6.1983	0.4626	1793.99	1794.188	6547.8	1	1681	69.4	10	K.VAVLGASGGIGQPLSLLLK.N
*	HsFLAG-p53-DNA-D	4.6117	0.3055	2366.01	2366.676	6427.8	1	694.7	47.6	1	R.LTLYDIAHTPGVAADLSHIETK.A
*	HsFLAG-p53-DNA-D	6.2351	0.3804	2366.92	2366.676	8119.5	1	2313.9	45.2	3	R.LTLYDIAHTPGVAADLSHIETK.A
*	HsFlag-NUFIP_Ti_1	2.7436	0.3209	1149.33	1148.351	3833.4	1	638.3	77.3	1	R.VNVPVIGGHAGK.T
*	HsFLAG-p53-DNA-D	3.5851	0.2351	1371.52	1371.626	5237.4	1	671.8	72.7	2	K.TIIPLISQCTPK.V
gi|13027644|r	7	42	19.20%	240	24614	11.2	small nuclear ribonucleoprotein polypeptide N [Homo sapiens]				
gi|4507135|re	7	42	19.20%	240	24614	11.2	small nuclear ribonucleoprotein polypeptide N [Homo sapiens]				
gi|4507125|re	7	42	19.90%	231	23656	10.9	small nuclear ribonucleoprotein polypeptide B/B' isoform B [Homo sapiens]				
gi|38150007|r	7	42	19.20%	240	24610	11.2	small nuclear ribonucleoprotein polypeptide B/B' isoform B' [Homo sapiens]				
gi|13027650|r	7	42	19.20%	240	24614	11.2	small nuclear ribonucleoprotein polypeptide N [Homo sapiens]				
gi|13027648|r	7	42	19.20%	240	24614	11.2	small nuclear ribonucleoprotein polypeptide N [Homo sapiens]				
gi|13027646|r	7	42	19.20%	240	24614	11.2	small nuclear ribonucleoprotein polypeptide N [Homo sapiens]				
	HsFLAG-p53-DNA-D	2.9621	0.1557	1075.95	1076.259	3894.5	2	693.3	92.9	4	K.MLQHIDYR.M
	HsFLAG-p53-DNA-D	4.4186	0.2476	1723.65	1723.873	7578.3	1	2143.8	87.5	2	K.HMNLILCDCDEFR.K
	HsFlag-NUFIP_Ti_1	4.987	0.3526	1852.53	1852.047	9814.2	1	2360.3	84.6	9	K.HMNLILCDCDEFRK.I
	HsFlag-NUFIP_Ti_1	4.4276	0.2012	1852.57	1852.047	7293.7	1	1494.6	51.9	9	K.HMNLILCDCDEFRK.I
	HsFLAG-p53-DNA-D	3.439	0.1259	1039.43	1039.353	6219.5	2	1117.9	93.8	13	K.RVLGLVLLR.G

	HsFLAG-p53-DNA-D	3.4075	0.1077	883.05	883.166	3444.4	4	848.7	92.9	2	R.VLGLVLLR.G
	HsFLAG-ARP6_Ti_1	4.6	0.4766	1555.72	1555.786	6102.5	1	1160.6	67.9	3	R.GENLVSMTVEGPPPK.D
gi|30581135|r	18	38	19.10%	1233	143233	7.6	SMC1 structural maintenance of chromosomes 1-like 1 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.556	0.3153	1524.57	1524.772	6479.6	1	1784.8	80.8	6	K.SNLMDAISFVLGEK.T
*	HsARP6-FLAG_Ti_1	3.1182	0.2614	1516.56	1516.743	4885.8	2	443.9	57.1	1	R.DLIHGAPVGKPAANR.A
*	HsFlag-VPS71_Ti_1	2.5058	0.2609	1038.61	1039.174	6286.4	1	727.5	72.2	1	R.VIVGGSSEYK.I
*	HsFLAG-Lin9_Ti_20	3.7722	0.2299	1603.03	1603.769	9364.4	1	1158.5	70.8	1	K.VVQLHEYSEELEK.L
*	HsYL1_Ti_101.1795.	2.7774	0.1412	1189.4	1189.308	4665.8	8	643.7	72.2	1	R.DLTLEENQVK.K
*	HsFlag-VPS71_Ti_1	2.9603	0.0933	1230.59	1230.407	6423.1	1	1411.4	90	1	K.RAATLAQELEK.F
*	HsFLAG-Lin9_Ti_20	2.8082	0.1962	1168.2	1168.341	9726.2	1	905.4	72.2	1	K.RLYPGSVYGR.L
*	HsFLAG-ARP6_Ti_1	4.5431	0.4053	2320.72	2321.586	4283.3	1	523.1	50	5	R.GEPETFLPLDYLEVKPTDEK.L
*	HsFlag-VPS71_Ti_1	2.5565	0.2308	1065.58	1066.246	5941.3	3	536.9	68.8	1	R.HLALNLQEK.S
*	HsARP6-FLAG_Ti_1	3.0265	0.2073	1066.13	1066.246	4155	2	830.8	87.5	1	R.HLALNLQEK.S
*	HsFLAG-p53-DNA-D	4.1869	0.2441	1448.47	1448.619	8444.9	1	1745.9	75	6	K.SKLESELANFGPR.I
*	HsFLAG-FLJ20729_	4.0029	0.1208	1518.91	1518.766	11949.9	5	1595.2	70.8	1	K.IIDETMAQLQDLK.N
*	HsYL1_Ti_101.1746.	4.6697	0.434	2486.32	2487.482	7715.9	1	1687.4	54.3	3	K.GTMDDISQEEGSSQGEDSVSGSQR.I
*	HsFLAG-FLJ20729_	4.6908	0.3986	1618.48	1618.96	7244.8	1	1075.3	67.9	1	K.TVAALALLFAIHSYK.P
*	HsFLAG-FLJ20729_	4.5259	0.2474	2261.33	2261.536	5318.7	1	1079.4	40	3	K.PAPFFVLDEIDAALDNTNIGK.V
*	HsFlag-DPCD_Ti_20	3.1817	0.2962	1965.56	1966.161	5186.6	3	446	47.1	2	K.AESLIGVYPEQGDCVISK.V
*	HsFLAG-p53-DNA-D	3.3366	0.2221	2177.71	2177.375	7657.5	2	382.2	38.9	1	K.VLTFDLTKYPDANPNPNEQ.-
*	HsFLAG-FLJ20309_	2.8542	0.2364	1258.31	1259.274	8229.8	3	897.7	65	2	K.YPDANPNPNEQ.-
gi|74136549|r	16	29	19.10%	1188	132375	8.7	AT rich interactive domain 5B (MRF1-like) [Homo sapiens]				
*	HsH2AZ-FLAG_293_	3.616	0.2477	1330.52	1330.532	8428	1	1782.3	85	1	K.AFQFHLEGKPR.I
*	HsH2AZ-FLAG_293_	3.6416	0.2511	1314.64	1314.57	4669.9	1	1126.8	90	3	R.ILSLGDFFFVR.C
*	HsH2AZ-FLAG_293_	5.1456	0.3975	1884.55	1886.121	6058	1	1748.9	78.6	6	K.DPICIAELQLLWEER.T
*	HsH2AZ-FLAG_293_	3.2116	0.3526	1629.24	1629.678	9903.3	1	803.8	57.1	1	R.NSDHGEDEVIAVSEK.V
*	HsH2AZ-FLAG_293_	3.2713	0.2065	1156.57	1156.451	6429.1	1	1450.4	88.9	1	K.VIVKLEDLVK.W
*	HsH2AZ-FLAG_293_	2.5441	0.1006	1006.35	1006.106	5162.1	4	586.6	85.7	1	K.WVHSDFSK.W
*	HsH2AZ-FLAG_293_	3.0342	0.204	973.33	973.086	6044.6	1	1079.8	87.5	2	R.CGFHAGPVK.T
*	HsH2AZ-FLAG_293_	3.577	0.3642	1368.24	1368.572	6718.9	1	1450.5	81.8	2	R.ADEQAFLVALYK.Y
*	HsH2AZ-FLAG_293_	6.0564	0.4727	2108.14	2108.195	5550.6	1	2626.2	84.2	1	K.HIYDELGGNPGSTSAATCTR.R
*	HsH2AZ-FLAG_293_	4.0225	0.2007	1865.9	1865.226	6965.5	1	1807.5	48.3	1	R.FIKGEEDKPLPPIKPR.K
*	HsH2AZ-FLAG_293_	2.7187	0.2892	1824.3	1825.075	8167.1	1	1178.8	63.3	1	K.KIEGYQEFSAKPLASR.V
*	HsH2AZ-FLAG_293_	3.2891	0.4197	1474.01	1472.725	4393.8	1	578.7	67.9	4	K.GPTPPLPSAPLAPEK.D
*	HsH2AZ-FLAG_293_	2.2438	0.3026	944.16	945.06	3117.9	4	377.5	66.7	1	K.DSALVPGASK.Q
*	HsH2AZ-FLAG_293_	4.3019	0.4794	2536.3	2536.885	7099.3	1	691.5	41.7	1	K.LLSQVSGASLSSSYPYGSPPPLISK.K
*	HsH2AZ-FLAG_293_	4.4308	0.3406	1927.27	1928.06	5045.7	1	911.4	61.1	1	K.SAAAEAPTDDQPTDLSLPK.N
*	HsH2AZ-FLAG_293_	4.4711	0.4484	1525.15	1525.702	7392	1	2099.8	82.1	2	K.VLGLAHSTTGPQESK.G
gi|4506675|re	6	13	19.10%	607	68569	6.4	ribophorin I precursor [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.9743	0.5636	1654.5	1654.864	6299.1	1	1497.3	71.9	2	K.VTAEVVLAHLGGGSTSR.A
*	HsFLAG-p53-DNA-D	2.9926	0.1405	1660.56	1660.908	9256.3	2	837.6	53.6	1	R.ATSFLLALEPELEAR.L
*	HsFLAG-ARP6_Ti_1	5.9435	0.4267	2883.8	2884.302	6775.8	1	813.5	30.2	3	K.ISVIVETVYTHVLHPYPTQITQSEK.Q
*	HsFLAG-ARP6_Ti_1	4.3329	0.3795	2010.51	2011.26	9294	1	1718.8	65.6	1	K.VHYENNSPFLTITSMTR.V

*	HsFLAG-ARP6_Ti_1	4.7308	0.3314	2998.99	2999.349	9375.4	1	1050.5	29.2	3	K.THYIVGYNLPSYEYLYNLGDQYALK.M
*	HsFLAG-ARP6_Ti_1	4.2853	0.3946	1992.53	1992.236	7226.6	1	844.2	56.2	3	R.FVDHVFDEQVIDSLTVK.I
gi|32454741|r	5	6	19.10%	418	46441	8.7	serine (or cysteine) proteinase inhibitor, clade H, member 1 precursor [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.7946	0.4455	2407.77	2406.701	8088.4	1	1550.7	38.1	1	K.AVLSAEQLRDEEVHAGLGELLR.S
*	HsFLAG-p53-DNA-D	3.8427	0.405	1660.69	1660.824	5500.2	1	1117.4	75	1	R.LYGPSSVSFADDFVR.S
*	HsFLAG-p53-DNA-D	3.841	0.3161	1984.63	1985.395	4891.1	1	867.7	59.4	1	K.LSSLIILMPHHVEPLER.L
*	HsFLAG-ARP6_Ti_1	3.761	0.2997	1338.11	1338.547	4661.5	1	1124.4	83.3	1	K.HLAGLGLTEAIDK.N
*	HsFLAG-p53-DNA-D	3.6341	0.3768	1640.25	1638.952	4840.4	1	881.8	75	2	K.LFYADHPFIFLVR.D
gi|5032087|re	12	59	19.00%	793	88886	5.2	splicing factor 3a, subunit 1, 120kDa isoform 1 [Homo sapiens]				
	HsFlag-VPS71_Ti_1	3.859	0.3669	1932.93	1932.104	4165	1	397.5	53.6	10	K.FNFLNPNDPYHAYYR.H
*	HsFLAG-ARP6_Ti_2	4.3272	0.2092	1943.18	1943.185	6043.6	1	1305.8	66.7	2	K.VMQQQQQTTQQQLPQK.V
*	HsFlag-VPS71_Ti_1	3.0923	0.2869	2660.34	2660.98	3677.5	6	241.3	34.8	4	K.EPPPEFEFIADPPSISAFDLDVVK.L
*	HsFLAG-FLJ20729_	3.9498	0.1546	2662.47	2660.98	6468.4	2	697.1	29.3	1	K.EPPPEFEFIADPPSISAFDLDVVK.L
	HsFLAG-p53-DNA-D	3.6132	0.3732	2465.63	2466.761	10276.1	1	869.3	47.2	1	R.NYQFDFLRPQHSLFNYFTK.L
	HsFLAG-UTX1_Ti_2	4.7779	0.3889	2378.04	2378.728	6818.9	1	970.2	34.1	10	K.ASKPLPPAPAPDEYLVSPITGEK.I
	HsFLAG-ARP6_Ti_1	4.7691	0.435	2378.48	2378.728	6011.4	1	991.2	54.5	12	K.ASKPLPPAPAPDEYLVSPITGEK.I
	HsFLAG-ARP5_Ti_1	3.7554	0.2665	2874.65	2875.335	7088.5	1	753.4	29.6	1	K.ASKPLPPAPAPDEYLVSPITGEKIPASK.M
	HsFlag-DPCD_Ti_20	3.114	0.1688	1966.3	1967.094	5247.9	2	407.6	44.1	2	K.QSDDEVYAPGLDIESSLK.Q
	HsFlag-VPS71_Ti_1	3.8107	0.1954	2185.89	2185.612	5534.5	3	428.7	44.7	10	K.LNGQVLVFTLPLTDQVSVIK.V
	HsFlag-VPS71_Ti_1	2.71	0.3374	1111.51	1112.289	4154.5	1	557.8	70	4	K.IHEATGMPAGK.Q
	HsFlag-VPS71_Ti_1	3.0433	0.3151	1112.52	1112.289	4427.2	1	810.5	80	2	K.IHEATGMPAGK.Q
gi|4504865|re	12	35	19.00%	711	73161	7.3	KH-type splicing regulatory protein (FUSE binding protein 2) [Homo sapiens]				
*	HsFlag-DPCD_Ti_20	5.379	0.5419	2154.54	2155.285	7451.4	1	1226.7	54.8	9	K.IGGDAATTVNNSTPDFGFGGQK.R
*	HsFLAG-Lin9_Ti_20	5.0483	0.3783	2186.29	2186.476	7546.3	1	1275	38.8	1	K.KLASQGDSISSQLGPIHPPPR.T
*	HsFLAG-Lin9_Ti_20	4.0752	0.3558	2057.48	2058.302	5468	1	554.2	47.4	2	K.LASQGDSISSQLGPIHPPPR.T
*	HsFLAG-Lin9_Ti_20	4.4356	0.3411	2057.54	2058.302	6643.9	1	920.6	39.5	1	K.LASQGDSISSQLGPIHPPPR.T
*	HsFLAG-Lin9_Ti_20	4.1787	0.1359	1080.03	1080.272	6347.8	1	1700.1	95	1	R.IGGGIDVPVPR.H
*	HsFLAG-Lin9_Ti_20	2.5466	0.1675	923.91	924.091	3957.1	1	605.7	87.5	1	R.HSVGVVIGR.S
*	HsFLAG-Lin9_Ti_20	4.0373	0.1484	1185.22	1185.409	6036.5	1	1465.2	94.4	3	R.IINDLLQSLR.S
*	HsFlag-DPCD_Ti_20	2.9382	0.2392	1534.33	1534.712	9747.8	1	1075.9	61.5	1	K.AINQQTGAFVEISR.Q
*	HsFlag-VPS71_Ti_1	4.0208	0.2559	2109.85	2110.334	5959.6	1	1092	61.1	4	K.KIGQQPQQPGAPPQQDYTK.A
*	HsFLAG-Lin9_Ti_20	4.2504	0.2378	2111.35	2110.334	7750.4	1	1854.6	45.8	1	K.KIGQQPQQPGAPPQQDYTK.A
*	HsFlag-DPCD_Ti_20	4.3743	0.2261	1981.18	1982.16	6044.2	1	2185.8	79.4	8	K.IGQQPQQPGAPPQQDYTK.A
*	HsFLAG-Lin9_Ti_20	3.8498	0.3892	2953.9	2954.141	3858.1	1	295.7	35.7	3	K.QAQVATGGGPGAPPGSQPDYSAAWAEYYR.Q
gi|46852398|r	1	2	19.00%	142	15961	4.9	biogenesis of lysosome-related organelles complex-1, subunit 2 isoform 1 [Homo sapiens]				
gi|47717129|r	1	2	27.30%	99	11489	8.7	biogenesis of lysosome-related organelles complex-1, subunit 2 isoform 2 [Homo sapiens]				
	HsFLAG-FLJ20729_	4.828	0.4089	3038.71	3039.412	8193.9	1	943.2	28.8	2	K.YAGLQPYLDQINVIEEQVAALEQAAYK.L
gi|14141170|r	7	11	18.90%	668	75023	9.7	metastasis-associated protein 2 [Homo sapiens]				
*	HsSrcap_Ti_202.257	4.8595	0.4336	2110.65	2110.287	10002.7	1	1877.4	64.7	3	R.VGDYVYFENSSSNPYLVR.R
*	HsSrcap_Ti_202.012	5.3455	0.4714	1551.97	1550.622	8666.8	1	2051.5	78.6	1	R.DISSSLNSLADSNAR.E
*	HsSrcap_Ti_205.584	3.8072	0.2453	4002.83	4003.424	10902.2	1	774.1	22.7	2	K.CSVTLLNETDILSQYLEKEDCFFYSLVFDPVQK.T
*	HsFlag-VPS71_Ti_1	3.4422	0.3526	1562.52	1561.796	6103.4	1	1004	70.8	1	R.DITLFHAMDTLQR.N
*	HsFlag-VPS71_Ti_1	3.7803	0.328	2173.87	2173.35	7682.6	1	888	50	1	R.GHLSRPEAQSLSPYTTSANR.A

*	HsSrcap_Ti_203.162	3.2389	0.1097	1182.38	1180.433	7443.7	1	1433.8	85	2	K.DLVAQAPLKPK.T
*	HsSrcap_Ti_202.244	3.0934	0.357	1654.57	1653.919	5600.4	1	737.2	63.3	1	K.LNPADAPNPVVFVATK.D
gi|66346679|r	6	9	18.90%	408	44965	8.6	SERPINE1 mRNA binding protein 1 isoform 1 [Homo sapiens]				
gi|66346685|r	6	9	19.90%	387	42427	8.4	SERPINE1 mRNA binding protein 1 isoform 4 [Homo sapiens]				
gi|66346683|r	6	9	19.60%	393	43135	8.4	SERPINE1 mRNA binding protein 1 isoform 3 [Homo sapiens]				
gi|66346681|r	6	9	19.20%	402	44257	8.7	SERPINE1 mRNA binding protein 1 isoform 2 [Homo sapiens]				
	HsFlag-NUFIP_Ti_10	5.0263	0.4505	1944.75	1945.089	7334.8	1	2405.7	83.3	2	R.FDQLFDDESDPFEVLK.A
	HsFLAG-TCF3_Ti_10	3.7444	0.3675	1460.46	1461.531	7805	1	958.6	56.7	1	K.SAAQAAAQTNSNAAGK.Q
	HsFLAG-p53-DNA-D	3.4864	0.1871	1368.66	1368.616	5829.8	5	655	68.2	2	K.KEETQPPVALKK.E
	HsFlag-NUFIP_Ti_10	3.931	0.2295	1256.65	1256.361	8796.1	1	1329.7	80	2	R.RPDQQLQGEGK.I
	HsFLAG-p53-DNA-D	3.033	0.0895	1176.46	1176.358	6890.1	4	1003.9	87.5	1	R.RFEKPLEEK.G
	HsFLAG-Lin9_Ti_202	3.0367	0.1481	1518.6	1516.602	9491.4	3	675.3	54.2	1	K.ENEVEEVKEEGPK.E
gi|7705805|re	2	3	18.90%	296	33249	9.3	mitochondrial ribosomal protein S2 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_10	5.0343	0.5595	4186.35	4188.64	8238.9	1	793.1	24.3	2	K.MNIPTVGIVDTNCNPCLITYPVPGNDDSPLAVHLYCR.L
*	HsFlag-NUFIP_Ti_10	3.8188	0.3452	1900.37	1901.017	5614.4	1	426.1	50	1	K.EPGDQGPAHPPGADMSHSL.-
gi|4505119|re	2	3	18.90%	291	32844	5.3	methyl-CpG binding domain protein 3 [Homo sapiens]				
*	HsSrcap_Ti_204.362	3.7358	0.3286	1747.02	1748.029	8254.6	1	770.8	53.3	2	K.KLSGLNAFDIAEELVK.T
*	HsSrcap_Ti_203.488	4.2047	0.2723	3884.17	3884.357	5862.5	1	489.6	21.1	1	K.GLQGVGPGCTDETLLSAIASALHTSTMPITGQLSAAVEK.N
gi|4507127|re	3	12	18.90%	159	17394	9.7	small nuclear ribonucleoprotein polypeptide C [Homo sapiens]				
*	HsFlag-VPS71_Ti_10	4.8225	0.3963	2299.76	2300.375	7780.1	1	1880.4	67.6	7	K.FYCDYCDTYLTHDSPSVR.K
*	HsSrcap_Ti_202.212	3.8683	0.3606	2300.74	2300.375	4077.2	1	672.9	41.2	2	K.FYCDYCDTYLTHDSPSVR.K
*	HsFlag-VPS71_Ti_10	4.7551	0.2307	1479.6	1478.66	6411.8	1	2148	90.9	3	K.WMEEQAQSLIDK.T
gi|88953190|r	3	13	18.90%	132	14501	7.2	PREDICTED: similar to ribosomal protein S12 [Homo sapiens]				
gi|88955046|r	3	13	18.90%	132	14502	6.8	PREDICTED: similar to ribosomal protein S12 [Homo sapiens]				
	HsFLAG-ARP8_Ti_2	5.2084	0.0988	1752.53	1753.015	7995.1	1	1992.1	78.6	1	K.LVEALCAEHQIDLIK.V
	HsFlag-NUFIP_Ti_10	3.2132	0.3059	1189.76	1190.394	5456.5	1	707	72.2	3	K.KLGEWVGLCK.T
	HsFlag-NUFIP_Ti_10	3.5234	0.3303	1190.63	1190.394	5208.3	1	1103.3	88.9	9	K.KLGEWVGLCK.T
gi|10835165|r	2	9	18.80%	128	14177	6.5	CD59 antigen p18-20 [Homo sapiens]				
gi|42761474|r	2	9	18.80%	128	14177	6.5	CD59 antigen p18-20 [Homo sapiens]				
gi|42716302|r	2	9	18.80%	128	14177	6.5	CD59 antigen p18-20 [Homo sapiens]				
gi|42716299|r	2	9	18.80%	128	14177	6.5	CD59 antigen p18-20 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	4.111	0.3687	1540.38	1540.598	5767.8	1	1270.2	86.4	7	K.FEHCNFNDVTTR.L
	HsFLAG-ARP6_Ti_1	4.6378	0.4188	1648.68	1649.773	8122.4	1	1987	86.4	2	R.LRENELTYYCCK.K
gi|38327634|r	8	33	18.70%	670	75407	9.5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18 [Homo sapiens]				
*	HsFLAG-FLJ20309_	3.7297	0.2141	1527.44	1527.931	4644.9	4	696.5	69.2	6	K.TLAFLIPAVELIVK.L
*	HsFLAG-Lin9_Ti_204	3.0875	0.0946	1395	1395.645	12131.1	5	1102.1	53.8	1	K.LGNGINIIVATPGR.L
*	HsFLAG-FLJ20729_	4.0243	0.3072	1695.53	1695.992	9892.1	1	1413.2	69.2	2	R.LLDHMQNTPGFMYK.N
*	HsFLAG-Lin9_Ti_202	3.9236	0.3429	1446.23	1446.566	9604.8	1	1793.1	81.8	3	K.NLQCLVIDEADR.I
*	HsFLAG-FLJ20729_	4.2422	0.2907	2311.33	2312.538	5294.6	1	647.6	50	4	R.GLDIPEVDWIVQYDPPDDPK.E
*	HsFLAG-p53-DNA-D	4.0279	0.2418	1835.62	1835.203	8335.9	1	1188.4	60	8	R.GHALLILRPEELGFLR.Y
*	HsFLAG-Lin9_Ti_202	5.283	0.4352	2265.33	2264.632	7882.2	1	1184.4	57.9	8	K.QIFNVNNLNLPQVALSFGFK.V
*	HsFLAG-FLJ20729_	2.9391	0.362	1630.94	1629.81	6536.2	1	953.8	64.3	1	K.VPPFVDLNVNSNEGK.Q
gi|46367787|r	8	33	18.70%	636	70671	9.5	poly(A) binding protein, cytoplasmic 1 [Homo sapiens]				

	HsFLAG-ARP6_Ti_1	3.0589	0.308	1929.23	1930.084	9460.6	1	1041	53.1	1	R.SLGYAYVNFQQPADAER.A
	HsFLAG-ARP6_Ti_1	3.0592	0.2797	1267.66	1267.483	5025.5	1	890.6	80	1	R.ALDTMNFDVIK.G
	HsFLAG-ARP6_Ti_1	4.5583	0.3978	1807.79	1808.007	7833.5	1	1601.2	70	1	K.ALYDTFSAFGNILSCK.V
*	HsFLAG-ARP6_Ti_1	4.2223	0.4991	1741.53	1741.857	6700	1	1406.3	71.4	3	K.GYGFVHFETQEAAER.A
	HsFLAG-ARP6_Ti_1	3.6131	0.4405	1663.85	1663.79	5123.3	1	681.7	57.1	3	K.GFGFVCFSSPEEATK.A
	HsFLAG-ARP6_Ti_1	4.0405	0.3767	1543.47	1543.893	2806.3	1	566.6	76.9	11	R.IVATKPLYVALAQR.K
	HsFLAG-ARP6_Ti_1	4.7173	0.4431	1637.21	1638.024	5919.7	1	1882.9	85.7	6	R.LFPLIQAMHPTLAGK.I
	HsFLAG-TCF3_Ti_1	5.1211	0.4253	1694.51	1694.928	8006.8	1	2427.4	80	7	R.SKVDEAVAVLQAHQAK.E
gi|14028877|r	2	4	18.50%	173	20116	8.8	mitochondrial ribosomal protein S25 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.5564	0.3569	1545	1544.836	7544.9	1	1536.6	86.4	2	K.FVFFNIPQIQYK.N
*	HsFlag-NUFIP_Ti_1	4.4758	0.4166	2312.04	2312.564	4005.6	1	661.9	52.6	2	R.ECICEVEGQVPCPSLVPLPK.E
gi|18105007|r	22	55	18.40%	2225	242981	6.5	carbamoylphosphate synthetase 2/aspartate transcarbamylase/dihydroorotase [Homo sapiens]				
*	HsSrcap_Ti_206.272	4.5749	0.4988	2286.83	2286.555	6434.3	1	860.9	55.3	1	R.TLHEWLQQHGIPGLQGVDTR.E
*	HsSrcap_Ti_202.413	4.6951	0.4428	4449.92	4449.831	6656.3	1	448.8	19.5	2	LSR.V
*	HsFLAG-ARP6_Ti_1	3.7982	0.136	3023.18	3024.442	12652.1	1	1086.7	25.9	1	K.ALKEENIQTLLINPNIATVQTSQGLADK.V
*	HsFLAG-ARP6_Ti_1	3.4266	0.3399	1946.68	1947.331	4464.3	1	1131.3	76.7	3	K.VYFLPITPHYVTQVIR.N
*	HsFLAG-ARP6_Ti_1	4.5793	0.3433	2681.19	2681.894	9006.4	1	1300.4	32	2	R.MAEIGEHVAPSEAANSLEQAQAAAER.L
*	HsFLAG-ARP6_Ti_1	5.8639	0.3482	3703.54	3704.177	4745.3	1	628.8	25	20	R.AAFALGGLGSGFASNREELSALVAPAFAHTSQVLVDK.S
*	HsFLAG-ARP6_Ti_1	3.6646	0.3709	2103.32	2102.271	5493.4	1	634.4	52.6	1	R.NSVTGGTAAFEPSVDYCVVK.I
*	HsFLAG-ARP6_Ti_1	4.1681	0.3792	1428.91	1429.665	9071.4	1	1613.6	77.3	1	R.IIAHAQLLEQHR.G
*	HsFLAG-ARP6_Ti_1	3.1961	0.2408	1486.64	1484.779	5432.9	1	496.7	57.7	1	K.QIALAVLSTELAVR.K
*	HsFLAG-ARP6_Ti_1	3.2615	0.2992	1398.9	1398.648	4128.9	1	1011	83.3	1	R.TPHVLVLGSGVYR.I
*	HsFLAG-ARP6_Ti_1	4.6741	0.3106	1527.54	1527.764	6301.3	1	1755.2	87.5	2	R.LLDTIGISQPQWR.E
*	HsSrcap_Ti_204.467	4.6331	0.2808	4384.87	4384.798	8819.6	1	760.7	18.6	1	TAK.T
*	HsSrcap_Ti_205.339	4.7069	0.4318	2446.49	2447.883	9715.8	1	1297.1	50	5	K.AIVHAVGQELQVTGPFNLQLIAK.D
*	HsFLAG-ARP6_Ti_1	4.2987	0.1219	2447.93	2447.883	7530.3	1	1221.3	37.5	1	K.AIVHAVGQELQVTGPFNLQLIAK.D
*	HsSrcap_Ti_205.331	4.5707	0.4083	3049.75	3047.525	8805.8	1	920.9	28.7	2	K.AIVHAVGQELQVTGPFNLQLIAKDDQLK.V
*	HsFLAG-ARP6_Ti_1	4.536	0.4527	2188.61	2188.603	4631.3	1	1285.3	66.7	2	R.VIMGEEVEPVGLMTGSGVVGVK.V
*	HsFLAG-ARP6_Ti_1	3.4896	0.3574	1651.44	1651.002	5813.7	1	1422	70	1	K.LFVEALGQIGPAPPLK.V
*	HsFLAG-ARP6_Ti_1	2.8327	0.2738	1205.2	1205.337	3947	3	684.2	83.3	1	K.VHVDCMTSQK.L
*	HsFLAG-ARP6_Ti_1	2.7569	0.2796	1201.25	1201.327	3704.4	1	729.9	83.3	3	K.AHWTPFEGQK.V
*	HsFLAG-ARP6_Ti_1	3.2166	0.3173	1668.89	1669.899	8362.2	1	1342.9	69.2	1	K.DQMSHLFNVAHTLR.M
*	HsSrcap_Ti_205.161	2.6536	0.2488	1218.46	1218.398	5336.3	1	479.9	68.2	1	R.HPQPGAVELAAK.H
*	HsFLAG-ARP6_Ti_1	4.0357	0.3145	1564.56	1562.775	6922.7	1	1856.6	83.3	2	R.TVHSLACLLTQYR.V
gi|6912542|re	12	42	18.40%	495	56369	9.2	nuclear fragile X mental retardation protein interacting protein 1 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_2	3.0368	0.1779	1167.23	1167.307	5026.9	1	857.2	88.9	1	K.FTDFSLPPSR.K
*	HsFlag-NUFIP_Ti_2	2.6411	0.2124	1295.19	1295.481	3955.9	1	357.5	65	1	K.FTDFSLPPSRK.Q
*	HsFlag-NUFIP_Ti_2	2.9498	0.3623	1729.8	1730.806	5769.2	1	500.4	62.5	3	K.EPVFHFFCDTCDR.G
*	HsFlag-NUFIP_Ti_2	4.6365	0.3035	1593.59	1594.65	7066.2	1	1180.8	75	7	K.CPELDCSFTAHEK.I
*	HsFLAG-TIP49a_Ti_	2.1154	0.3154	885.25	886.075	3906.8	6	320.7	64.3	2	R.NMHAPGMK.K
*	HsFlag-NUFIP_Ti_2	2.6069	0.1296	1045.2	1044.15	5324.7	3	804.1	93.8	1	K.LDTPEEIAR.W
*	HsFlag-NUFIP_Ti_2	2.2721	0.2914	1294.54	1295.481	3388.2	7	213.5	59.1	2	K.RGAVLTTTQYGK.M
*	HsFlag-NUFIP_Ti_2	4.2133	0.3231	1297.17	1295.481	8452.1	1	1825	81.8	8	K.RGAVLTTTQYGK.M

*	HsFLAG-TIP49a_Ti_	2.2468	0.1253	1344.26	1345.461	4480.6	5	344.8	50	1	R.AVTGSGSHLCDLK.L
*	HsFLAG-TIP49a_Ti_	3.6492	0.2511	1346.17	1345.461	6231.3	1	908.7	66.7	9	R.AVTGSGSHLCDLK.L
*	HsFLAG-TIP49a_Ti_	3.2442	0.2514	1582.56	1583.7	3813.5	1	392.7	63.6	2	K.DYHNYQTLFEPR.T
*	HsFlag-NUFIP_Ti_20	4.0014	0.2576	1583.06	1583.7	8177.7	1	1163.8	72.7	5	K.DYHNYQTLFEPR.T
gi|5453539|re	4	6	18.40%	425	47079	7.2	phosphoribosylaminoimidazole carboxylase [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.9152	0.256	1721.29	1722.001	8813.6	1	1263.4	64.3	3	K.ITSCIFQLLQEAGIK.T
*	HsFLAG-ARP6_Ti_1	3.2707	0.3242	1733.36	1732.956	7281.4	1	703.9	53.3	1	R.VVVLMGSTSDLGHCEK.I
*	HsFLAG-p53-DNA-D	3.0976	0.2708	1411.59	1411.558	4878.1	2	417.3	54.2	1	R.VTSAHKGPDETLR.I
*	HsFLAG-ARP8_Ti_2	4.6424	0.1415	3562.78	3560.998	10741.7	1	938.9	22.7	1	R.LPSGLGCSTVLSPEGSAQFAAQIFGLSNHLVWSK.L
gi|4885063|re	5	16	18.40%	364	39456	6.9	fructose-bisphosphate aldolase C [Homo sapiens]				
*	HsFlag-VPS71_Ti_1(	5.5085	0.1357	2272.92	2274.447	5367.9	1	699.8	52.3	1	K.GVVPLAGTDGETTTQGLDGLSER.C
	HsFlag-VPS71_Ti_1(	4.0335	0.3068	3022.16	3022.348	5181.6	2	408.1	36.5	3	R.YASICQQNGIVPIVEPEILPDGDHDLK.R
	HsFlag-VPS71_Ti_1(	5.5709	0.2217	3022.85	3022.348	6479.9	2	791.7	30.8	6	R.YASICQQNGIVPIVEPEILPDGDHDLK.R
	HsH2AZ-FLAG_293_	1.9697	0.1264	763.69	763.955	6757.4	3	659.4	75	4	K.VLAAVYK.A
	HsFlag-VPS71_Ti_1(	3.5725	0.2934	1198.81	1198.367	5068.6	1	1115.9	88.9	2	R.PWALTFSYGR.A
gi|4506609|re	6	18	18.40%	196	23466	11.5	ribosomal protein L19 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	5.6615	0.4915	2070.48	2072.242	3782.6	1	1121.4	76.5	1	K.KVWLDPNETNEIANANSR.Q
*	HsFLAG-ARP6_Ti_1	3.8022	0.2483	2072.4	2072.242	6850.1	3	702.2	35.3	1	K.KVWLDPNETNEIANANSR.Q
*	HsFlag-NUFIP_Ti_1(	4.6806	0.4358	1943.1	1944.068	6976.1	1	1530.8	71.9	4	K.VWLDPNETNEIANANSR.Q
	HsFLAG-TCF3_Ti_1(	2.4383	0.1493	923.58	924.091	3542.2	5	229.1	71.4	6	R.KPVTVHSR.A
	HsFLAG-TCF3_Ti_1(	2.4727	0.2212	1114.69	1115.275	6134.6	2	495.8	66.7	3	K.KLLADQAEAR.R
	HsFlag-NUFIP_Ti_1(	3.93	0.1888	1115.56	1115.275	7096.2	1	1799.9	94.4	3	K.KLLADQAEAR.R
gi|48928058|r	2	3	18.40%	103	11637	5.5	small ubiquitin-like modifier protein 3 [Homo sapiens]				
gi|89062887|r	2	3	20.00%	95	10814	7.4	PREDICTED: similar to SMT3 suppressor of mif two 3 homolog 2 [Homo sapiens]				
gi|89060987|r	2	3	11.90%	160	17755	6.3	PREDICTED: similar to SMT3 suppressor of mif two 3 homolog 2 [Homo sapiens]				
gi|89060008|r	2	3	11.90%	160	17755	6.3	PREDICTED: similar to SMT3 suppressor of mif two 3 homolog 2 [Homo sapiens]				
gi|89026922|r	2	3	20.00%	95	10814	7.4	PREDICTED: similar to SMT3 suppressor of mif two 3 homolog 2 [Homo sapiens]				
gi|89024911|r	2	3	20.00%	95	10814	7.4	PREDICTED: similar to SMT3 suppressor of mif two 3 homolog 2 [Homo sapiens]				
gi|54792071|r	2	3	26.80%	71	8111	5.4	small ubiquitin-like modifier 2 isoform b precursor [Homo sapiens]				
gi|54792069|r	2	3	20.00%	95	10871	5.5	small ubiquitin-like modifier 2 isoform a precursor [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	2.9752	0.1648	1236.07	1235.382	7731.2	2	973.8	68.2	1	K.VAGQDGSVVQFK.I
	HsFLAG-Lin9_Ti_20	2.8395	0.087	838.91	838.985	7791.2	2	1060	100	2	K.RHTPLSK.L
gi|4502303|re	2	4	18.30%	213	23277	10	mitochondrial ATP synthase, O subunit precursor [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.413	0.2906	1873.54	1874.147	7773.7	1	692.3	50	2	R.FSPLTTNLINLLAENGR.L
*	HsFLAG-ARP6_Ti_1	2.7803	0.2958	2318.29	2319.534	5896.9	1	407.4	38.1	2	R.GEVPCTVTSASPLEEATLSELK.T
gi|19913428|r	6	8	18.20%	511	56501	5.8	ATPase, H+ transporting, lysosomal 56/58kD, V1 subunit B, isoform 2 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.3263	0.2449	2000.45	2001.293	5536.4	5	428.8	42.9	1	R.GIVNGAAPELPVPTGGPAVGAR.E
*	HsFLAG-ARP6_Ti_1	2.6947	0.2944	1649.63	1648.943	5265.4	2	349.7	43.3	1	K.TVSGVNGPLVILDHVK.F
*	HsFLAG-ARP6_Ti_1	4.8506	0.2906	2410.54	2410.763	10063.1	1	1552.4	52.4	2	R.IYPEEMIQTGISAIDGMNSIAR.G
	HsFLAG-ARP6_Ti_1	3.2549	0.2484	2180.28	2179.493	3727.4	1	385.5	50	1	K.IPIFSAAGLPHNEIAAQICR.Q
	HsFLAG-ARP6_Ti_1	4.6346	0.429	2180.59	2179.493	6682.9	1	1722	47.4	2	K.IPIFSAAGLPHNEIAAQICR.Q
*	HsFLAG-ARP6_Ti_1	2.8562	0.0972	1594.38	1594.811	6402	1	745.4	58.3	1	K.RIPQSTLSEFYPR.D
gi|42544123|r	8	21	18.10%	548	59712	9.5	splicing factor 1 isoform 3 [Homo sapiens]				

gi|42544130|r	8	21	15.50%	639	68330	9	splicing factor 1 isoform 1 [Homo sapiens]				
gi|42544125|r	8	21	15.50%	638	68633	9.2	splicing factor 1 isoform 2 [Homo sapiens]				
	HsFLAG-p53-DNA-D	2.93	0.3099	1649.51	1650.032	5042.6	1	591.5	53.3	1	K.TVIPGMPTVIPPGLTR.E
	HsARP6-FLAG_Ti_1	2.6753	0.1248	1562.38	1562.806	8780.7	3	1078.1	66.7	1	R.AYIVQLQIEDLTR.K
	HsFlag-VPS71_Ti_1	5.9685	0.5456	2937.4	2937.386	7196	1	1238.7	35	2	R.HNLITEMVALNPDFKPPADYKPPATR.V
	HsFLAG-p53-DNA-D	4.9347	0.3723	2401.39	2401.826	5345.7	1	879.7	57.5	3	K.VMIPQDEYPEINFVGLLIGPR.G
	HsFlag-VPS71_Ti_1	5.1074	0.2923	2402.49	2401.826	8326.1	1	2558.8	46.2	7	K.VMIPQDEYPEINFVGLLIGPR.G
	HsFlag-VPS71_Ti_1	1.9711	0.2148	1124.44	1125.23	5709.3	7	335.6	61.1	1	R.SITNTTVCTK.C
	HsFlag-VPS71_Ti_1	2.5483	0.1384	1125.38	1125.23	6062.2	3	749.7	77.8	2	R.SITNTTVCTK.C
	HsFLAG-p53-DNA-D	4.2015	0.3738	1473.77	1474.573	3708.8	2	657.7	75	4	K.FQRPGDPQSAQDK.A
gi|42476281|r	3	6	18.00%	294	31566	7.6	voltage-dependent anion channel 2 [Homo sapiens]				
gi|88955151|r	3	6	18.10%	293	31445	7.6	PREDICTED: similar to voltage-dependent anion channel 2 [Homo sapiens]				
gi|88953242|r	3	6	18.10%	293	31479	7.6	PREDICTED: similar to voltage-dependent anion channel 2 [Homo sapiens]				
	HsFLAG-TIP49b_Ti_	2.6608	0.2457	1908.24	1908.893	7701.3	7	356.1	38.9	1	K.SCSGVEFSTSGSSNTDTGK.V
	HsFLAG-ARP6_Ti_1	2.817	0.2873	1557.77	1557.744	6784.3	3	634.4	57.7	1	K.LTFDTTFSPNTGKK.S
	HsFLAG-ARP6_Ti_1	4.0312	0.3206	2103.61	2104.414	5550.4	1	487.2	42.1	4	K.VNNSSLIGVGYTQTLRPGVK.L
gi|89040213|r	1	2	18.00%	183	20343	5.6	PREDICTED: hypothetical protein XP_934593 [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	4.2715	0.2447	3373.83	3374.744	6138.6	1	564.6	24.2	2	R.YSVEASSPGHGSPLSSLLPSASVPESMTISELR.Q
gi|20070160|r	4	17	17.70%	372	40060	9.8	cold shock domain protein A [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.925	0.3759	1745.19	1745.93	6667.6	1	1504.7	75	2	R.NDTKEDVFVHQTAIK.K
	HsFlag-NUFIP_Ti_1	3.8133	0.4608	1797.85	1796.882	6497.5	1	815	59.4	9	R.SVGDGETVEFDVVEGEK.G
*	HsFlag-NUFIP_Ti_1	3.8893	0.3622	1784.56	1783.893	7328	1	986.4	55.6	2	K.GAEAANVTGPDGVPVEGSR.Y
*	HsFlag-NUFIP_Ti_1	3.3468	0.3039	1560.66	1560.71	5644	1	602	60.7	4	K.DGVPEGAQLQGPVHR.N
gi|4759098|re	3	11	17.70%	288	33666	11.2	splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila) [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.5982	0.4821	2383.76	2385.568	4774.7	1	941.9	57.5	6	R.ANPDPNCCLGVFGLSLYTTER.D
*	HsFLAG-Lin9_Ti_20	3.5389	0.1814	1812.07	1811.989	8848.3	1	1113.3	56.7	4	K.YGPIADVSIVYDQQSR.R
*	HsFLAG-ARP6_Ti_1	2.5692	0.2786	1621.64	1622.774	7676.5	1	863.6	61.5	1	R.GFAFVYFENVDDAK.E
gi|19923466|r	32	144	17.60%	2752	299676	12.1	splicing coactivator subunit SRm300 [Homo sapiens]				
*	HsFLAG-FLJ20309_	4.0953	0.2887	1734.18	1734.866	7688.5	1	977.3	69.2	2	R.RGERPDYKGEEELR.R
*	HsFLAG-p53-DNA-D	2.1001	0.0856	927.64	928.036	4137.2	9	203.6	62.5	2	K.THTTALAGR.S
*	HsFLAG-Lin9_Ti_20	4.4592	0.4211	2792.41	2792.933	8607	2	876.3	27.9	2	R.RGEGDAPFSEPGTTSTQRPSSPETATK.Q
*	HsMRGBP-FLAG_Ti_	3.7999	0.4457	1720.7	1720.92	4110.7	1	545.1	62.5	9	R.SSTGPEPPAPTPLLAER.H
*	HsFlag-NUFIP_Ti_2	4.8677	0.3426	2853.18	2854.106	8918.4	1	1158.5	31.5	3	R.HGGSPQPLATTPLSQEPVNPPSEASPTR.D
*	HsFlag-DPCD_Ti_20	4.4346	0.5054	1841.18	1841.97	6182	1	1048.5	61.8	3	K.LPQSSSSESSPPSPQPTK.V
*	HsFLAG-FLJ20729_	3.0355	0.3726	1897.02	1898.045	7319.1	1	624.8	47.2	1	R.HASSSPESPKPAPAPGSHR.E
*	HsFLAG-FLJ20729_	4.6321	0.3672	1897.93	1898.045	6590.9	1	2178.3	52.8	2	R.HASSSPESPKPAPAPGSHR.E
*	HsFLAG-ARP6_Ti_2	2.5594	0.1798	1019.59	1020.094	4042.5	1	590.2	77.8	1	R.SLSGSSPCPK.Q
*	HsARP6-FLAG_Ti_1	3.133	0.1733	1396.32	1396.46	8676.2	1	810.8	63.6	2	R.SCFESSPDPELK.S
*	HsFLAG-ARP6_Ti_2	4.8206	0.3454	1879.16	1879.05	4131.1	1	1054.8	70.6	5	K.DSLVQSCPGSLSLCAGVK.S
*	HsFLAG-ARP6_Ti_2	5.73	0.572	2274.58	2276.378	3589	1	951.9	67.5	11	R.FQSDSSSYPTVDSNSLLGQSR.L
*	HsFLAG-Lin9_Ti_20	4.5951	0.4173	1981.64	1981.258	7215	1	956.3	62.5	17	K.FSPFPVQDRPESSLVFK.D
*	HsFlag-DPCD_Ti_20	2.9215	0.2339	2362.83	2364.54	3938.8	1	229.3	37.5	1	K.EQNSALPTSSQDEELMEVVEK.S
*	HsFLAG-ARP6_Ti_1	3.777	0.4414	1825.19	1826.013	6856.4	1	1148.9	62.5	10	K.SEEPAGQILSHLSSELK.E

*	HsFLAG-ARP6_Ti_2	2.8484	0.267	1855.55	1856.014	9705.2	1	609.7	41.2	1	R.NSGPLGTEMNTGFSSEVK.E
*	HsFLAG-ARP6_Ti_2	4.9985	0.3839	1616.93	1617.667	8700.7	1	1848.8	70	2	R.SSGHSSSELSPDAVEK.A
*	HsFLAG-ARP6_Ti_2	4.4278	0.5055	1916.54	1917.144	5907.1	1	762.1	52.8	3	K.AGMSSNQSISSPVLDAVPR.T
*	HsFLAG-Lin9_Ti_20	2.7127	0.1077	1035.71	1036.222	4636.7	1	641.4	81.2	2	K.ALPQTPRPR.S
*	HsFLAG-ARP6_Ti_2	3.7094	0.3561	1901.9	1903.013	5402.1	1	928.7	58.8	2	R.SGSSQELDVKPSASPQER.S
*	HsFlag-NUFIP_Ti_2	2.7361	0.1153	1526.98	1526.896	4762.8	5	375	50	1	R.MSQVPAPVPLMSLR.T
*	HsFlag-DPCD_Ti_20	5.3137	0.5086	1414.57	1415.651	8154.8	1	2525.6	85.7	9	R.IPAASAAAMNLASAR.T
*	HsARP6-FLAG_Ti_1	3.4017	0.2499	1426.34	1426.613	3432.4	1	539.7	65.4	4	R.TPAIPTAVNLADSR.T
*	HsFlag-VPS71_Ti_1	3.9352	0.51	1343.89	1342.556	5348.3	1	1642.3	88.5	2	R.TPAAAAAMNLASPR.T
*	HsARP6-FLAG_Ti_1	3.1186	0.3243	1239.09	1239.417	4085.4	1	579.1	70.8	3	R.TPTAPAVNLAGAR.T
*	HsFLAG-Lin9_Ti_20	3.6587	0.4761	2560.64	2560.823	5440	1	348.2	34.6	2	R.TPAALAALSLTGSGTPPTAANYPSSSR.T
*	HsFLAG-FLJ20309_	3.9074	0.2205	1380.51	1379.559	3763.1	1	836.5	76.9	20	R.TPQAPASANLVGPR.S
*	HsFlag-VPS71_Ti_1	3.8854	0.3463	1351.66	1352.493	4459.9	1	373.6	57.7	3	R.SAHATAPVNIAGSR.T
*	HsFLAG-FLJ20309_	3.3066	0.3289	1352.27	1352.493	6083.9	1	815.5	65.4	15	R.SAHATAPVNIAGSR.T
*	HsFlag-DPCD_Ti_20	3.7562	0.3063	1385.72	1386.609	4959	1	1292	84.6	2	R.MAPALSGANLTSPR.V
*	HsFLAG-ARP6_Ti_2	2.1511	0.2435	934.45	935.068	2965.5	1	214.4	71.4	1	R.VPLSAYER.V
*	HsFLAG-TIP49b_Ti_	3.1	0.1126	1021.78	1022.152	5728.6	6	610.9	75	1	R.RPSPQPSPR.D
gi|9966805|re	9	21	17.60%	859	96332	9.1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24 [Homo sapiens]				
*	HsYL1_Ti_101.1202.	2.8834	0.2548	1564.43	1564.557	5728.8	1	950.9	69.2	2	K.AQAVSEEEEEEEGK.S
*	HsFLAG-p53-DNA-D	2.6483	0.1503	1219.39	1217.365	6442	5	548.9	63.6	1	K.KGLEPSQSTAAK.V
*	HsFLAG-p53-DNA-D	3.4715	0.1636	2356.56	2356.814	5954.4	1	388.8	38.6	3	R.ALSFLGFSAPTPIQALTLAPAIR.D
*	HsFLAG-FLJ20729_	4.7659	0.43	1967.49	1968.411	3413.9	1	783.6	71.9	3	K.TLAFAIPMIHAVLQWQK.R
*	HsFlag-DPCD_Ti_20	4.3907	0.3077	1864.44	1862.997	9198.4	1	1342.3	61.8	1	K.RNAAPPPSNTEAPPGETR.T
*	HsFLAG-Lin9_Ti_20	4.005	0.3513	2578.16	2579.737	8338.2	1	1094.5	46	1	K.TGGTVSDQALLFGDDDAGEGPSSLIR.E
*	HsFLAG-Lin9_Ti_20	3.1935	0.1681	1195.55	1195.407	5748	1	564.7	75	2	R.RPEIVVATPGR.L
*	HsFLAG-Lin9_Ti_20	3.8602	0.3219	1528.46	1528.748	6367.6	1	1183	75	4	R.HLLSQPLFTESQK.T
*	HsFLAG-Lin9_Ti_20	4.1469	0.3762	1770.89	1771.067	4826.9	1	851.8	62.5	4	K.YPTQSGKPPLLVSAPSK.S
gi|41327771|r	9	18	17.60%	820	95583	9.6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23 [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	3.2055	0.2471	1312.5	1312.549	2756.6	1	482.4	77.3	2	K.AQPLSLEELLAK.K
*	HsFlag-ZnF-HIT2_Ti_	2.7407	0.1611	1236.55	1236.42	5463	1	790.3	83.3	2	K.ERHQVQLLGR.G
*	HsFLAG-FLJ20729_	4.7963	0.3309	1898.16	1898.382	4038	1	991.5	71.9	7	K.TAAFLIPLLVWITTLPK.I
*	HsFlag-VPS71_Ti_1	3.0528	0.1473	2258.48	2258.536	6813.4	4	507.2	44.7	1	K.IDRIEESDQGPYAIILAPTR.E
*	HsFlag-ZnF-HIT2_Ti_	4.436	0.3386	2523.98	2523.731	6910.6	1	1662.8	42.9	1	K.ILEHMPVSNQKPDTDEAEDPEK.M
*	HsARP6-FLAG_Ti_1	4.387	0.3418	2269.9	2269.732	7952.3	1	1551.6	42.1	2	K.LLAILEQGFDPPIIIFVNQK.K
*	HsFlag-ZnF-HIT2_Ti_	2.9357	0.1974	2272.11	2269.733	5593.6	1	454	44.7	1	K.LLAILEQGFDPPIIIFVNQK.K
*	HsFlag-VPS71_Ti_1	2.9199	0.3075	1308.66	1309.449	9571.8	1	947.5	68.2	1	K.MGYNACTLHGGK.G
*	HsFLAG-p53-DNA-D	3.6413	0.2264	3336.58	3337.723	5577.3	1	451.6	24.2	1	K.QAILESPVSSCPPELANHPDAQHKPGTILTK.K
gi|21327708|r	3	9	17.60%	391	45374	4.5	nucleosome assembly protein 1-like 1 [Homo sapiens]				
gi|4758756|re	3	9	17.60%	391	45374	4.5	nucleosome assembly protein 1-like 1 [Homo sapiens]				
	HsH2AZ-FLAG_293_	4.5432	0.4097	1860.25	1861.102	4916.5	1	1003.1	68.8	6	R.LDGLVETPTGYIESLPR.V
	HsH2AZ-FLAG_293_	3.7752	0.2178	1358.75	1357.592	5528.8	1	1187.2	85	2	K.YAVLYQPLFDK.R
	HsFLAG-TCF3_Ti_1	3.564	0.4069	4516.85	4517.862	4304.2	1	543.8	22.5	1	.E
gi|5453634|re	4	9	17.50%	492	54099	6.4	dynein, cytoplasmic, light intermediate polypeptide 2 [Homo sapiens]				

*	HsFLAG-ARP6_Ti_1	5.1326	0.4931	3630.37	3631.084	6958.9	1	814.5	26.5	4	R.GPLTSGSDEENVALPLGDNVLTHNLGIPVLVVCTK.C
*	HsFLAG-p53-DNA-D	3.8521	0.28	1710.4	1710.97	6752.6	1	1144.5	67.9	1	K.TYGFHFTTPALVVEK.D
*	HsFLAG-FLJ20729_	4.3622	0.4124	1969.53	1970.189	7851.8	1	962	52.8	3	K.NNAASEGVLASFFNSLLSK.K
*	HsFLAG-ARP6_Ti_2	2.9241	0.2632	1459.31	1459.556	4131.5	1	501.4	59.4	1	K.TGSPGSPGAGGVQSTAK.K
gi|4506741|re	3	27	17.50%	194	22127	10.1	ribosomal protein S7 [Homo sapiens]				
	HsARP6-FLAG_Ti_1	3.6651	0.3402	1338.2	1338.72	4583.2	2	756.2	72.7	11	K.AIIIFVPVPQLK.S
*	HsFLAG-TCF3_Ti_1	4.5887	0.1584	2368.22	2368.733	5082.2	1	814.9	35.7	6	R.TLTAVHDAILEDLVFPSEIVGK.R
*	HsFLAG-TCF3_Ti_1	5.5915	0.3068	2369.03	2368.733	8008.2	1	1388.8	52.4	10	R.TLTAVHDAILEDLVFPSEIVGK.R
gi|71361682|r	25	84	17.40%	2115	238257	5.8	nuclear mitotic apparatus protein 1 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.3673	0.3193	3396.47	3395.89	7129.2	1	1258.1	31.7	2	R.GAALLSWVNSLHVADPVEAVLQLQDCSIFIK.I
*	HsFLAG-FLJ20729_	2.9912	0.2523	1440.12	1440.562	5388.9	2	415.9	62.5	2	K.HPSSPECLVSAQK.V
*	HsFLAG-Lin9_Ti_20	4.5141	0.377	2837.96	2838.106	9417.8	1	1328	32.6	1	K.LREFASHLQQLQDALNELTEEHSK.A
*	HsFLAG-p53-DNA-D	7.1502	0.3838	2567.15	2568.759	12002.2	1	2326.8	39.3	2	R.EFASHLQQLQDALNELTEEHSK.A
*	HsFLAG-Lin9_Ti_20	3.8991	0.2676	1515.01	1514.759	10363.8	1	1371	69.2	1	K.GEVLGDVLQLETLK.Q
*	HsARP6-FLAG_Ti_1	4.0714	0.3317	2262.61	2262.522	8877.1	1	1192.4	36.2	1	K.QQLSSLITDLQSSISNLSQAK.E
*	HsFlag-DPCD_Ti_20	3.7364	0.4273	2262.64	2262.522	7634.7	1	510.7	40	1	K.QQLSSLITDLQSSISNLSQAK.E
*	HsFlag-DPCD_Ti_20	5.6936	0.2952	3187.41	3187.572	11686.4	1	1560	30.2	7	R.LTAQVASLTSELTTLNATIQQQDQELAGLK.Q
*	HsFLAG-Lin9_Ti_20	5.5699	0.4418	2126.94	2127.322	11392.5	1	2089.1	63.9	1	K.QAQLAQTLQQQEQASQGLR.H
*	HsARP6-FLAG_Ti_1	3.3941	0.3168	1257.44	1256.401	5880.4	1	1072.1	85	8	R.HQVEQLSSSLK.Q
*	HsFLAG-p53-DNA-D	5.364	0.457	1871.79	1872.128	8231.9	1	1955.5	71.9	9	R.VEFATLQEALAHALTEK.E
*	HsARP6-FLAG_Ti_1	3.902	0.2838	1872.05	1872.128	3953.6	1	734.7	43.8	1	R.VEFATLQEALAHALTEK.E
*	HsYL1_Ti_103.1104.	3.519	0.1933	1448.54	1448.582	5429.5	1	951.5	77.3	2	R.AEVSKLEQQCQK.Q
*	HsFlag-VPS71_Ti_1	5.2739	0.4996	1654.32	1654.78	7438.4	1	1892	76.7	11	K.AQELGHSQSALASAQR.E
*	HsFLAG-Lin9_Ti_20	4.595	0.3859	1803.48	1804.007	8417.5	1	2249.6	73.3	1	K.NSLISSLEEEVSILNR.Q
*	HsARP6-FLAG_Ti_1	3.9881	0.4178	1260.31	1261.377	9398.6	1	1982.1	86.4	2	R.LLQAETASNSAR.A
*	HsMRGBP-FLAG_Ti_	5.9266	0.3472	1725.74	1725.865	6371.3	1	1794.5	82.1	10	K.HLCQQLQAEQAAAEK.R
*	HsYL1_Ti_104.1398.	3.1522	0.2007	1193.54	1194.376	4316.6	2	592.9	70	2	R.LGHELQQAGLK.T
*	HsFlag-NUFIP_Ti_2	3.068	0.121	1194.09	1194.376	7179.5	3	847.8	70	5	R.LGHELQQAGLK.T
*	HsFLAG-Lin9_Ti_20	4.4267	0.331	1566.57	1566.714	7061	1	1469.8	76.9	6	R.SLEAQVAHADQQLR.D
*	HsFlag-DPCD_Ti_20	2.738	0.1884	1925.08	1925.062	4426.8	1	527.8	55.6	1	R.TQPDGTSVPGEPASPISQR.L
*	HsYL1_Ti_105.2507.	5.2305	0.4987	2158.85	2158.546	8998.5	1	2334.6	69.4	3	R.LPPKVESLESLYFTPIPAR.S
*	HsFlag-DPCD_Ti_20	4.1815	0.4507	2194.52	2194.36	9229.8	1	1168.4	52.5	2	R.SQAPLESSLDSLGDVFLDSGR.K
*	HsFLAG-Lin9_Ti_20	4.353	0.3551	2046.69	2046.155	4740.4	1	627.3	55.9	2	K.KLDVEEPDSANSSFYSTR.S
*	HsFLAG-p53-DNA-D	3.8993	0.3935	1564.77	1563.707	7242	1	1204.7	71.4	1	R.VSLEPHQGPGTPESK.K
gi|8922789|re	5	32	17.40%	357	41739	6.2	paraspeckle protein 1 [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	4.4363	0.4019	1840	1839.052	3373	1	603.2	70	7	R.LFVGNLPTDITEEDFK.R
*	HsARP6-FLAG_Ti_1	2.6053	0.26	1115.44	1116.305	4985.7	1	563.9	65	3	R.FATHGAALTVK.N
*	HsFLAG-Lin9_Ti_20	5.1027	0.3989	2533.23	2533.841	9525.6	1	1309.3	47.7	12	K.NLSPVVSNELLEQAFSQFGPVEK.A
*	HsFLAG-FLJ20729_	5.0848	0.2917	2535.31	2533.841	9751.6	1	1480.2	35.2	2	K.NLSPVVSNELLEQAFSQFGPVEK.A
*	HsFlag-NUFIP_Ti_2	3.8033	0.2105	1290.4	1290.508	5702.6	1	957.5	77.3	8	K.GFVEFAAKPPAR.K
gi|4507521|re	5	5	17.30%	623	67878	7.7	transketolase [Homo sapiens]				
*	HsFLAG-p53-DNA-D	2.9249	0.216	2020.99	2021.278	4332.5	1	375.7	50	1	K.ILATPPQEDAPSVDIANIR.M
*	HsH2AZ-FLAG_293_	4.139	0.4987	1886.48	1886.066	5439.2	1	594.7	55.9	1	R.SVPTSTVFYPSDGVATEK.A

*	HsFlag-VPS71_Ti_1(	4.315	0.387	2508.94	2509.695	5839.5	1	889.7	52.4	1	R.TSRPENAIIYNNNEDFQVGQAK.V
*	HsFlag-VPS71_Ti_1(	2.6051	0.1577	1542.85	1542.862	4808.3	4	344.8	58.3	1	R.VLDPFTIKPLDRK.L
*	HsFlag-VPS71_Ti_1(	3.6418	0.2667	3756.88	3755.176	8123.3	1	764.9	24.3	1	R.ILTVEDHYYEGGIGEAVSSAVVGEPGITVTHLAVNR.V
gi|56676330|r	7	44	17.20%	553	61207	9.7	HP1-BP74 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1(	5.0428	0.4266	1559.57	1559.892	6528	1	1436.3	75	19	K.ALPLIVGAQLIHADK.L
*	HsFLAG-p53-DNA-D	4.0934	0.3407	1730.01	1731.005	4687.4	1	805.2	66.7	6	K.KTIPSWATLSASQLAR.A
*	HsFLAG-ARP6_Ti_1	4.3757	0.4619	1602	1602.831	4501.9	1	824.4	75	2	K.TIPSWATLSASQLAR.A
*	HsFlag-VPS71_Ti_1(	4.8071	0.2846	2393.1	2390.859	8714.4	1	1468.5	35.2	1	K.PLLGGSLMEYAILSAIAAMNEPK.T
*	HsFlag-NUFIP_Ti_11	3.3467	0.1707	2258.84	2259.544	5617.6	4	282.4	41.7	1	K.YVLENHPGTNSNYQMHLLK.K
*	HsFlag-NUFIP_Ti_11	3.7768	0.1786	2260.71	2259.544	4133.5	2	538.6	36.1	1	K.YVLENHPGTNSNYQMHLLK.K
*	HsFLAG-p53-DNA-D	4.3587	0.4321	2508.83	2510.86	5563.4	1	560.2	42.9	14	K.GFSGTFQLCFPYYPSPGVLFPK.K
gi|4505939|re	22	58	17.10%	1970	217204	7.4	PolII_Rpb1 {DNA directed RNA polymerase II polypeptide A; polymerase (RNA) II (DNA directed) polypeptide				
*	HsFlag-NUFIP_Ti_1(	4.4352	0.37	1596.5	1596.724	5483.5	1	1034.8	70	2	-.MHGGGPPSGDSACPLR.T
*	HsFlag-NUFIP_Ti_1(	4.0079	0.217	1488.85	1488.727	7112.6	1	1436.1	75	5	K.RVQFGVLSPDELK.R
*	HsFlag-NUFIP_Ti_1(	3.5655	0.1773	1488.66	1488.727	6854.7	1	1118.6	75	2	R.VQFGVLSPDELKR.M
*	HsFlag-NUFIP_Ti_1(	6.2476	0.444	2527.42	2528.003	4903.9	1	1570.5	44.3	5	R.MIVTPQSNRPVMGIVQDTLTAVR.K
*	HsFlag-NUFIP_Ti_1(	3.1581	0.2137	2529.22	2528.003	5802.2	3	274.5	34.1	1	R.MIVTPQSNRPVMGIVQDTLTAVR.K
*	HsFlag-NUFIP_Ti_11	3.293	0.1521	1119.48	1119.396	4485.9	1	771.3	88.9	2	K.VPQPAILKPR.P
*	HsFlag-NUFIP_Ti_11	3.1534	0.1143	1781.91	1782.105	3966.2	1	472	60.7	1	K.QIFSLIIPGHINCIR.T
*	HsFlag-NUFIP_Ti_1(	4.665	0.4131	2445.43	2445.753	6801.8	1	942.7	35.2	4	K.SLGTSAGSLVHISYLEMGHDITR.L
*	HsFlag-NUFIP_Ti_11	5.8363	0.4427	3433.11	3433.886	7908.4	1	1423	30.8	3	R.LFYSNIQTVINNWLLIEGHTIGIGDSIADSK.T
*	HsFLAG-p53-DNA-D	4.7134	0.4161	1663.42	1663.787	5246.9	1	1047.3	71.4	4	K.AHNNELEPTPGNTLR.Q
*	HsFlag-NUFIP_Ti_1(	4.3557	0.3519	1775.54	1775.958	6651.4	1	1450	71.4	7	R.TLPHFIKDDYGPESR.G
*	HsFlag-NUFIP_Ti_1(	4.2462	0.3374	2649.38	2649.983	6732.5	1	705.5	29.3	1	R.GFVENSYLAGLTPTEFFFHAMGGR.E
*	HsFlag-NUFIP_Ti_1(	3.9607	0.299	2650.12	2649.983	6080.3	1	491.9	39.1	3	R.GFVENSYLAGLTPTEFFFHAMGGR.E
*	HsFlag-NUFIP_Ti_1(	2.0101	0.1919	1019.45	1020.217	4845.9	8	446.5	68.8	1	R.LPSDLHPIK.V
*	HsFlag-NUFIP_Ti_1(	3.1165	0.2522	1020.39	1020.217	4552.6	1	928.8	93.8	2	R.LPSDLHPIK.V
*	HsFLAG-UTX1_Ti_2(	4.7236	0.4523	1794.09	1794.999	7083.1	1	2411.6	80	5	R.LSGEAFDWLLGEIESK.F
*	HsFlag-NUFIP_Ti_11	5.1292	0.3778	4130.69	4131.67	7538.3	1	1297.9	26.3	1	K.N
*	HsFLAG-p53-DNA-D	4.0103	0.3555	1490.37	1490.743	9593	1	1618.7	73.1	4	K.TPSLTVFLLGQSAR.D
*	HsFlag-NUFIP_Ti_1(	5.1986	0.4084	2244.68	2243.314	8309.6	1	1159.9	55.3	2	K.INAGFGDDLNCIFNDDNAEK.L
*	HsFLAG-UTX1_Ti_2(	3.0345	0.3536	2079.01	2078.37	10793.9	1	761	47.2	1	R.TTSNDIVEIFTVLGIEAVR.K
*	HsFlag-NUFIP_Ti_1(	3.368	0.2251	1492.87	1491.678	9589	1	1560.3	77.3	1	R.HLALLCDTMTCR.G
*	HsFlag-FLJ20643_Ti	4.494	0.3947	2258.95	2259.474	7030.3	1	836	50	1	K.YSPTSPTYSPTSPVYTPTSPK.Y
gi|44889481|r	14	31	17.10%	1078	124951	9.2	myosin IB [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.793	0.3233	1710.23	1710.924	4783	1	765.7	69.2	2	R.SLPIYSPEKVEEYR.N
*	HsFLAG-ARP6_Ti_1	5.6172	0.4449	2172.29	2173.389	6982.7	1	1915.6	76.5	2	R.NFYELSPHIFALSDEAYR.S
*	HsFLAG-ARP6_Ti_1	3.5012	0.237	2175.92	2173.389	4543.5	1	834.4	39.7	1	R.NFYELSPHIFALSDEAYR.S
	HsFLAG-Lin9_Ti_20	4.1894	0.306	1860.62	1859.089	6844	1	882.5	59.4	2	K.EQLLQSNPVLEAFGNAK.T
*	HsFLAG-BC014022_	4.5693	0.2081	2211.54	2210.494	9029.6	1	2106.7	44.4	5	R.NFHVFYQLLSGASEELLNK.L
*	HsFLAG-ARP6_Ti_1	2.7631	0.0822	1290.8	1290.462	6512.2	1	1177.7	80	1	K.LGNIEFKPESR.V
*	HsVPS71-FLAG_Ti_	2.0694	0.1664	1102.6	1103.261	2226.3	3	122.4	66.7	4	R.VNGLDESKIK.D
*	HsMRGBP-FLAG_Ti_	2.6079	0.1645	1103.32	1103.261	4972.4	3	864.2	72.2	1	R.VNGLDESKIK.D

*	HsFLAG-ARP6_Ti_1	3.9177	0.4246	1594.34	1594.733	3958.9	1	655.3	75	2	R.FLNDTSLPHSCFR.I
*	HsFLAG-Lin9_Ti_20	2.5222	0.1512	1088.28	1089.239	10236.3	2	1204.1	77.8	1	K.RPPTAGSQFK.A
*	HsFLAG-ARP6_Ti_1	4.2948	0.3468	2414.64	2414.674	4684.9	1	851.1	57.5	6	R.SGVEVLFNELEIPVEEYSFGR.S
*	HsFLAG-ARP6_Ti_1	2.9735	0.3234	1803.86	1804.015	7933.4	2	752.5	50	1	K.EAVTTIAAYWHGTQVR.R
*	HsFLAG-ARP6_Ti_1	4.3965	0.352	2182.21	2183.469	5692.4	1	1627.1	71.1	2	K.ALYPSSVGQPFQGAYLEINK.N
*	HsFLAG-Lin9_Ti_20	4.1894	0.2854	1730	1731.045	12151.4	1	1680.9	67.9	1	R.IFLLTNNNLLLADQK.S
gi|4504895|re	5	11	17.10%	538	60307	5	karyopherin alpha 1 [Homo sapiens]				
*	HsFlag-FLJ90652_2	3.7797	0.3161	2150.02	2149.501	4161.1	1	774.6	64.7	4	R.DYVLDCNILPPLLQLFSK.Q
*	HsFLAG-Lin9_Ti_20	4.6445	0.2998	3507.17	3506.988	6230.4	1	807.4	28.1	3	R.AVGNIVTGDDIQTQVILNCSALQSLLHLLSSPK.E
	HsFLAG-TIP49a_Ti_	3.4162	0.2619	1393.24	1392.617	5742.1	1	859.8	72.7	1	K.PLCDLLTVMDSK.I
	HsFLAG-Lin9_Ti_20	5.0013	0.2717	1553.05	1552.858	10861.1	1	2767	80.8	2	K.IVQVALNGLENILR.L
	HsFlag-FLJ90652_2	4.8161	0.3707	1909.07	1907.09	9756.6	1	2054.1	75	1	K.IEFLQSHENQEIYQK.A
gi|5803207|re	4	23	17.10%	240	27872	8.8	U2 small nuclear RNA auxillary factor 1 isoform a [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.1585	0.2502	1374.44	1374.41	6433.8	1	721.8	70.8	2	R.NPQNSSQSADGLR.C
	HsFlag-NUFIP_Ti_1	5.3315	0.4411	2114.92	2115.356	7142.3	1	1334.7	64.7	14	R.WFNGQPIHAELSPVTDFR.E
	HsFlag-VPS71_Ti_1	4.8516	0.3722	2116.79	2115.356	5141.9	1	639.7	39.7	5	R.WFNGQPIHAELSPVTDFR.E
	HsFlag-NUFIP_Ti_11	3.1112	0.2405	1211.42	1211.39	7349.4	3	871.1	72.2	2	R.GGFCNFMHLK.P
gi|31563378|r	2	3	17.10%	245	26599	4.7	integrin beta 4 binding protein isoform a [Homo sapiens]				
gi|4504771|re	2	3	17.10%	245	26599	4.7	integrin beta 4 binding protein isoform a [Homo sapiens]				
	HsFlag-NUFIP_Ti_11	4.171	0.4071	2086.21	2086.315	7569.1	1	1169.2	41.2	1	R.HGLLVPNNTTDQELQHIR.N
	HsFLAG-Lin9_Ti_20	3.7703	0.3265	2584.75	2585.871	6813	1	535.1	39.1	2	K.TSIEDQDELSSLLQVPLVAGTVNR.G
gi|4506635|re	2	7	17.00%	135	15860	11.3	ribosomal protein L32 [Homo sapiens]				
gi|89026739|r	2	7	17.00%	135	15751	10.9	PREDICTED: similar to 60S ribosomal protein L32 [Homo sapiens]				
gi|89025918|r	2	7	17.00%	135	15751	10.9	PREDICTED: similar to 60S ribosomal protein L32 [Homo sapiens]				
gi|89024761|r	2	7	17.00%	135	15751	10.9	PREDICTED: similar to 60S ribosomal protein L32 [Homo sapiens]				
gi|55743130|r	2	7	17.00%	135	15860	11.3	ribosomal protein L32 [Homo sapiens]				
gi|55743128|r	2	7	17.00%	135	15860	11.3	ribosomal protein L32 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.0516	0.2325	1249.29	1249.474	7572.3	1	910.4	72.2	2	K.ELEVLLMCNK.S
	HsFLAG-ARP6_Ti_1	4.8985	0.2369	1466.43	1466.557	7715.1	1	2179.8	87.5	5	K.SYCAEIAHNVSSK.N
gi|14110407|r	6	10	16.90%	420	46437	9.6	heterogeneous nuclear ribonucleoprotein D-like [Homo sapiens]				
gi|4885423|re	6	10	16.90%	420	46437	9.6	heterogeneous nuclear ribonucleoprotein D-like [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.6223	0.3153	1470.54	1470.727	6240.3	1	1070.9	75	3	K.MFIGGLSWDTSKK.D
	HsFLAG-p53-DNA-D	2.9122	0.228	914.45	915.123	2938.3	3	645.5	85.7	3	R.GFGFVLFK.D
	HsFLAG-p53-DNA-D	2.0301	0.1206	915.7	915.123	8175.2	7	803	78.6	1	R.GFGFVLFK.D
	HsFLAG-FLJ20729_	2.8998	0.1693	1706.56	1706.89	5612.5	8	612.2	56.7	1	K.VFVGGLSPDTSEEQIK.E
	HsFLAG-p53-DNA-D	4.1704	0.3201	2202.93	2204.456	11103	1	1002.2	50	1	K.EYFGAFGEIENIELPMDTK.T
	HsFLAG-Lin9_Ti_20	3.7759	0.2304	1862.74	1863.043	6623.9	1	807.5	60.7	1	R.RGFCFITYTDEEPVK.K
gi|6912618|re	4	9	16.90%	361	40877	6.6	glutaminyl-peptide cyclotransferase precursor [Homo sapiens]				
*	HsFlag-DPCD_Ti_20	4.2244	0.272	1492.78	1493.7	6254.6	1	868.4	65.4	5	R.SFSNIISTLNPTAK.R
*	HsFLAG-p53-DNA-D	2.9875	0.251	1746.43	1744.044	10475.6	1	1298.5	64.3	1	R.LQAIEHELHELGLLK.D
*	Hs293Flag-Ies2_Ti_1	2.8927	0.3226	2433.59	2433.685	10521	1	824.4	47.4	1	R.YFQNYSYGGVIQDDHIPFLR.R
*	HsFLAG-RPB5MP_2	4.6145	0.3193	1488.6	1487.825	10272.9	1	1745	77.3	2	K.ILQVFVLEYLHL.-
gi|14110428|r	4	23	16.80%	303	33299	5.2	heterogeneous nuclear ribonucleoprotein C isoform a [Homo sapiens]				

gi|4758544|re	4	23	17.60%	290	31966	5.2	heterogeneous nuclear ribonucleoprotein C isoform b [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.8904	0.2855	1318.32	1317.615	5847.6	2	1082.2	77.3	10	R.VFIGNLNTLVVK.K
	HsFLAG-p53-DNA-D	4.4725	0.3306	1330.48	1330.486	7228.3	1	1555	85	7	K.GFAFVQYVNER.N
	HsFLAG-ARP6_Ti_1	4.1489	0.1617	1684.74	1684.004	6637.3	1	1515.6	73.3	4	R.MIAGQVLDINLAAEPK.V
	HsFLAG-ARP6_Ti_1	3.2624	0.2046	1415.91	1416.615	4012.8	1	313.1	63.6	2	K.QKVDSLLENLEK.M
gi|4506411|re	5	8	16.70%	587	63542	4.7	Ran GTPase activating protein 1 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	6.4994	0.458	4753.63	4751.431	7699.6	1	1085.9	23.3	2	EALLK.S
*	HsFlag-VPS71_Ti_1	3.3712	0.2485	1255.53	1255.426	6882.6	2	963.5	75	2	K.ILAAALTECHR.K
*	HsFLAG-Lin9_Ti_20	3.7303	0.2224	1383.48	1383.6	11075.6	1	2147.2	81.8	1	K.ILAAALTECHRK.S
*	HsYL1_Ti_101.1718.	2.5941	0.3101	1720.28	1719.843	6328.7	2	701	56.7	1	K.SSVLIAQQTDTSDPEK.V
*	HsSrcap_Ti_206.311	4.4151	0.4039	2577.56	2577.993	4997.2	1	534.8	43.5	2	K.ALAPLLLAFVTKPNSALESCSFAR.H
gi|16950609|r	4	5	16.70%	414	47669	6	mitochondrial ribosomal protein S27 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_11	2.526	0.2382	1201.57	1201.452	3641.5	1	476.3	75	1	R.KLPVSSLTISR.L
*	HsFlag-NUFIP_Ti_1	2.7571	0.1583	1230.87	1230.493	9136.7	1	1251.5	72.7	1	R.NFGASLLLPGLK.Q
*	HsFlag-NUFIP_Ti_11	4.1788	0.4304	2073.31	2074.451	7332.4	1	1093.6	59.4	1	R.AVYHNMPLIWKPGYLDR.A
*	HsFlag-NUFIP_Ti_1	4.6418	0.4175	3516.23	3516.855	7412.8	1	864.5	26.8	2	K.LSTCEAEDIATYEQNLQQWHLDLVQLIQR.E
gi|19923935|r	2	2	16.70%	293	33238	8.1	hypothetical protein LOC112869 [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	4.3015	0.1974	1522.09	1521.841	6853.9	1	1233.3	75	1	R.IAELLTELHQLIK.Q
*	HsFLAG-TCF3_Ti_1	4.2913	0.2764	4033.54	4033.403	9177	1	655.7	21.4	1	R.ALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQR.Y
gi|5803036|re	3	12	16.70%	305	30841	9.3	heterogeneous nuclear ribonucleoprotein A0 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	5.3732	0.392	1691.42	1691.925	7672.2	1	2342.7	83.3	4	K.LFIGGLNVQTSESGLR.G
*	HsFLAG-p53-DNA-D	5.5703	0.4512	2178.35	2179.348	9580.1	1	1372.4	55.3	3	K.GDVAEGDLIEHFSQFGTVEK.A
*	HsFLAG-p53-DNA-D	4.4573	0.3648	1716.45	1716.85	7604.8	1	2086.5	82.1	5	R.GFGFVYFQNHDAADK.A
gi|16306492|r	2	10	16.70%	240	27503	7.1	cell division cycle 2 protein isoform 2 [Homo sapiens]				
gi|4502709|re	2	10	13.50%	297	34095	8.4	cell division cycle 2 protein isoform 1 [Homo sapiens]				
	HsSrcap_Ti_203.551	3.9631	0.3312	2213.18	2213.535	6186.4	1	674.6	44.7	8	R.YSTPVDIWSIGTIFAELATK.K
	HsScrap_Ti_102.288	2.8432	0.3312	2289.3	2290.491	4294.8	1	276.9	39.5	2	R.ALGTPNNEVWPEVESLQDYK.N
gi|4504183|re	2	4	16.70%	210	23356	5.6	glutathione transferase [Homo sapiens]				
*	HsFLAG-ARP8_Ti_1	2.5811	0.1856	1884.57	1885.084	7681.7	1	924.8	56.7	1	K.FQDGDLTLYQSNTILR.H
*	HsFLAG-ARP6_Ti_1	3.6829	0.2612	2117.47	2118.28	7107.6	1	972.9	55.6	3	K.DQQEAALVDMVNDGVEDLR.C
gi|4506711|re	2	8	16.70%	84	9461	9.5	ribosomal protein S27 [Homo sapiens]				
gi|89035892|r	2	8	16.70%	84	9461	9.5	PREDICTED: similar to ribosomal protein S27 [Homo sapiens]				
gi|89035229|r	2	8	16.70%	84	9461	9.5	PREDICTED: similar to ribosomal protein S27 [Homo sapiens]				
gi|88952642|r	2	8	15.40%	91	10338	9.2	PREDICTED: similar to ribosomal protein S27 [Homo sapiens]				
gi|88948822|r	2	8	16.70%	84	9461	9.5	PREDICTED: similar to ribosomal protein S27 [Homo sapiens]				
gi|88943618|r	2	8	15.40%	91	10338	9.2	PREDICTED: similar to ribosomal protein S27 [Homo sapiens]				
gi|88942612|r	2	8	16.70%	84	9461	9.5	PREDICTED: similar to ribosomal protein S27 [Homo sapiens]				
gi|7705706|re	2	8	16.70%	84	9477	9.5	ribosomal protein S27-like [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	4.4005	0.4347	1685.38	1684.951	5820.2	1	784.3	65.4	6	K.RLVQSPNSYFMDVK.C
	HsFLAG-ARP6_Ti_1	4.0078	0.2386	1528.3	1528.763	6360.4	1	1372.7	79.2	2	R.LVQSPNSYFMDVK.C
gi|4506891|re	2	7	16.60%	277	32134	4.2	SET translocation (myeloid leukemia-associated) [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.2229	0.1428	3729.93	3728.155	7078.9	1	527	23.4	1	K.IPNFWVTTFVNHPQVSALLGEEDEEALHYLTR.V
	HsFlag-VPS71_Ti_1	4.6723	0.2036	1842.17	1841.971	7638.5	1	1833	76.9	6	R.IDFYFDENPYFENK.V

gi|15431295|r	5	27	16.60%	211	24261	11.7	ribosomal protein L13 [Homo sapiens]				
gi|15431297|r	5	27	16.60%	211	24261	11.7	ribosomal protein L13 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.7995	0.3286	1346.02	1346.534	6524.8	1	987.2	80	2	R.RVATWFNQPAR.K
	HsFlag-Ies6_293_Ti_	3.0108	0.2332	1190.59	1190.347	4958.9	5	664.6	77.8	2	R.VATWFNQPAR.K
	HsFLAG-TCF3_Ti_1	4.2455	0.3621	1232.9	1233.324	7060.5	1	1488.9	85	6	K.STESLQANVQR.L
	HsFLAG-TCF3_Ti_1	2.4416	0.2962	1382.64	1383.692	5796.7	3	239	54.2	2	K.LATQLTGPVMPVR.N
	HsFLAG-ARP6_Ti_1	3.9852	0.3167	1383.38	1383.692	7011.3	2	1304.2	75	15	K.LATQLTGPVMPVR.N
gi|45446743|r	9	20	16.50%	938	102975	7	DEAD box polypeptide 42 protein [Homo sapiens]				
gi|45446747|r	9	20	16.50%	938	102975	7	DEAD box polypeptide 42 protein [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	5.1331	0.5017	1982.43	1982.117	8348	1	1563.7	63.2	2	K.LPQQSHSAFGATSSSSGFGK.S
	HsFlag-VPS71_Ti_1	3.2239	0.2496	2464.15	2464.821	6129.7	1	441	40	1	K.KIIDPLPPIDHSEIDYPPFEK.N
	HsFLAG-FLJ20729_	4.2082	0.3397	2464.57	2464.821	8695.6	1	1316.2	36.2	2	K.KIIDPLPPIDHSEIDYPPFEK.N
	HsFLAG-p53-DNA-D	4.4489	0.2166	2588.29	2588.836	7590.7	2	1171.3	37.5	1	K.NFYNEHEEITNLTPQQLIDLR.H
	HsFlag-VPS71_Ti_1	4.9045	0.4981	2416.93	2417.69	5121.6	1	955.6	57.1	3	R.KSEYTQPTPIQCQGVPVALSGR.D
	HsFlag-NUFIP_Ti_2	4.2127	0.3211	2417.67	2417.69	6048.1	1	825.1	36.9	1	R.KSEYTQPTPIQCQGVPVALSGR.D
	HsFlag-DPCD_Ti_20	3.5569	0.3402	1823.99	1824.05	4040.6	1	516.5	56.2	5	K.ELEPGDGPIAVIVCPTR.E
	HsARP6-FLAG_Ti_1	4.2007	0.4392	1340.59	1340.563	6195.4	1	1454.2	83.3	2	K.DIPVLVATDVAAR.G
	HsFLAG-Lin9_Ti_20	4.4095	0.4394	3813.51	3814.975	5750	1	534.5	21.9	3	AAK.G
gi|8400738|re	3	5	16.50%	393	43712	6.9	tumor protein p53 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	3.1495	0.3453	2750.63	2752.142	6382.4	2	393.1	33.9	2	R.VAPAPAAPTPAAPAPAPSWPLSSSVPSQK.T
*	HsFLAG-Lin9_Ti_20	3.7304	0.4139	1910.73	1912.119	6091.6	1	848.3	59.4	2	K.TCPVQLWVDSTPPPGTR.V
*	HsFLAG-p53-DNA-D	3.3678	0.3611	2069.54	2069.409	7335.4	1	856.2	55.6	1	R.RPILTIITLEDSSGNLLGR.N
gi|4885371|re	4	19	16.50%	194	20863	10.8	H1 histone family, member 0 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.7507	0.296	1440.6	1439.667	5972.4	1	1757	87.5	11	K.YSDMIVAAIQAEK.N
*	HsFLAG-p53-DNA-D	2.8416	0.1223	1060.45	1061.137	7450.5	1	694.2	72.2	1	K.VGENADSQIK.L
*	HsFLAG-p53-DNA-D	3.2552	0.2584	1061.28	1061.137	8105.2	1	1559	88.9	2	K.VGENADSQIK.L
*	HsFlag-NUFIP_Ti_1	2.9542	0.1795	987.31	987.231	4392.9	7	1026.3	100	5	K.RLVTTGVLK.Q
gi|10863997|r	3	6	16.40%	531	57491	8.7	polypyrimidine tract binding protein 2 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.2675	0.441	2101.76	2099.475	10544.5	1	1854.8	60.5	2	R.KLPGEVTETEVIALGLPFGK.V
*	HsFLAG-Lin9_Ti_20	5.5024	0.393	3668.11	3666.123	10107	2	878.2	22.2	2	R.AQAVLQAVTAVQTANTPLSGTTVSESAVTPAQSPVLR.I
*	HsFLAG-FLJ20729_	4.2807	0.3662	2689.01	2688.1	9043	1	1409.4	31	2	K.ETSLLAVPGALSPLAIPNAAAAAAAAAAGR.V
gi|21361350|r	3	4	16.40%	354	39038	4.8	serologically defined colon cancer antigen 3 [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	4.4819	0.5264	2311.75	2312.458	7099.4	1	1118.3	52.2	1	R.VSPASPAGSPSADFAVHGESLGDR.H
*	HsFLAG-TCF3_Ti_1	4.0485	0.3191	2003.27	2003.309	6381.7	1	1092.7	42.2	2	K.LKQEISLLQAQVSNFQR.E
*	HsFLAG-TCF3_Ti_1	4.7245	0.3901	1799.42	1799.118	8082.4	1	1377.1	65.6	1	K.QLVSGAETLNLVAEILK.S
gi|5453599|re	3	9	16.40%	286	32949	5.8	capping protein (actin filament) muscle Z-line, alpha 2 [Homo sapiens]				
	HsFlag-FLJ90652_2	3.7224	0.1765	1199.09	1198.408	6513.5	1	1344.7	94.4	5	R.LLLNNDNLLR.E
*	HsFlag-FLJ90652_2	6.009	0.4242	2315.76	2316.585	8428.9	1	2162.4	47.4	2	K.KIDGQQTIIACIESHQFQAK.N
	HsFlag-FLJ90652_2	4.9973	0.4721	2029.62	2030.247	9558.4	1	2401.2	75	2	K.IQVHYYEDGNVQLVSHK.D
gi|51100974|r	11	22	16.30%	1006	116202	9.4	myosin ID [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.6592	0.1029	2104.36	2105.401	7802.3	1	550.6	47.1	1	R.ELYERPPHLFAIADAAYK.A
*	HsFLAG-ARP6_Ti_1	3.4498	0.269	2130.36	2129.398	11402.8	1	843.3	44.1	1	R.SFHSFYQLLQGGSEQMLR.S
*	HsFLAG-Lin9_Ti_20	2.9098	0.3113	1680.57	1680.901	8104.7	1	984.3	60.7	1	K.SLSSYNYIHVGAQLK.S

*	HsFLAG-ARP6_Ti_1	3.7705	0.3839	1651.44	1651.943	3665.8	1	719.8	76.9	4	K.VIGFKPEEIQTVYK.I
*	HsFLAG-ARP6_Ti_1	2.5693	0.1153	1422.52	1422.686	6700.5	5	561.8	59.1	1	K.RLMYNSSNPVLK.N
*	HsFLAG-ARP6_Ti_1	2.5835	0.1126	1118.82	1118.365	5241.9	6	548.8	72.2	1	K.RPLTAATLFK.N
*	HsFLAG-Lin9_Ti_20	4.025	0.3734	1570.53	1570.789	7027.7	1	1397.5	79.2	3	R.HQVEYLGLLENVR.V
*	HsFLAG-Lin9_Ti_20	4.3807	0.366	1524.86	1524.72	8695.9	1	1899	86.4	3	R.RFEEALQTIFNR.W
*	HsFLAG-ARP6_Ti_1	6.3534	0.4724	3021.65	3022.341	8096.9	1	2140.2	38	4	R.AWEGNYLASKPDTPQTSGTFVPVANELK.R
*	HsFLAG-ARP6_Ti_1	3.3469	0.1608	1426.51	1426.642	6067.1	3	764.3	70	1	K.YMNVLFSCHVR.K
*	HsFLAG-Lin9_Ti_20	4.1938	0.3697	1425.34	1425.714	5989	1	1089.8	75	2	R.IGELVGVLVNHFK.S
gi|21359884|r	8	12	16.30%	884	99992	9.2	calcium homeostasis endoplasmic reticulum protein [Homo sapiens]				
*	HsFlag-NUFIP_Ti_11	4.0654	0.4192	1504.71	1505.701	7284.3	1	1536	79.2	3	K.SPPHCELMAGHLR.N
*	HsFLAG-Lin9_Ti_20	3.56	0.39	1970.03	1970.236	4817.1	1	752.6	65.6	1	K.VVVPIYCTSFLAVEEDK.Q
*	HsFlag-NUFIP_Ti_10	5.6584	0.4152	4084.5	4085.469	8277.6	1	1194	26.5	1	K.TQHEEFVTSLAQQQQQQQQQQQQLQMPQMEAEVK.A
*	HsFlag-NUFIP_Ti_10	4.3608	0.3103	3888.95	3891.042	7600.8	1	902.4	26.5	1	R.DAPWNNQPDAAWNSQFEGPWNSQHEQPPWGGGQR.E
*	HsFlag-NUFIP_Ti_11	3.7234	0.25	2027.26	2027.29	4418.9	1	687.6	41.2	2	R.LLAAVEAFYSPPSHDRPR.N
*	HsFLAG-UTX1_Ti_2	2.6455	0.2155	2028.03	2027.29	8263.8	2	469.3	44.1	1	R.LLAAVEAFYSPPSHDRPR.N
*	HsFLAG-p53-DNA-D	5.0325	0.4758	1876.21	1876.979	8280.4	1	1542.8	71.4	2	R.NSEGWEQNGLYEFFR.A
*	HsFLAG-ARP5_Ti_1	2.8885	0.1831	1482.61	1483.726	9925.4	1	1176.7	66.7	1	R.LGEENKGHQMLVK.M
gi|23110925|r	1	2	16.30%	239	25358	4.9	proteasome beta 6 subunit [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.8525	0.3301	4058.11	4058.494	8066.2	1	852.3	21.7	2	R.SGSAADTQAVADAVTYQLGFHSIELNEPPLVHTAASLFK.E
gi|7705320|re	2	6	16.30%	203	22620	8	hepatoma-derived growth factor, related protein 3 [Homo sapiens]				
	HsARP6-FLAG_Ti_1	4.2542	0.3495	1971.51	1973.281	5668.1	1	836.9	59.4	5	K.YPIFFFGTHETAFLGPK.D
*	HsFLAG-Lin9_Ti_20	2.5886	0.2553	1803.29	1803.969	8622.8	1	422.4	46.7	1	K.GFNEGLWEIENNPGVK.F
gi|4507131|re	1	3	16.30%	86	9725	4.7	small nuclear ribonucleoprotein polypeptide F [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.0158	0.2227	1501.49	1501.871	10130.3	1	2040.9	76.9	3	K.PFLNGLTGKPVMVK.L
gi|4885403|re	19	45	16.20%	1938	198471	7.3	host cell factor C1 (VP16-accessory protein) [Homo sapiens]				
*	HsFLAG-FLJ20436_	3.2219	0.2499	1459.18	1459.555	5286.1	1	684.7	68.2	2	K.YSNDLYELQASR.W
*	HsFLAG-FLJ20436_	4.1291	0.4177	1686.31	1686.782	6458.8	1	1245.5	67.9	1	K.CYLFGGLANDSEDPK.N
*	HsFLAG-FLJ20729_	3.0285	0.2884	1906.01	1905.158	9699.7	1	1074.4	56.7	1	R.LGDLWTLDIDTLTWNK.P
*	HsFlag-VPS71_Ti_1	5.3692	0.4394	2980.47	2980.434	4790.1	1	485	26.9	1	R.LGDLWTLDIDTLTWNKPSLSGVAPLPR.S
*	HsFLAG-FLJ20436_	2.7854	0.1788	1094.6	1094.299	5288.5	8	681.6	65	1	K.PSLSGVAPLPR.S
*	HsFLAG-p53-DNA-D	2.8377	0.2456	1128.48	1129.258	5494.9	1	714.5	75	6	R.SLHSATTIGNK.M
*	HsFlag-VPS71_Ti_1	4.9849	0.5343	1857.79	1857.236	5228.2	1	1316.7	76.7	6	K.MYVFGGWVPLVMDDVK.V
*	HsFLAG-FLJ20436_	2.3811	0.2304	1169.44	1170.28	4094.4	1	323	60	3	R.AGHCAVAINTR.L
*	HsFLAG-FLJ20436_	3.103	0.4336	2679.86	2680.974	6646.3	1	623.9	39.6	1	R.ANTNSLEVSWGAVATADSYLLQLQK.Y
*	HsFLAG-Lin9_Ti_20	3.4936	0.3878	2675.34	2675.998	7755	1	586.9	36.5	2	K.YDIPATAATATSPTPNPVPSVPANPPK.S
*	HsFlag-VPS71_Ti_1	3.4428	0.3015	2270.48	2270.609	5799.1	1	386.8	36.4	1	K.VTGPQATTGTPLVTMRPASQAGK.A
*	HsFLAG-p53-DNA-D	3.6003	0.4127	1597.78	1597.852	3228.2	1	422	59.4	2	K.SPISVPGGSALISNLGK.V
*	HsFLAG-FLJ20436_	4.4782	0.3394	1638.32	1636.892	8249.3	1	1375	66.7	7	K.IATGHGQQGVTQVVLK.G
*	HsFLAG-FLJ20436_	3.3272	0.2404	1346.74	1345.582	6726.5	2	984.7	66.7	2	R.SPAFVQLAPLSSK.V
*	HsFLAG-Lin9_Ti_20	2.9097	0.151	2925.59	2926.296	5238.6	1	236.2	28.6	1	R.AVTTVTQSTPVPGPSVPPPEELQVSPGPR.Q
*	HsFLAG-p53-DNA-D	4.4515	0.361	2916.07	2915.357	7540.1	1	852.7	26.8	1	K.LQAAATLTEVANGIESLGVKPDLPPPPSK.A
*	HsFlag-VPS71_Ti_1	3.1817	0.1127	1263.48	1263.436	8112.3	1	1289	80	2	K.KQELQPGTAYK.F
*	HsARP6-FLAG_Ti_1	3.1266	0.1452	1490.22	1489.687	4458.1	6	624.8	65.4	1	K.TCLPGFPGAPCAIK.I

*	HsFlag-VPS71_Ti_1	3.9974	0.5024	1866.7	1867.025	5547.8	1	880.7	55.9	4	K.SPDGAHLTWEPPSVTSGK.I
gi|6677723|re	3	4	16.20%	340	38497	7.2	replication factor C 5 isoform 1 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	3.6483	0.3053	2236.5	2238.594	8354.2	1	804.3	42.1	1	K.FINEDRLPHLLLYGPPGTGK.T
	HsFLAG-Lin9_Ti_20	3.8369	0.4142	1735.33	1735.898	5791.4	1	541.4	53.6	1	K.VTEETVYTCTGHPLK.S
	HsFlag-VPS71_Ti_1	5.4382	0.4518	2389.23	2388.657	8339.1	1	1754.8	60.5	2	K.SDIANILDWMLNQDFTTAYR.N
gi|66933016|r	6	10	16.10%	514	55805	6.9	inosine monophosphate dehydrogenase 2 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.0381	0.259	1822.43	1822.111	6527.7	1	644.7	53.3	1	K.KYEQGFITDPVVLSPK.D
*	HsFlag-FLJ90652_2	2.7049	0.156	1432.14	1431.557	7572.7	2	729.2	62.5	1	R.HGFCGIPITDTGR.M
*	HsFlag-VPS71_Ti_1	2.6203	0.2131	1480.23	1482.764	11214.2	3	901.2	57.7	1	K.REDLVVAPAGITLK.E
	HsFlag-FLJ90652_2	2.7468	0.1511	1064.34	1064.186	5710.3	7	642.7	75	1	K.NRDYPLASK.D
*	HsFLAG-p53-DNA-D	4.8738	0.507	1892.78	1893.196	6978.9	1	1402.1	63.9	4	R.FGVPVIADGGIQNVGHIAK.A
*	HsFlag-VPS71_Ti_1	2.92	0.3439	1160.23	1159.285	5502.2	1	958.8	77.3	2	K.VAQGVSGAVQDK.G
gi|89030025|r	4	6	16.10%	461	49351	8.4	PREDICTED: far upstream element (FUSE) binding protein 3 isoform 4 [Homo sapiens]				
gi|89030643|r	4	6	15.30%	485	52239	8.6	PREDICTED: similar to Far upstream element binding protein 3 (FUSE binding protein 3) isoform 5 [Homo sap				
gi|89030641|r	4	6	16.10%	461	49351	8.4	PREDICTED: similar to Far upstream element binding protein 3 (FUSE binding protein 3) isoform 8 [Homo sap				
gi|89030027|r	4	6	15.30%	485	52239	8.6	PREDICTED: far upstream element (FUSE) binding protein 3 isoform 1 [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.071	0.2823	1938.96	1940.326	8454	3	554.5	47.1	1	K.MVMIQDGPLPTGADKPLR.I
	HsFlag-VPS71_Ti_1	3.5539	0.376	2247.9	2248.454	3782.6	1	469	47.6	2	R.GDWSVGAPGGVQEITYTVPADK.C
	HsFLAG-FLJ20729_	3.1778	0.2306	1567	1567.702	7095.6	1	580.2	57.7	2	K.SINQQSGAHVELQR.N
	HsFLAG-Lin9_Ti_20	3.8672	0.5558	2219.35	2220.363	9502.7	1	851.1	44.7	1	R.QQVAFYGQTLGQAQAHSQEQ.-
gi|6005854|re	3	5	16.10%	299	33296	9.8	prohibitin 2 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.7083	0.2361	1724.83	1725.043	7442.7	1	1357.6	75	2	R.IPWFQYPIIYDIR.A
*	HsFLAG-ARP6_Ti_1	4.5322	0.2963	1889.59	1890.167	6841.6	2	939.8	60	2	R.VLSRPNAQELPSMYQR.L
*	HsFLAG-TCF3_Ti_1	3.6061	0.337	2226.35	2226.491	10500.8	1	752	47.2	1	R.IYLTADNLVLNLQDESFTR.G
gi|4507357|re	2	11	16.10%	199	22391	8.2	transgelin 2 [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.6551	0.3875	2102.66	2101.32	6519.7	1	1298.9	64.7	6	R.YGINTTDIFQTVDLWEGK.N
	HsFLAG-p53-DNA-D	4.282	0.353	1596.44	1595.708	8697.8	1	1347.5	69.2	5	R.DDGLFSGDPNWFPK.K
gi|19923653|r	6	27	16.00%	530	60103	9.1	PC4 and SFRS1 interacting protein 1 isoform 2 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	2.5212	0.2536	1251.4	1251.468	2960.5	1	380.7	75	2	R.DFKPGDLIFAK.M
	HsFLAG-Lin9_Ti_20	2.9228	0.138	1566.12	1566.751	5550.6	8	680.2	60.7	1	R.VDEVPDGAVKPPTNK.L
	HsFLAG-FLJ20729_	5.2072	0.5052	1923.42	1923.265	5752.4	1	1632.1	78.1	17	K.LPIFFFGTHETAFLGPK.D
	HsFLAG-Lin9_Ti_20	3.463	0.3436	1633.82	1633.758	8029	1	881.1	65.4	2	K.GFNEGLWEIDNNPK.V
	HsFLAG-p53-DNA-D	1.9517	0.1876	1084.71	1085.252	3450.9	8	153.1	55.6	1	K.RGRPAATEVK.I
*	HsFLAG-p53-DNA-D	5.3113	0.3886	1964.8	1965.272	9670.8	1	1726.5	64.7	4	K.NMFLVGEGDSVITQVLNK.S
gi|77404397|r	7	19	15.90%	910	101997	7.2	staphylococcal nuclease domain containing 1 [Homo sapiens]				
*	HsFlag-DPCD_Ti_20	4.6334	0.387	1961.28	1961.093	9999.2	1	2112.2	63.9	2	K.DTNGENIAESLVAEGLATR.R
*	HsFlag-VPS71_Ti_1	3.6152	0.3002	1148.54	1148.351	5600	1	1183.1	88.9	3	K.PVNAIIEHVR.D
*	HsFlag-VPS71_Ti_1	3.9986	0.4247	2011.19	2010.483	3649.2	1	534.1	58.8	2	R.ALLLPDYYLVTVMLSGIK.C
*	HsFLAG-FLJ20729_	4.6376	0.3809	2306.39	2307.562	5338.1	1	760.6	55	8	R.NLPGLVQEGEPFSEEATLFTK.E
*	HsFLAG-FLJ20729_	3.4754	0.4268	1710.38	1710.844	3620.6	1	519.8	63.3	2	R.NDIASHPPVEGSYAPR.R
*	HsFLAG-Lin9_Ti_20	4.0621	0.4073	3509.15	3509.854	6195.5	1	1241.1	31.5	1	R.VLPAQATEYAFAFIQVPQDDDARTDAVDSVVR.D
*	HsFLAG-Lin9_Ti_20	3.9112	0.214	3299.88	3297.581	12429.3	1	778.4	22.3	1	R.DIQNTQCLLNVEHLSAGCPHVTLQFADSK.G
gi|5453595|re	4	7	15.80%	475	51673	8	adenylyl cyclase-associated protein [Homo sapiens]				

*	HsFLAG-FLJ20729_	5.3109	0.4578	2353.52	2352.692	6947	1	1415.6	59.1	4	K.AGAAPYVQAFDSLLAGPVAEYLK.I
*	HsFLAG-FLJ20729_	3.3533	0.2373	1758.36	1758.935	7472.6	1	703.2	53.3	1	R.ALLVTASQCQQPAENK.L
*	HsFLAG-FLJ20729_	2.8638	0.1788	1928.12	1929.183	10952.3	1	877.7	50	1	R.SALFAQINQGESITHALK.H
*	HsFLAG-Lin9_Ti_20	2.9734	0.236	2075.62	2074.249	8457.6	1	661.3	47.1	1	R.VENQENVSNLVIEDTELK.Q
gi|8393159|re	1	3	15.80%	146	15921	4.4	calmodulin-like skin protein [Homo sapiens]				
*	HsYL1-FLAG_Ti_20	4.5624	0.439	2265.04	2264.454	7874.6	1	680.2	40.9	3	K.AFSAVDTDGNGTINAQELGAALK.A
gi|57164975|r	22	52	15.70%	1411	144314	9	Treacher Collins-Franceschetti syndrome 1 isoform b [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.4659	0.2728	1517.6	1517.858	4878.9	1	930.6	81.8	4	R.ELLPLIYHHLLR.A
	HsSrcap_Ti_205.461	4.6284	0.3437	2878.19	2878.223	4642.8	1	476.2	30.4	2	K.CFLAQPVTLLDIYTHWQQTSELGR.K
	HsFLAG-p53-DNA-D	2.8321	0.1301	1090.01	1088.206	6541.4	1	1022.8	72.7	3	K.TSQVGAASAPAK.E
	HsFLAG-p53-DNA-D	2.7946	0.2215	1557.63	1557.704	6734.6	1	682	56.7	1	K.TSQVGAASAPAKESPR.K
	HsFLAG-p53-DNA-D	3.339	0.2444	893.65	894.062	5100.3	1	1519.9	100	3	R.KGAAPAPPGK.T
	HsFLAG-p53-DNA-D	2.6671	0.2232	893.68	894.062	4322.4	1	708.9	72.2	2	R.KGAAPAPPGK.T
	HsFLAG-p53-DNA-D	2.4207	0.2025	864.71	865.023	5194.2	6	448.9	75	1	R.KGAAPAPPR.K
	HsFLAG-p53-DNA-D	4.2051	0.2378	1613.35	1612.867	9721.1	6	818	53.3	13	K.SLGNILQAKPTSSPAK.G
	HsFLAG-p53-DNA-D	2.1986	0.1507	868.56	869.052	6023.1	6	451.7	62.5	1	K.AGPVAVQVK.A
	HsARP6-FLAG_Ti_1	3.2048	0.3615	1282.29	1282.483	7223	1	898.1	61.5	1	K.GSLGQGTAPVLPGK.T
	HsFLAG-p53-DNA-D	2.1616	0.1628	930.5	931.077	6378.3	4	500.3	68.8	1	K.TGPTVTQVK.A
	HsFlag-VPS71_Ti_1	2.8238	0.3319	931.48	931.077	4185.9	3	614.9	81.2	1	K.TGPTVTQVK.A
	HsFLAG-p53-DNA-D	2.5064	0.1651	858.56	859.013	9432.8	7	754.3	68.8	1	K.VVTAAAQAK.Q
	HsFLAG-p53-DNA-D	2.6336	0.0943	859.19	859.013	3747.6	2	521.4	81.2	1	K.VVTAAAQAK.Q
	HsFLAG-p53-DNA-D	2.6389	0.1696	1099.57	1100.22	3109.7	3	214.3	72.2	1	R.NPQNSTVLAR.G
	HsFLAG-p53-DNA-D	2.2368	0.1466	923.63	924.088	4292.4	3	565.3	72.2	2	R.KGAAPTPPGK.T
	HsFLAG-p53-DNA-D	4.7369	0.4991	1751.65	1750.909	4614.7	1	786.3	61.1	3	R.SPAGPAATPAQAQAASTPR.K
	HsFlag-VPS71_Ti_1	3.52	0.3591	1325.59	1324.541	4675.2	1	815.1	72.7	3	R.TNVVTMPTAHPR.I
*	HsFlag-VPS71_Ti_1	3.2037	0.2691	1323.71	1324.563	5802.1	2	503.7	58.3	2	K.NPASLPLTQAALK.V
*	HsFLAG-Lin9_Ti_20	3.3285	0.2885	1324.35	1324.563	4153	1	547.6	70.8	3	K.NPASLPLTQAALK.V
	HsFLAG-FLJ20729_	3.1059	0.2714	1388.37	1388.474	6167.5	1	816.7	64.3	2	K.LGAGEGGEASVSPEK.T
	HsFLAG-p53-DNA-D	2.9988	0.1156	1379.7	1377.469	8777.6	1	1110.9	65.4	1	K.GMGTVEGGDQSNPK.S
gi|42476130|r	7	12	15.70%	719	79728	5.4	retinoid x receptor interacting protein [Homo sapiens]				
*	HsScrap_Ti_106.216	3.7549	0.4305	1710.43	1710.844	8128.1	1	887.5	60	3	R.SRPLATGPSSQSHQEK.T
*	HsSrcap_Ti_202.451	3.3851	0.2571	2190.59	2190.501	4429.8	3	483.1	47.4	2	K.TTDSGLTEGIWQLVPPSLFK.G
*	HsSrcap_Ti_204.167	2.2396	0.2677	1125.53	1126.264	6462.1	1	493.4	61.1	1	R.HCLPTLADAK.G
*	HsSrcap_Ti_202.245	4.6924	0.3126	4229.63	4229.509	4641.1	1	420.2	21.9	1	K.R
*	HsSrcap_Ti_201.076	4.0224	0.3895	1509.31	1509.567	6513.3	1	1177.6	67.9	2	K.SDSGTAAQTSLDIDK.N
*	HsSrcap_Ti_203.202	2.9025	0.1338	1330.49	1331.511	4871.8	8	382.6	65	1	R.LLSFLEQSEHK.T
*	HsSrcap_Ti_203.202	3.1226	0.1585	1331.46	1331.511	8557	1	1186.9	80	2	R.LLSFLEQSEHK.T
gi|4502389|re	1	2	15.70%	89	10059	6.1	barrier to autointegration factor 1 [Homo sapiens]				
gi|88959141|r	1	2	16.30%	86	9740	6.1	PREDICTED: similar to barrier to autointegration factor 1 [Homo sapiens]				
gi|88953904|r	1	2	16.30%	86	9740	6.1	PREDICTED: similar to barrier to autointegration factor 1 [Homo sapiens]				
	HsFlag-VPS71_Ti_1	4.7041	0.359	1297.67	1297.538	6028.1	1	1685.5	84.6	2	K.PVGSLAGIGEVLGK.K
gi|19923142|r	8	23	15.60%	876	97170	4.8	karyopherin beta 1 [Homo sapiens]				
*	HsFlag-FLJ90652_2	3.2663	0.1423	1557.97	1557.744	7128.2	5	633.4	61.5	1	K.TVSPDRLELEAAQK.F

*	HsFLAG-p53-DNA-D	4.085	0.3033	1659.67	1659.923	4574.5	1	1141.1	75	8	R.AAVENLPTFLVELSR.V
*	HsFlag-DPCD_Ti_20	3.767	0.3816	2566.7	2566.744	8126.7	1	979.4	47.6	1	K.ESTLEAIGYICQDIDPEQLQDK.S
*	HsFLAG-ARP6_Ti_1	4.7285	0.3513	1608.1	1606.86	7838.5	1	1962.6	78.6	4	K.LAATNALLNSLEFTK.A
*	HsFLAG-p53-DNA-D	3.4827	0.2163	1761.42	1760.127	3920.9	3	540.5	60	3	K.GALQYLVPILTQTLTK.Q
*	HsFLAG-ARP6_Ti_1	3.53	0.375	1766.17	1766.651	10410.5	1	1028.5	61.5	2	K.QDENDDDDDWNPCK.A
*	HsFLAG-p53-DNA-D	3.5391	0.3946	2290.47	2290.708	10387	1	992.3	45.2	1	R.SVKPQILSVFGDIALAIGGEFK.K
*	HsFLAG-Lin9_Ti_20	5.543	0.4555	2147.95	2148.421	11871	1	2349.3	63.9	3	K.YLEVVLNTLQQASQAQVDK.S
gi|41872577|r	5	8	15.60%	578	63146	5.7	raft-linking protein [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.427	0.398	1997.98	1997.255	6065.8	1	959.1	61.1	1	R.FLEFTTLSAAELPGSSAVR.L
*	HsFLAG-ARP6_Ti_1	3.3342	0.229	1173.5	1173.355	6717.9	1	1261.4	80	2	K.KIQEAASQGLK.F
*	HsFLAG-ARP6_Ti_1	5.4422	0.361	3136.18	3137.346	5391.6	1	732.6	30.8	2	K.FVGVIPQYHSSVNSAGSSAPVSTANSTEDAR.D
*	HsFLAG-ARP6_Ti_1	3.233	0.3634	1246.09	1245.301	6863.4	1	862.5	66.7	2	K.PGTGDVCSAPAGR.N
*	HsFLAG-ARP6_Ti_1	2.6011	0.1432	1761.94	1762.781	7437.4	2	678.1	53.3	1	R.DGDAEEVRELGTVEEN.-
gi|7661920|re	5	21	15.60%	411	46871	6.7	DEAD (Asp-Glu-Ala-Asp) box polypeptide 48 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	2.3621	0.254	1047.39	1048.183	9240.5	1	837.8	75	2	R.GIYAYGFEK.P
	HsFLAG-ARP6_Ti_1	4.6012	0.3935	1829.59	1829.065	4460.2	1	954.3	73.3	7	R.GIYAYGFEKPSAIQQR.A
*	HsFLAG-ARP6_Ti_1	3.4378	0.2988	1404.24	1404.523	7366.4	1	650.6	61.5	3	K.GRDVIAQSQSGTGK.T
*	HsFLAG-Lin9_Ti_20	4.4609	0.3604	1598.38	1598.802	9859.5	1	1928.3	75	2	R.KLDYGQHVVAGTPGR.V
*	HsFLAG-Lin9_Ti_20	4.6985	0.3577	2140.75	2141.432	9536	1	2016.8	61.1	7	R.GLDVPQVSLIINYDLPNNR.E
gi|16554627|r	3	7	15.60%	334	36589	8.3	WD repeat domain 5 [Homo sapiens]				
gi|16554629|r	3	7	15.60%	334	36589	8.3	WD repeat domain 5 [Homo sapiens]				
	HsFLAG-FLJ20436_	2.9323	0.3416	2279.4	2280.45	9468.2	1	519.9	35.7	1	K.LGISDVAWSSDSNLLVSASDDK.T
	HsFLAG-Lin9_Ti_20	3.456	0.5083	1748.42	1748.939	5681.3	1	819	66.7	2	K.TLPAHSDPVSAVHFNR.D
	HsFLAG-FLJ20436_	4.0442	0.3787	1559.76	1560.744	5002.1	1	1211.2	76.9	4	K.TLIDDDNPPVSFVK.F
gi|23308579|r	2	2	15.60%	160	18697	4.5	unactive progesterone receptor, 23 kD [Homo sapiens]				
gi|88950407|r	2	2	15.60%	160	18695	4.6	PREDICTED: similar to unactive progesterone receptor, 23 kD [Homo sapiens]				
gi|27481323|r	2	2	15.60%	160	18694	4.6	PREDICTED: similar to unactive progesterone receptor, 23 kD [Homo sapiens]				
	HsFLAG-RPB5MP_2	2.7614	0.1706	1448.47	1446.566	8513	1	1210.9	70.8	1	K.LTFSCLGGSDNFK.H
	HsFlag-FLJ90652_2	2.7645	0.1441	1538.65	1536.73	7438.5	9	508.8	54.5	1	K.LNWLSVDFNNWK.D
gi|46276893|r	1	5	15.50%	161	17911	6.1	elongin B isoform b [Homo sapiens]				
gi|6005890|re	1	5	21.20%	118	13133	4.9	elongin B isoform a [Homo sapiens]				
	HsFlag-NUFIP_Ti_1	5.4914	0.4288	2637.65	2637.921	6981.7	1	1408.2	37.5	5	K.TLGECGFTSQTARPQAPATVGLAFR.A
gi|46249412|r	12	38	15.40%	1396	152978	5.1	latent transforming growth factor beta binding protein 1 isoform LTBP-1S [Homo sapiens]				
gi|46249414|r	12	38	12.50%	1722	186838	6	latent transforming growth factor beta binding protein 1 isoform LTBP-1L [Homo sapiens]				
	Hs293Flag-Ies2_Ti_	3.8279	0.2544	1406.41	1406.634	4178.3	1	723.6	75	7	K.LCQIPVHGASVPK.L
	HsFLAG-ARP6_Ti_1	3.2833	0.2383	1584.75	1585.763	3585.1	1	407	69.2	1	K.HPPEASVQIHQVSR.I
	HsFLAG-ARP6_Ti_1	4.8605	0.1708	2606.2	2606.944	8964	1	842.4	30.7	2	K.TQTIHSTYSHQQVIPHVYPVAAK.T
	HsFlag-NUFIP_Ti_1	3.7018	0.2608	2475.8	2476.708	4944.7	1	560.9	45.5	6	K.IGFGPDPTFSSCVPDPPVISEEK.G
	HsFLAG-ARP6_Ti_1	3.7745	0.2397	2304.51	2304.608	5106.2	4	439	31.2	1	K.STHPPPLPAKEEPVEALTFSR.E
	Hs293Flag-Ies2_Ti_	3.5202	0.4362	1815.22	1815.977	8026.1	1	947.1	55.9	3	R.EHGPGVAEPEVATAPPEK.E
	HsFLAG-ARP6_Ti_1	3.8508	0.2979	2038.76	2039.062	8190	1	1737.9	68.8	3	R.DIDECQQGNLCVNGQCK.N
	HsFLAG-Lin9_Ti_20	3.9637	0.2599	1819.06	1819.917	8909.8	2	1196.2	60	1	R.TSTDLDVDVDQPKEEK.K
	HsFLAG-TCF3_Ti_1	3.7096	0.428	1786.69	1786.849	6379.7	1	1245.6	67.6	4	K.GFVPAGESSSEAGGENYK.D

	HsFLAG-RPB5MP_2	3.2069	0.2752	1698.29	1698.799	7334.1	1	1179.9	65.4	2	K.DADECLLFGQEICK.N
	Hs293Flag-Ies2_Ti_1	4.5331	0.4552	2039.23	2040.138	7626.4	1	850.9	60	2	K.NGFCLNTRPGYECYCK.Q
	HsFLAG-ARP6_Ti_1	5.1086	0.4391	2620.27	2620.788	4962	1	928.6	54.8	6	R.DALVDFSEQYTPEADPYFIQDR.F
gi|17402900|r	6	13	15.40%	644	67560	7.6	far upstream element-binding protein [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.2866	0.4116	1975.73	1975.036	6345.3	1	1342.5	57.9	3	K.IGGDAGTSLNSNDYGYGGQK.R
*	HsFlag-VPS71_Ti_1	3.3498	0.3584	1261.81	1261.525	5887	1	1438.5	90.9	1	K.VPDGMVGFIIGR.G
*	HsFlag-VPS71_Ti_1	3.5228	0.2469	1354.94	1353.518	3943.9	2	745.6	70.8	1	K.IQIAPDSGGLPER.S
*	HsFlag-VPS71_Ti_1	3.8088	0.1738	1505.69	1504.64	3714	2	677.4	75	2	R.IQFKPDDGTTPER.I
*	HsFlag-VPS71_Ti_1	4.4256	0.3462	1540.68	1540.726	7611.8	1	1801.8	83.3	5	R.CQHAAEIITDLLR.S
*	HsFlag-VPS71_Ti_1	3.9121	0.4022	2910.12	2910.19	4711.8	1	498.7	44.4	1	K.MGQAVPAPTGAPPGGQPDYSAAWAEYYR.Q
gi|4506031|re	3	4	15.40%	306	34193	6.5	palmitoyl-protein thioesterase 1 (ceroid-lipofuscinosis, neuronal 1, infantile) [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.3587	0.3612	1530.75	1530.891	4402.9	1	889.4	76.9	1	K.KIPGIYVLSLEIGK.T
*	HsFLAG-ARP6_Ti_1	5.0171	0.4902	2003.75	2003.243	6182.2	1	1791.7	76.5	1	K.LQQGYNAMGFSQGGQFLR.A
*	HsFLAG-ARP6_Ti_1	3.0879	0.2176	1794.49	1794.956	4840.5	1	579	60.7	2	K.ETIPLQETSLYTQDR.L
gi|8922498|re	2	2	15.30%	261	29988	7.1	pyridoxine 5'-phosphate oxidase [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.691	0.3573	2297.4	2298.56	7577.4	1	1034.1	52.8	1	K.ELDSNPFASLVFYWEPLNR.Q
*	HsFLAG-ARP8_Ti_2	3.7284	0.4303	2546.66	2547.85	4319.8	1	336.2	40	1	K.SWGGYVLYPQVMEFWQGQTNR.L
gi|11415026|r	5	10	15.30%	176	20762	10.7	ribosomal protein L18a [Homo sapiens]				
gi|88954764|r	5	10	16.30%	166	19523	10.7	PREDICTED: similar to ribosomal protein L18a isoform 6 [Homo sapiens]				
gi|88954757|r	5	10	15.30%	176	20767	10.7	PREDICTED: similar to ribosomal protein L18a isoform 4 [Homo sapiens]				
gi|88953058|r	5	10	16.30%	166	19523	10.7	PREDICTED: similar to ribosomal protein L18a isoform 3 [Homo sapiens]				
gi|27480190|r	5	10	15.30%	176	20767	10.7	PREDICTED: similar to ribosomal protein L18a isoform 1 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	2.5593	0.0829	1095.4	1096.318	5570.4	2	792.6	77.8	1	R.IFAPNHVVAK.S
	HsFLAG-ARP6_Ti_1	2.637	0.2489	1217.21	1218.44	8745.7	1	944.7	75	1	R.FWYFVSQLK.K
	HsFLAG-ARP6_Ti_1	3.0529	0.2647	1218.36	1218.44	3211.1	1	716.7	87.5	6	R.FWYFVSQLK.K
	HsFLAG-TCF3_Ti_1	2.4451	0.1928	927.46	928.138	5634.2	6	702.6	78.6	1	R.AHSIQIMK.V
	HsFLAG-ARP6_Ti_1	2.7211	0.1453	928.29	928.138	3776.4	2	519.4	85.7	1	R.AHSIQIMK.V
gi|89052285|r	10	14	15.20%	1278	138244	8.4	PREDICTED: hypothetical protein LOC57662 [Homo sapiens]				
gi|89057109|r	10	14	15.20%	1278	138244	8.4	PREDICTED: similar to Protein KIAA1543 [Homo sapiens]				
	HsARP6-FLAG_Ti_1	4.0941	0.4387	2216.15	2214.613	6698.6	1	1219.2	38.8	1	R.QALPQLETPPNPSALLALLAR.R
	HsFLAG-Lin9_Ti_20	3.644	0.1595	3660.68	3661.094	10033	2	568.1	21.1	1	R.RAPCFPTVTSLQDLASGAALAATIHCYCPQLLR.L
	HsFLAG-p53-DNA-D	2.6436	0.1841	1446.77	1446.649	3241.5	1	350	65.4	1	R.HPLLSSGGPQSPLR.G
	HsFLAG-p53-DNA-D	3.5426	0.242	3037.1	3035.381	4367	2	358.8	27.8	1	R.TPTQPPPEPGDLPTIEEALQIIHSAEPR.L
	HsFLAG-ARP6_Ti_2	2.8946	0.3326	1332.12	1332.453	3651.1	1	485.4	65.4	3	K.AVASSPAATNSEVK.M
	HsFLAG-p53-DNA-D	4.0054	0.4408	2256.74	2256.48	5624.3	1	489.7	45	2	K.AVTFSPDLGPVPHEGLGEYNR.A
	HsFLAG-p53-DNA-D	3.553	0.341	1696.6	1696.947	4186.7	1	553.6	64.3	1	R.VLTPPHDVDSLPHLR.K
	HsARP6-FLAG_Ti_1	2.5729	0.2878	1057.2	1055.133	8232.7	6	854.9	77.8	1	R.APAEEEVGPR.K
	HsFlag-VPS71_Ti_1	3.318	0.3609	2447.45	2447.707	8288.2	1	415.7	31.8	1	K.IYSQSTLSLSTVANEAHNNLGVK.R
	HsFLAG-p53-DNA-D	3.6657	0.3019	1741.78	1741.963	9859.5	1	658.7	50	2	K.FIIHNALSHCCLAGK.V
gi|68509926|r	8	20	15.20%	795	90933	7.5	DEAH (Asp-Glu-Ala-His) box polypeptide 15 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	3.2916	0.1637	1332.54	1332.588	4728.1	1	693.3	77.8	2	K.RLQLPVWEYK.D
*	HsFLAG-ARP6_Ti_1	3.6624	0.2988	1448.14	1446.603	7460.4	1	960.4	69.2	3	R.HQSFVLVGETGSGK.T
*	HsFLAG-ARP6_Ti_1	4.0161	0.3048	1275.93	1275.59	5368.4	2	1078.9	81.8	2	R.TLATDILMGVLK.E

*	HsFLAG-Lin9_Ti_20	4.4843	0.4076	1954.7	1955.23	8541.3	1	1494.2	66.7	5	K.FQIYFDNCPLLTIPGR.T
*	HsARP6-FLAG_Ti_1	3.0881	0.2929	1430.32	1429.743	9565.2	1	1219.4	70.8	2	R.IRVESLLVTAISK.A
*	HsFLAG-ARP6_Ti_1	3.9616	0.3185	1158.38	1158.384	6707.8	1	1328	85	3	R.SNLGSVVLQLK.K
*	HsFLAG-ARP6_Ti_1	4.0309	0.3509	1735.4	1736.042	8206.7	1	1403.3	67.9	2	K.ALVTGYFMQVAHLER.T
*	HsFLAG-p53-DNA-D	4.6177	0.2047	3551.49	3552.024	7975.4	1	775.5	25	1	K.DNQVVQLHPSTVLDHKPEWVLYNEFVLTTK.N
gi|34419635|r	12	269	15.20%	643	71028	6.1	heat shock 70kDa protein 6 (HSP70B') [Homo sapiens]				
	HsFlag-FLJ90652_2	3.6517	0.3726	1487.89	1488.594	3812.9	1	610.4	75	34	R.TTPSYVAFTDTER.L
	Hs293Flag-Ies2_Ti_1	3.2174	0.4318	1488.58	1488.594	3710.2	1	167.1	54.2	6	R.TTPSYVAFTDTER.L
	HsFlag-FLJ90652_2	5.0718	0.2176	1688.21	1688.921	6740.8	1	1838.4	51.7	10	R.IINEPTAAAIAYGLDR.R
	HsFLAG-ARP6_Ti_1	5.4263	0.43	1689.04	1688.921	5489.6	1	1548.3	80	52	R.IINEPTAAAIAYGLDR.R
	HsFlag-ZnF-HIT2_Ti_	4.6766	0.4075	1675.9	1676.696	6824.2	1	1767	76.7	48	K.ATAGDTHLGGEDFDNR.L
	HsFLAG-ARP6_Ti_1	3.982	0.2027	1543.2	1543.686	7726	1	1819.5	56.8	8	R.ARFEELCSDLFR.S
	HsFLAG-TIP49b_Ti_	2.8901	0.2543	1543.7	1543.686	5209.7	8	240.3	54.5	1	R.ARFEELCSDLFR.S
	HsFlag-FLJ90652_2	4.4813	0.316	1544.45	1543.686	5279.2	1	1248.6	86.4	92	R.ARFEELCSDLFR.S
	HsFLAG-TCF3_Ti_1	3.5157	0.2378	1316.78	1316.419	6306.6	3	1058.7	83.3	9	R.FEELCSDLFR.S
	HsFLAG-ARP6_Ti_1	2.1699	0.1805	902.57	903.02	3454.5	4	265.1	64.3	2	R.STLEPVEK.A
	HsTIP60_Ti_105.226	2.8115	0.2224	1082.24	1082.244	4474.4	5	672.9	87.5	2	K.LLQDFFNGK.E
	HsFlag-NUFIP_Ti_11	4.3835	0.3141	2535.03	2532.81	10078.3	1	898.2	39.1	5	R.GVPQIEVTFDIDANGILSVTATDR.S
gi|31377603|r	5	15	15.20%	381	43563	9.8	HIV-1 rev binding protein 2 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	4.4459	0.2859	2552.59	2553.788	8342.3	1	1047.2	50	5	R.NQKPKPENQDESELLTVPDGWK.E
*	HsFlag-NUFIP_Ti_1	4.5776	0.2758	2553.94	2553.788	8815.8	1	1510.7	36.9	2	R.NQKPKPENQDESELLTVPDGWK.E
*	HsFlag-NUFIP_Ti_1	4.6369	0.4261	1538.75	1539.769	7997.1	1	1825.6	76.9	6	R.GLLEESSFATLFPK.Y
*	HsFlag-NUFIP_Ti_1	2.4208	0.1001	1111.54	1112.317	5047.6	8	524.4	75	1	K.NIHPIYNIK.S
*	HsFlag-NUFIP_Ti_1	3.7395	0.2091	1357.17	1357.634	8038.4	1	1787.7	83.3	1	K.KLGALTAEEIALK.M
gi|10863889|r	7	13	15.10%	800	90255	6.1	squamous cell carcinoma antigen recognized by T cells 1 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.9913	0.2494	1814.77	1814.907	6510.4	1	772.5	50	2	K.EAAGTTAAAGTGGATEQPPR.H
*	HsFlag-VPS71_Ti_1	5.4884	0.4183	2104.99	2104.237	5911.7	1	1937.6	76.5	4	K.TLGEDDPWLDDTAAWIER.S
*	HsFLAG-p53-DNA-D	4.1097	0.4359	1701.73	1701.877	9027.6	1	1662	67.9	2	R.DLQGLTVEHAIDSFR.E
*	HsFLAG-p53-DNA-D	2.7828	0.2665	2292.63	2293.498	11537.1	1	546.7	38.9	1	R.SILSKYDEELEGERPHSFR.L
*	HsFlag-VPS71_Ti_1	2.8856	0.2975	2020.57	2021.105	4127.3	1	416.6	52.8	1	R.ADDLLPLGDQTQDGDFGSR.L
*	HsARP6-FLAG_Ti_1	4.4006	0.3439	1272.43	1272.497	7719.8	1	1641	81.8	2	R.GLAAALLLCQNK.G
*	HsFLAG-p53-DNA-D	4.7141	0.4894	1905.35	1906.202	6183.8	1	1370	67.6	1	K.KMSSSDTPLGTVALLQEK.Q
gi|5901928|re	6	53	15.10%	551	59209	7.4	cleavage and polyadenylation specific factor 6, 68 kD subunit [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	2.5429	0.3915	1340.68	1341.506	8186.5	1	667.7	54.2	1	K.GAAPNVVYTYTGK.R
*	HsFLAG-Lin9_Ti_20	4.3874	0.2815	1749.64	1749.933	8545	1	1086.4	60.7	4	K.RELHGQNPVVTPCNK.Q
*	HsFLAG-p53-DNA-D	4.6428	0.4379	1666.69	1666.843	8622	1	1797.2	76.9	1	R.TPLSEAEFEEIMNR.N
*	HsFLAG-p53-DNA-D	6.3787	0.5289	2451.93	2453.749	9126.1	1	2670.4	62.5	39	R.AVSDASAGDYGSAIETLVTAISLIK.Q
*	HsFLAG-FLJ20729_	4.7093	0.4179	2453.37	2453.749	7305.8	1	1539.4	37.5	2	R.AVSDASAGDYGSAIETLVTAISLIK.Q
*	HsFLAG-p53-DNA-D	5.3452	0.4975	1799.32	1800.028	10404.7	1	2132	73.3	6	K.VLISSLQDCLHGIESK.S
gi|13540586|r	4	5	15.10%	518	57341	5.2	hypothetical protein LOC81556 [Homo sapiens]				
	HsFlag-FLJ90652_2	3.6699	0.38	2331.27	2331.637	7702.2	1	468.3	37.5	1	R.LIDLNNGEGQIFTIDGPLCLK.N
	HsFlag-FLJ90652_2	3.3922	0.3903	2243.97	2244.672	6122.7	1	603.6	47.4	1	K.SNLMMSLFEPGPEPLPWLGK.M
	HsFlag-FLJ90652_2	3.4517	0.3109	1279.42	1279.565	5055.7	1	1059.6	81.8	2	K.AALAFGFLDLLK.G

	HsFlag-FLJ90652_2	2.7376	0.4166	2791.47	2792.087	6210.9	1	278.6	33.3	1	R.ECTLLPETAHPDAAFQLTHAAQQLK.L
gi|5729730|re	4	21	15.10%	504	56770	5.9	apoptosis inhibitor 5 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.7445	0.3917	1744.82	1744.902	8600.9	1	1550	70	3	R.NYGILADATEQVGQHK.D
*	HsFlag-VPS71_Ti_1	3.4126	0.1403	1472.27	1472.641	4666	4	576.7	62.5	3	K.ELPQFATGENLPR.V
*	HsFLAG-Lin9_Ti_20	3.8216	0.2932	3206.84	3207.648	10985.6	1	929.1	25	4	R.VADILTQLLQTDDSAEFNLVNNALLSIFK.M
*	HsFLAG-p53-DNA-D	5.3073	0.3912	1904.38	1904.174	8968.1	1	2199.4	70.6	11	K.GTLGGLFSQILQGEDIVR.E
gi|29568103|r	5	8	15.10%	437	51557	9.9	U1 small nuclear ribonucleoprotein 70 kDa isoform a [Homo sapiens]				
	HsFLAG-p53-DNA-D	2.8374	0.231	1886.67	1887.229	4667.4	1	378.4	53.3	1	R.DPIPYLPPLEKLPHEK.H
	HsFlag-NUFIP_Ti_2	2.771	0.1414	1726.58	1726.901	6906.4	5	434.4	53.8	1	K.HHNQPYCGIAPYIR.E
	HsFlag-VPS71_Ti_1	1.9489	0.2275	1081.78	1082.241	2420.7	2	204.9	68.8	1	R.EFEVYGPIK.R
*	HsFLAG-p53-DNA-D	3.3583	0.2381	958.41	958.065	5306	1	995.9	93.8	4	R.RGGADVNIR.H
*	HsFLAG-p53-DNA-D	4.022	0.3501	1660.3	1660.654	9792.2	1	855	50	1	R.GGGGGQDNGLEGLGNDSR.D
gi|5730027|re	10	53	15.10%	443	48227	8.7	KH domain containing, RNA binding, signal transduction associated 1 [Homo sapiens]				
*	HsFLAG-FLJ20309_	3.9825	0.3305	1385.08	1385.494	4742.2	1	735.2	69.2	15	R.SGSMDPSGAHPSVR.Q
	HsFlag-VPS71_Ti_1	2.1849	0.0959	1093.71	1094.311	3855.9	5	409	62.5	2	K.YLPELMAEK.D
*	HsFLAG-p53-DNA-D	4.1746	0.2053	3321.79	3322.813	7073.4	1	705	27.7	2	K.YLPELMAEKDSLDPSFTHAMQLLTAEIEK.I
*	HsFLAG-FLJ20729_	3.9239	0.3297	2247.55	2247.525	4854	1	552.1	35.5	6	K.DSLDPSFTHAMQLLTAEIEK.I
*	HsFLAG-FLJ20729_	5.5552	0.4788	2248.36	2247.525	5634	1	1006.1	60.5	16	K.DSLDPSFTHAMQLLTAEIEK.I
*	HsFLAG-ARP5_Ti_1	4.3077	0.252	1753.15	1753.863	9463.5	1	1868.8	76.9	7	K.KDDEENYLDLFSHK.N
*	HsFLAG-Lin9_Ti_20	3.992	0.1469	1753.91	1753.863	6532.3	8	1109.4	50	1	K.KDDEENYLDLFSHK.N
*	HsFLAG-FLJ20729_	3.9398	0.2629	1626.14	1625.689	8757.2	1	835.5	62.5	1	K.DDEENYLDLFSHK.N
*	HsFLAG-p53-DNA-D	2.2212	0.1215	1040.6	1041.236	5803.5	1	449.8	66.7	1	K.ILGPQGNTIK.R
*	HsFLAG-p53-DNA-D	2.9817	0.2319	1041.32	1041.236	3815.7	2	577	83.3	2	K.ILGPQGNTIK.R
gi|56118234|r	2	4	15.10%	272	29731	9.7	proline rich 6 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.6485	0.3817	1926.3	1927.128	5390.1	1	878.7	59.5	2	K.RSGASAAPAASAAAALAPSATR.T
*	HsFLAG-ARP6_Ti_1	4.5998	0.4725	1984.34	1985.13	5742.4	1	1412.6	69.4	2	R.SNPGGFGIAPHCLDEGTVR.S
gi|13775200|r	1	4	15.10%	86	10135	6.4	SF3b10 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.2003	0.3297	1584.35	1584.772	10659.8	1	1835.4	75	4	R.YTIHSQLEHLQSK.Y
gi|51599156|r	15	43	15.00%	1912	218003	5.9	chromodomain helicase DNA binding protein 4 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.8052	0.2455	1448.86	1448.751	8337.7	1	1274	70.8	2	K.AFSQFVRPLIAAK.N
*	HsSrcap_Ti_205.215	3.0713	0.1063	1426.59	1426.574	6400.5	1	1079.5	80	2	K.WREFSTNNPFK.G
*	HsSrcap_Ti_206.354	6.9596	0.4306	3756.55	3757.337	8784.6	1	1959.6	29.5	4	.A
*	HsSrcap_Ti_204.332	5.6905	0.4002	4267.6	4266.541	8491.3	1	909.5	23.6	1	K.DGGELLCCDTCPSSYHIHCLNPPLPEIPNGEWLCPR.C
	HsFlag-VPS71_Ti_1	2.7171	0.3393	2040.89	2041.283	6293.3	1	574.1	44.4	1	R.FSWAQGTDTILADEMGLGK.T
	HsSrcap_Ti_203.417	4.7188	0.4454	1902.17	1901.216	4477.5	1	929.1	68.8	14	K.GPFLVSAPLSTIINWER.E
	HsFLAG-Lin9_Ti_20	4.5874	0.4438	3037.87	3037.529	4231.5	1	517.6	30	2	K.LLLTGTPLQNNLEELFHLLNFLTPER.F
*	HsSrcap_Ti_205.264	4.441	0.3476	2007.19	2006.259	6637.9	1	1232.5	65.6	3	K.CCNHPYLFPVAAMEAPK.M
	HsSrcap_Ti_204.333	5.2483	0.5175	1857.91	1858.073	4627.8	1	861.4	73.3	3	R.FNAPGAQQFCFLLSTR.A
	HsFLAG-ARP5_Ti_1	2.8267	0.2021	1554.29	1554.619	6562.7	3	601.9	68.2	1	R.HHYEQQQEDLAR.N
*	HsSrcap_Ti_201.079	4.0155	0.4212	2303.52	2304.392	7021.5	1	603.4	42.9	2	K.STAPETAIECTQAPAPASEDEK.V
*	HsFlag-VPS71_Ti_1	3.0932	0.1956	1176.44	1175.281	8517.5	4	1040.8	70	1	K.GAADVEKVEEK.S
	HsSrcap_Ti_203.304	3.709	0.2644	1554.79	1554.827	7815.9	1	1364.1	75	1	K.LLEQALVIEEQLR.R
*	HsSrcap_Ti_204.178	4.1667	0.4912	1885.72	1886.037	9484	1	1726.8	66.7	1	R.FAEVECLAESHQHLSK.E

*	HsSrcap_Ti_203.152	4.6379	0.4045	1876.74	1877.067	7857.4	1	1357.2	62.5	5	R.LANRAPEPTPQQVAQQQ.-
gi|56550051|r	5	9	14.90%	565	65381	8.9	ubiquitin specific protease 39 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	2.5052	0.2244	1908.98	1910.177	4474.7	3	326.9	41.2	1	R.AYDGTTYLPGIVGLNNIK.A
*	HsFLAG-p53-DNA-D	4.7522	0.4446	2026.53	2027.288	5238.3	1	1121.3	66.7	5	K.ANDYANAVLQALSNVPPLR.N
*	HsARP6-FLAG_Ti_1	2.827	0.2489	1264.61	1264.56	4275	1	450.1	72.2	1	K.LPPYLIFCIK.R
*	HsFLAG-p53-DNA-D	2.7646	0.2025	1713.44	1713.974	6898.6	1	488.8	53.6	1	K.NPTIVNFPITNVDLR.E
*	HsFLAG-p53-DNA-D	3.6734	0.2491	2451.5	2451.655	7438.1	7	621.3	28.6	1	K.NTTYDLIANIVHDGKPSEGSYR.I
gi|4885661|re	4	7	14.90%	543	60801	6.7	viral oncogene yes-1 homolog 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	5.8741	0.4418	3520.71	3521.742	6495.6	1	811.9	27.3	1	K.YRPENTPEPVSTSVSHYGAEPTTVSPCPSSSAK.G
*	HsFLAG-ARP6_Ti_1	5.2404	0.4049	1881.24	1880.026	8078.2	1	1752.3	78.6	1	R.FQIINNTEGDWWEAR.S
*	HsFLAG-ARP6_Ti_1	3.5571	0.4259	1842.4	1843.14	4747.5	1	330.4	46.9	2	K.LTTVCPTVKPQTQGLAK.D
*	HsFLAG-ARP6_Ti_1	3.7758	0.3305	1823.12	1824.084	9176.6	1	1194.8	60	3	K.SDVWSFGILQTELVTK.G
gi|7705738|re	3	10	14.90%	242	28162	10	mitochondrial ribosomal protein S7 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_11	3.7302	0.2934	1332.58	1332.545	8340.4	1	1037.6	75	4	R.NPYTIFHQALK.N
*	HsFlag-NUFIP_Ti_1	2.8154	0.2006	1488.51	1487.745	8291.4	1	798	63.6	2	R.FYQVPVPLPDRR.R
*	HsFlag-NUFIP_Ti_1	3.9701	0.2867	1466.58	1466.723	9529.7	1	1161.2	70.8	4	K.LLEAFHNQGPVIK.R
gi|23397666|r	9	21	14.80%	1273	145175	7.3	transcriptional co-repressor Sin3A [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.4829	0.3983	2143.77	2144.45	3362.3	1	369.5	50	1	K.LQFGSQPQVYNDFLDIMK.E
*	HsFLAG-p53-DNA-D	3.7178	0.3865	2005.9	2005.342	8002.7	1	1358.8	61.8	1	K.GHPDLIMGFNTFLPPGYK.I
*	HsFLAG-Lin9_Ti_20	3.9669	0.2655	4010.74	4011.486	8269.6	2	395.7	18.1	1	R.SPPVQPHTPVTISLGTAPSLQNNQPVEFNHAINYVNK.I
*	HsFlag-VPS71_Ti_1	4.4328	0.2569	1363.42	1363.599	7383.3	1	1620.5	85	5	K.AFLEILHTYQK.E
*	HsScrap_Ti_102.244	4.2557	0.4367	2267.55	2268.445	3474.9	1	425.8	47.5	2	K.EAGGNYTPALTEQEVYAQVAR.L
*	HsSrcap_Ti_202.452	5.277	0.4478	2652.66	2652.918	5957	1	872.1	47.8	6	K.NQEDLLSEFGQFLPDANSSVLLSK.T
*	HsScrap_Ti_103.239	3.0176	0.3206	1150.49	1151.435	5481.4	1	630.5	70	2	K.NPSIAVPIVLK.R
*	HsSrcap_Ti_203.367	4.9783	0.345	4147.15	4146.468	5056.5	1	606	25	2	K.SLLNEIESIYDERQEQATEENAGVPVGPHLSLAYEDK.Q
*	HsFLAG-p53-DNA-D	3.6746	0.1567	1434.93	1435.712	6369	1	955.1	72.7	1	R.EHLAQKPVFLPR.N
gi|17017991|r	6	19	14.80%	847	96576	8.2	FtsJ homolog 3 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_11	5.6862	0.5012	3621.27	3622.298	6291.8	1	1057.4	29.7	1	K.FMPVSSLIVGVDLVPIKPLPNVVTLQEDITTER.C
*	HsFlag-NUFIP_Ti_11	4.6933	0.4872	1867.7	1868.188	7262	1	1853.4	76.9	4	R.DYQPLLWIFQQLFR.R
*	HsFLAG-TCF3_Ti_1	3.8404	0.3205	2839.94	2840.029	8862	1	797.8	38	1	K.GSFAGIEDDADEALEISQAQLLFENR.R
*	HsFLAG-ARP6_Ti_1	2.7454	0.2257	1747.22	1747.853	4567.9	1	549.7	50	3	K.SDDDGFEIVPIEDPAK.H
*	HsFLAG-p53-DNA-D	4.8675	0.4607	1654.7	1654.944	7319.3	1	2085.6	78.1	5	R.ILDPEGLALGAVIASSK.K
*	HsFLAG-TCF3_Ti_1	4.7098	0.4273	2389.71	2390.521	6430.6	1	723.2	52.8	5	R.YTFNEDEGELPEWFVQEEK.Q
gi|4507241|re	6	9	14.80%	709	81075	6.9	structure specific recognition protein 1 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	2.6385	0.2097	951.07	951.16	5577.4	1	1142.2	93.8	1	R.RVALGHGLK.L
*	HsFLAG-Lin9_Ti_20	4.8964	0.258	3257.2	3256.603	6459.8	1	624.6	26.7	1	K.FGGQLLSFDIGDQPVFEIPLSNVSQCTTGK.N
*	HsFLAG-p53-DNA-D	3.0086	0.4045	2652.04	2651.932	3545	1	249.9	39.1	1	R.FYVPPTQEDGVDPVEAFAQNVLSK.A
*	HsFLAG-FLJ20729_	2.7188	0.3142	1325.84	1326.584	4322.1	1	450.4	75	3	R.IYPTFLHLHGK.T
*	HsFLAG-p53-DNA-D	2.8064	0.2371	1267.31	1267.517	4667.8	2	844.6	83.3	2	R.LFLLPHKDQR.Q
*	HsFLAG-Lin9_Ti_20	3.791	0.3094	2325.55	2326.503	5388.5	1	346	40	1	K.ITVPGNFQGHSGAQCITCSYK.A
gi|40217805|r	5	11	14.80%	702	79277	9.2	hypothetical protein LOC79707 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.0732	0.0958	3820.9	3820.334	4093.5	1	365.7	22	1	K.TATVNFITSYPGSSYIFVQESPTPQIKPEYLALR.S
*	HsH2AZ-FLAG_293_	3.8209	0.2938	1386.36	1385.516	6514.8	1	1369.7	90	2	K.NNYENYIDIVK.Y

*	HsH2AZ-FLAG_293_	4.2173	0.2522	2752.61	2752.994	6278.2	9	449.8	26	1	R.LAAFADALEFADEEKESPVEFTGHK.L
*	HsH2AZ-FLAG_293_	3.181	0.2536	1978.11	1979.346	7009.3	2	461.2	41.2	5	R.TVNCLLVGAIAIPHCVLK.C
*	HsH2AZ-FLAG_293_	3.7285	0.3326	1804.28	1804.994	3020.7	1	652.4	76.7	2	R.GIEGTVPYVTTDYNFK.L
gi|58535459|r	5	10	14.80%	418	48758	8.6	cell division cycle 10 isoform 1 [Homo sapiens]				
gi|58535461|r	5	10	14.90%	417	48659	8.6	cell division cycle 10 isoform 2 [Homo sapiens]				
	HsFLAG-p53-DNA-D	2.5067	0.298	1954.13	1955.18	8925.3	1	490.8	43.8	1	K.NLEGYVGFANLPNQVYR.K
	HsFLAG-p53-DNA-D	4.1606	0.4343	2608	2608.91	8137	1	546.7	36.4	4	K.STLINSLFLTDLYSPEYPGPSHR.I
	HsFlag-VPS71_Ti_1	4.3148	0.18	2611.12	2608.91	6126.2	1	730.9	29.5	3	K.STLINSLFLTDLYSPEYPGPSHR.I
	HsFlag-VPS71_Ti_1	3.8122	0.3835	1524.12	1524.59	4946.9	1	931.2	77.3	1	K.DVTNNVHYENYR.S
	HsFLAG-p53-DNA-D	3.0314	0.2095	1189.24	1189.311	6819.8	1	893.1	83.3	1	K.LKDSEAELQR.R
gi|89036402|r	5	189	14.80%	229	25758	7.5	PREDICTED: similar to ubiquitin C isoform 5 [Homo sapiens]				
gi|89036412|r	5	126	12.80%	266	29892	6.9	PREDICTED: similar to ubiquitin C isoform 10 [Homo sapiens]				
gi|89036410|r	5	189	14.80%	229	25758	7.5	PREDICTED: similar to ubiquitin C isoform 9 [Homo sapiens]				
gi|89036408|r	5	315	8.90%	381	42851	7.6	PREDICTED: similar to CG11624-PA, isoform A isoform 8 [Homo sapiens]				
gi|89036406|r	5	189	14.80%	229	25758	7.5	PREDICTED: similar to ubiquitin C isoform 7 [Homo sapiens]				
gi|89036404|r	5	315	8.90%	381	42851	7.6	PREDICTED: similar to CG11624-PA, isoform A isoform 6 [Homo sapiens]				
	HsH2AZ-FLAG_293_	4.2324	0.2617	1788.49	1788.99	4419.2	1	862.9	70	78	K.TITLEVEPSDTIENVK.A
	HsFlag-VPS71_Ti_1	2.5095	0.1457	1081.52	1082.199	7176.1	4	468.2	68.8	3	R.TLSDYNIQK.E
	HsFlag-VPS71_Ti_1	2.5377	0.1147	1082.36	1082.199	2680.1	3	487.2	87.5	3	R.TLSDYNIQK.E
	HsFlag-VPS71_Ti_1	2.164	0.1434	1067.63	1068.261	3540.1	1	262.4	62.5	12	K.ESTLHLVLR.L
	HsFLAG-TCF3_Ti_1	3.1021	0.3261	1068.54	1068.261	4839.9	3	563.2	81.2	93	K.ESTLHLVLR.L
gi|19424130|r	15	27	14.70%	1445	161719	5.8	CD109 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.7669	0.3034	2145.64	2146.445	3570.3	1	748.4	63.9	3	K.TLTLPSLPLNSADEIYELR.V
*	HsFLAG-ARP6_Ti_1	3.1576	0.1016	1207.21	1207.415	7500.2	4	963.4	77.8	1	K.RISVFIQTDK.A
*	HsFLAG-ARP6_Ti_1	6.2851	0.4162	2145.82	2145.42	7882.4	1	1734.6	66.7	2	K.SNLIQQWLSQQSDLGVISK.T
*	HsFLAG-ARP6_Ti_1	2.8502	0.2285	1761.55	1762.01	6074.8	1	1209	71.4	1	K.IEFPILEDSSELQLK.A
*	HsFLAG-ARP6_Ti_1	3.0799	0.3637	1107.5	1107.313	5725.4	1	1233.3	88.9	1	K.SSMAVHSLFK.S
*	HsFLAG-ARP6_Ti_1	3.8226	0.319	1333.26	1333.527	7780.5	1	1686.4	83.3	1	K.VGSPFELVVSGNK.R
*	HsFLAG-ARP6_Ti_1	4.5351	0.4141	2315.99	2315.589	10816.1	1	1499.7	55.3	6	K.ACVIVYYIEDDGEIISDVLK.I
*	HsFLAG-ARP6_Ti_1	3.4567	0.3364	1743.14	1742.023	2821.6	1	345.6	50	1	R.ISVTQPDSIVGIVAVDK.S
*	HsFLAG-ARP6_Ti_1	3.5511	0.3261	1794.17	1793.841	5234.2	1	1098	75	2	K.DYIDGVYDNAEYAER.F
*	HsFLAG-ARP6_Ti_1	3.4683	0.3088	1625.47	1625.776	7329	1	1200.1	69.2	2	K.SYSQSILLDLTDNR.L
*	HsFLAG-ARP6_Ti_1	3.3914	0.2026	2208.47	2208.607	6053.3	1	468.8	38.1	2	R.VQITAIGDVLGPSINGLASLIR.M
*	HsFLAG-ARP6_Ti_1	5.2067	0.4109	2209.52	2208.607	8400.1	1	1165	36.9	2	R.VQITAIGDVLGPSINGLASLIR.M
*	HsFLAG-ARP6_Ti_1	3.8867	0.4616	1856.09	1855.185	8164.2	1	1264.8	65.6	1	K.SPVTLTAYIVTSLLGYR.K
*	HsFLAG-ARP6_Ti_1	2.7072	0.2326	1982.09	1983.359	10646.5	3	453.2	35.3	1	K.SPVTLTAYIVTSLLGYRK.Y
*	HsFLAG-ARP6_Ti_1	2.7182	0.1988	2438.52	2439.643	7654.6	1	382.4	36.8	1	K.YQPNIDVQESIHFLESEFSR.G
gi|21327701|r	5	23	14.70%	592	61830	8	TBP-associated factor 15 isoform 1 [Homo sapiens]				
gi|4507353|re	5	23	14.80%	589	61558	8	TBP-associated factor 15 isoform 2 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	5.3149	0.3497	3626.54	3624.72	9408.9	1	1256.5	27.3	7	R.TDADSESDNSDNNTIFVQGLGEGVSTDQVGEFFK.Q
	HsFLAG-FLJ20309_	2.8393	0.2065	1381.81	1381.63	3911.7	1	431.3	68.2	1	K.TGKPMINLYTDK.D
	HsFlag-VPS71_Ti_1	4.1712	0.4305	1421.9	1421.503	4776.8	1	1058.8	76.9	3	K.GEATVSFDDPPSAK.A
	HsFlag-VPS71_Ti_1	2.5337	0.1023	1022.72	1023.133	6069	2	567.1	68.8	1	K.AAIDWFDGK.E

	HsFLAG-ARP6_Ti_2	4.5086	0.3845	2070.38	2070.176	4415.9	1	803.2	61.8	11	K.SGDWVCPNPSCGNMNFAR.R
gi|4506623|re	2	6	14.70%	136	15798	10.6	ribosomal protein L27 [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	3.7499	0.2921	1408.76	1408.618	8324.4	1	1722.8	85	4	K.VYNYNHLMPTR.Y
*	HsFLAG-TCF3_Ti_1	2.1916	0.2589	1049.56	1050.197	4703.9	3	418.6	68.8	2	R.YSVDIPLDK.T
gi|32189392|r	2	4	14.60%	198	21892	6	peroxiredoxin 2 isoform a [Homo sapiens]				
gi|33188452|r	2	4	19.70%	147	15989	6.6	peroxiredoxin 2 isoform b [Homo sapiens]				
	HsFLAG-p53-DNA-D	5.194	0.5205	1863.47	1864.195	6725.6	1	1609.2	70.6	3	R.KEGGLGPLNIPLLADVTR.R
	HsFLAG-KIAA0515_	2.9532	0.1804	1212.33	1212.392	5537	2	805.4	80	1	R.QITVNDLPVGR.S
gi|22208973|r	1	2	14.60%	96	10679	10.3	high mobility group AT-hook 1 isoform b [Homo sapiens]				
gi|4504433|re	1	2	14.60%	96	10679	10.3	high mobility group AT-hook 1 isoform b [Homo sapiens]				
gi|22208979|r	1	2	14.60%	96	10679	10.3	high mobility group AT-hook 1 isoform b [Homo sapiens]				
gi|22208975|r	1	2	14.60%	96	10679	10.3	high mobility group AT-hook 1 isoform b [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.2926	0.3	1562.52	1562.806	4407.9	3	336.2	57.7	2	R.KQPPKEPSEVPTPK.R
gi|28557709|r	3	9	14.50%	318	34839	6.4	phosphoribosyl pyrophosphate synthetase 1-like 1 [Homo sapiens]				
gi|4506127|re	3	9	14.50%	318	34834	7	phosphoribosyl pyrophosphate synthetase 1 [Homo sapiens]				
	HsFlag-FLJ90652_2	3.6906	0.2358	1434.09	1434.549	8568.7	1	1399.4	75	4	K.IFSGSSHQDLSQK.I
	HsFlag-FLJ90652_2	5.1766	0.4416	1802.79	1803.114	7236.7	1	2295.9	84.4	4	R.VYAILTHGIFSGPAISR.I
	HsFLAG-TCF3_Ti_1	2.7646	0.2012	1788.05	1787.97	6945.4	1	540.5	53.3	1	R.THNGESVSYLFSHVPL.-
gi|7661806|re	3	5	14.50%	296	33420	10	mitochondrial ribosomal protein L15 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.4736	0.2291	1325.26	1325.551	5534.9	1	1077.8	75	1	R.VSLANLKPNPGSK.K
*	HsFLAG-ARP6_Ti_1	4.8399	0.5058	1843.23	1843.985	7276.7	1	2089.7	75	3	R.DYGVQLVEEGADTFTAK.V
*	HsFLAG-ARP6_Ti_1	2.7354	0.1185	1398.08	1397.53	8234.7	1	949.5	62.5	1	K.NGGVVTTAFYDPR.S
gi|16117791|r	3	8	14.50%	110	12538	11.1	ribosomal protein L35a [Homo sapiens]				
	HsFLAG-TCF3_Ti_1	1.9154	0.1016	769.47	769.919	6868.4	4	538.9	75	3	K.AIFAGYK.R
*	HsFlag-Ies6_293_Ti_	1.8472	0.1999	1101.17	1102.186	6286	5	400	62.5	1	R.DETEFYLGK.R
*	HsFLAG-ARP6_Ti_1	2.7693	0.2309	1101.91	1102.186	4690.4	5	593.9	75	4	R.DETEFYLGK.R
gi|14249398|r	1	2	14.50%	110	12405	8.4	PHD-finger 5A [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.5782	0.4155	1806.3	1806.908	7904.4	1	1504.5	70	2	R.CVICGGPGVSDAYYCK.E
gi|7661606|re	5	8	14.40%	749	84878	5.5	nucleolar complex associated 2 homolog [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.6071	0.2465	2839.26	2839.355	11375.2	1	784.5	25	1	R.VLSTAGPSEALQPLVYPLAQVIIGCIK.L
*	HsFLAG-Lin9_Ti_20	6.2328	0.4135	4152.05	4152.786	8206	1	1568.4	28.6	1	R.DGLVEQLYDLTLEYLHSQAHCIGFPELVLPVVLQLK.S
*	HsFLAG-p53-DNA-D	3.3471	0.3625	1752.61	1752.924	8302	1	562.8	50	1	R.EEGTPLTLYYSHWR.K
*	HsFLAG-ARP6_Ti_1	3.782	0.2241	1503.89	1503.695	6623.5	1	1206.9	77.3	2	K.ERLEDLNFPEIK.R
*	HsFLAG-ARP6_Ti_1	4.8222	0.4815	2205.34	2206.194	10282.9	1	2548	66.7	3	K.DLFDLNSSEEDDTEGFSER.G
gi|14141193|r	4	10	14.40%	194	22591	10.7	ribosomal protein S9 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.205	0.198	1189.13	1189.403	6969.7	1	1239.2	83.3	7	R.RLFEGNALLR.R
*	HsFLAG-ARP6_Ti_1	3.0027	0.237	1034.05	1033.216	3129.2	8	602	87.5	1	R.LFEGNALLR.R
*	HsFLAG-ARP6_Ti_1	2.541	0.1	1022.16	1020.22	4135.8	1	700.2	92.9	1	R.RLQTQVFK.L
*	HsFlag-NUFIP_Ti_11	2.6881	0.2129	1004.52	1004.093	7052.2	2	713.9	72.2	1	R.SPYGGGRPGR.V
gi|16554609|r	2	6	14.40%	194	20616	10.8	mitochondrial ribosomal protein S11 isoform a [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	3.4975	0.2181	1324.71	1325.594	6059.6	1	1107	85	4	K.KFEEIPIAHIK.A
	HsFLAG-ARP6_Ti_1	3.531	0.2873	1530.54	1528.752	7999.2	1	1108.8	59.4	2	K.KGTGIAAQTAGIAAAAR.A
gi|27436904|r	1	3	14.40%	153	17811	9.7	mitochondrial ribosomal protein L23 [Homo sapiens]				

*	HsFlag-NUFIP_Ti_1	4.1051	0.2683	2563.46	2563.919	8407.7	1	1276.3	33.3	3	R.TNFFIQLVRPGVAQPEDTVQFR.I
gi|4757880|re	2	5	14.30%	328	37155	6.8	BUB3 budding uninhibited by benzimidazoles 3 isoform a [Homo sapiens]				
gi|56550081|r	2	5	14.40%	326	36955	6.8	BUB3 budding uninhibited by benzimidazoles 3 isoform b [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.5054	0.2597	2172.02	2172.402	9851.7	1	646.1	41.7	2	K.FSPNTSQFLLVSSWDTSVR.L
	HsFLAG-Lin9_Ti_20	3.7197	0.1877	3189.72	3189.436	11202.4	1	790.7	25	3	K.YQHTGAVLDCAFYDPTHAWSGGLDHQLK.M
gi|4502281|re	3	4	14.30%	279	31513	8.3	Na+/K+ -ATPase beta 3 subunit [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.9637	0.3186	1628.72	1628.868	4807.4	1	754.9	69.2	2	K.LFIYNPTTGEFLGR.T
	HsFLAG-ARP6_Ti_1	2.8561	0.3412	1687.33	1687.844	5405.5	1	835.1	64.3	1	R.SDPTSYAGYIEDLKK.F
	HsFLAG-ARP6_Ti_1	3.0223	0.2277	1179.13	1179.448	4700	2	963.5	85	1	R.IIGLKPEGVPR.I
gi|15011916|r	2	2	14.30%	217	22348	10.9	nucleolar protein family A, member 1 [Homo sapiens]				
gi|9506713|re	2	2	14.30%	217	22348	10.9	nucleolar protein family A, member 1 [Homo sapiens]				
	HsFLAG-FLJ20309_	2.5062	0.279	2143.83	2144.405	8978.4	4	363	38.2	1	R.VVLLGEFLHPCEDDIVCK.C
	HsFLAG-ARP6_Ti_1	3.8491	0.3009	1554.37	1554.786	7344.9	1	1763.6	83.3	1	K.VPYFNAPVYLENK.E
gi|4507349|re	8	16	14.20%	1083	109944	9.9	TBP-associated factor 4 [Homo sapiens]				
*	HsFLAG-FLJ20729_	3.3736	0.2655	1354.35	1354.508	4998.6	1	877.6	68.8	2	R.AGPGPGPGPGPGPGPGK.P
*	HsFLAG-FLJ20729_	4.6118	0.4534	1843.44	1844.035	5920.6	1	1018	68.8	4	K.QVSQAQTTVQPSATLQR.S
*	HsFLAG-p53-DNA-D	3.72	0.3317	3064.33	3064.426	6800.7	1	494.4	23.4	1	R.SPGVQPQLVLGGAAQTASLGTATAVQTGTPQR.T
*	HsFLAG-FLJ20729_	4.4	0.2899	2178.08	2178.404	10115.2	1	1358.2	37.5	1	K.ELVQNLLDGKIEAEDFTSR.L
*	HsFLAG-FLJ20729_	5.1723	0.395	1287.24	1287.459	8331.6	1	2359.1	84.6	4	K.ALSAVSAQAAAAQK.N
*	HsFLAG-Lin9_Ti_20	4.005	0.3725	1488.49	1488.725	6972	1	933.1	65.4	2	R.ILATNSELVGTLTR.S
*	HsFLAG-FLJ20729_	3.528	0.1138	1297.11	1297.45	7204.4	1	1558.8	88.9	1	K.FFEQLDQIEK.Q
*	HsFLAG-FLJ20729_	5.5294	0.3613	2867.42	2867.071	5736.8	1	1693.6	38.3	1	K.RKVDCPGPGSGAEGSGPGSVVPGSSGVGTPR.Q
gi|55749531|r	11	30	14.20%	895	100228	5.7	splicing factor 3B subunit 2 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_2	2.8738	0.2865	1316.33	1315.423	6815.9	1	998.5	72.7	1	R.VGEPVALSEEER.L
*	HsFLAG-ARP6_Ti_2	4.6233	0.408	1758.6	1758.003	9987.1	1	1902.7	75	4	K.LAQQQAALLMQQEER.A
*	HsFlag-NUFIP_Ti_2	3.8007	0.1741	1185.36	1185.369	7740.7	1	1198.9	83.3	5	K.RAAVLLEQER.Q
*	HsFLAG-Lin9_Ti_20	4.1721	0.4733	1941.67	1941.998	8229.8	1	1184.3	55.6	2	R.SSLGQSASETEEDTVSVSK.K
*	HsFlag-VPS71_Ti_1	4.4464	0.2812	1788.13	1787.112	8310.4	1	1235.8	67.9	4	K.RGIEKPPFELPDFIK.R
*	HsFlag-NUFIP_Ti_11	2.7431	0.24	1788.24	1787.112	4717.8	1	314.4	50	1	R.GIEKPPFELPDFIKR.T
*	HsFlag-NUFIP_Ti_2	3.2977	0.1825	1130.14	1130.243	8801.9	1	1375.7	83.3	2	K.KPGDLSDELR.I
*	HsFLAG-BC014022_	3.4398	0.3089	1321.05	1321.58	3752.1	1	486.6	70.8	4	R.ISLGMPVGPNAHK.V
*	HsFlag-NUFIP_Ti_1	2.5583	0.2254	1308.84	1308.627	3903.8	1	456.2	80	2	K.VPPPWLIAMQR.Y
*	HsFLAG-FLJ20729_	3.9288	0.2705	2363.24	2363.685	8725.3	1	1103.9	36.2	1	K.KIEEAMDGSETPQLFTVLPEK.R
*	HsFlag-VPS71_Ti_1	5.504	0.3967	2364.12	2363.685	7015.8	1	2481.8	72.5	4	K.KIEEAMDGSETPQLFTVLPEK.R
gi|14249678|r	4	13	14.20%	401	44962	6	RNA binding motif protein 17 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	3.224	0.2096	1446.38	1446.69	5687.8	1	905.9	73.1	4	R.QIVDTPPHVAAGLK.D
*	HsFlag-VPS71_Ti_1	2.5755	0.2068	1146.64	1146.208	6346.8	3	737.8	77.8	1	K.DRHEASGFAR.R
*	HsFlag-NUFIP_Ti_11	4.099	0.1991	1685.57	1685.979	5622.7	2	1039.2	68.8	7	K.RSMGGAAIAPPTSLVEK.D
*	HsFlag-DPCD_Ti_20	4.0758	0.3198	1788.61	1788.961	3939.6	1	584.1	63.3	1	K.CVIFEIPGAPDDEAVR.I
gi|5032069|re	3	22	14.20%	424	44386	8.6	splicing factor 3b, subunit 4 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	5.1939	0.3795	2607.66	2607.086	5614.2	1	1291.4	38.6	2	K.VSEPLLWELFLQAGPVVNTHMPK.D
*	HsFLAG-FLJ20729_	4.5297	0.3847	2186.94	2187.411	7692.2	1	1507.6	60.5	7	K.NLDVGANIFIGNLDPEIDEK.L
*	HsFLAG-p53-DNA-D	5.0847	0.4063	1913.71	1914.252	9495.7	1	1845.9	65.6	13	K.LLYDTFSAFGVILQTPK.I

gi|16950603|r	2	4	14.20%	323	36844	8.2	mitochondrial ribosomal protein S35 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_11	5.3148	0.4066	2938.41	2939.445	4192.7	1	588.7	30.8	3	K.MAVDQDWPSVYPVAAPFKPSAVPLPVR.M
*	HsFlag-NUFIP_Ti_1	3.5622	0.3956	2105.96	2107.284	6358	1	494	47.2	1	K.HFPIEIDSTDYVSSGPSVR.N
gi|89044285|r	16	36	14.10%	1949	220240	7.7	PREDICTED: structural maintenance of chromosomes flexible hinge domain containing 1 [Homo sapiens]				
gi|89047296|r	16	36	14.10%	1949	220240	7.7	PREDICTED: similar to SMC hinge domain containing 1 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	4.7629	0.3821	2190.58	2191.573	8722.7	1	1207.8	52.6	6	K.DGVTLYLLQSVNQLLLTATK.E
	HsFLAG-Lin9_Ti_20	3.3712	0.3025	1747.19	1747.004	8879.7	1	671.6	57.7	2	K.ERIDFLPHYDTLVK.S
	HsFLAG-FLJ20729_	4.0016	0.3685	3496.11	3496.827	10868.1	1	845.2	25	1	K.SGMYEYYASEGQNPLPFALAELIDNSLSATSR.N
	HsFLAG-p53-DNA-D	4.5229	0.3546	2044.48	2044.315	5060.3	1	814.5	55.6	1	K.LLFDETQGKPAVAVIDNGR.G
	HsARP6-FLAG_Ti_1	3.1224	0.2352	1444.44	1444.584	7878.2	5	596.7	57.7	2	R.SLNSDISYFGVGGK.Q
	HsARP6-FLAG_Ti_1	2.9451	0.3973	1266.26	1266.526	3327.3	1	602.9	80	2	K.TLPLFYGSIVR.F
	HsFLAG-p53-DNA-D	3.8069	0.2597	1311.71	1312.554	6971.6	1	1462.1	85	6	K.FSFGLLDLPFR.V
	HsFLAG-p53-DNA-D	3.3661	0.1727	1541.75	1541.828	5235.6	1	530.5	61.5	2	K.VTLPGLKEDSQILK.I
	HsFLAG-Lin9_Ti_20	5.5994	0.3375	3746.69	3745.175	11210.7	1	1302.2	25	1	K.VKPDSEILVIENGTAFPFQVEVLDESDNITAQPK.L
	HsFLAG-Lin9_Ti_20	3.6004	0.1751	2829.51	2829.151	6481.8	1	633.1	29.3	1	R.DLQNPIIVQLCDQWDNPAPVQHVK.I
	HsARP6-FLAG_Ti_1	3.8043	0.3203	1278.41	1278.497	6749.9	1	961.8	72.7	3	R.ANLGVFSVFAPR.G
	HsFLAG-p53-DNA-D	2.2562	0.1178	911.56	912.034	4038.8	2	399.7	71.4	1	R.GEHTLQVK.A
	HsFlag-DPCD_Ti_20	4.7208	0.3916	2051.01	2052.174	10507.8	1	1049	50	4	K.LSTSGNRPPANAETFSCNK.I
	HsARP6-FLAG_Ti_1	2.8796	0.1477	1503.19	1503.651	10191.8	1	1067	63.6	1	R.DSTEYFIVFEPR.L
	HsFLAG-FLJ20729_	2.9639	0.2347	1989.77	1991.352	6577.3	4	512.3	50	1	R.TLEPYILPFMFYNDVK.K
	HsARP6-FLAG_Ti_1	3.5718	0.2278	1639.17	1638.876	8814.1	1	1591.3	69.2	2	K.SLFEASQQLLNEMK.C
gi|4506193|re	2	2	14.10%	241	26489	8.1	proteasome beta 1 subunit [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.9884	0.3143	2005.61	2005.296	4091.6	1	509.6	50	1	K.AGGSASAMLQPLLDNQVGFK.N
*	HsFlag-VPS71_Ti_1	3.5398	0.3399	1652.61	1652.866	5342.9	3	556.4	57.7	1	K.NMQNVEHVPLSLDR.A
gi|4827071|re	3	4	14.10%	177	19463	7.7	zinc finger protein 9 [Homo sapiens]				
*	HsMRGBP-FLAG_Ti	3.1711	0.3782	1486.43	1486.556	5730.3	1	871.7	72.7	1	K.CYSCGEFGHIQK.D
*	HsFlag-VPS71_Ti_1	4.1862	0.4355	1433.29	1433.493	7649.4	1	1512.1	75	2	R.CGETGHVAINCSK.T
*	HsFlag-VPS71_Ti_1	2.542	0.0885	1434.46	1433.493	3224.9	1	313.2	62.5	1	R.CGETGHVAINCSK.T
gi|22202629|r	5	11	14.00%	609	66295	8.9	programmed cell death 8 isoform 2 [Homo sapiens]				
gi|4757732|re	5	11	13.90%	613	66901	9	programmed cell death 8 isoform 1 [Homo sapiens]				
	HsYL1_Ti_101.1586.	3.6678	0.3074	1531.7	1531.616	4767.7	1	829.1	67.9	3	K.AALSASEGEEVPQDK.A
	HsFLAG-ARP6_Ti_1	3.8461	0.3318	2026.87	2025.361	4535.6	1	679.6	52.5	1	K.APSHVPFLLIGGGTAAFAAAR.S
	HsFLAG-ARP6_Ti_1	3.7574	0.3757	1992.07	1993.277	10767.7	1	1164.6	52.6	3	K.SITIIGGGFLGSELACALGR.K
	HsFLAG-ARP6_Ti_1	3.4649	0.1792	1445.68	1445.699	6349.8	1	1178.9	75	2	R.ALGTEVIQLFPEK.G
	HsFLAG-ARP6_Ti_1	4.2223	0.4904	1573.51	1573.848	3591	1	719.3	70	2	K.VMPNAIVQSVGVSSGK.L
gi|20070125|r	5	12	14.00%	508	57116	4.9	prolyl 4-hydroxylase, beta subunit [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.8872	0.3452	2937.35	2937.273	8311.1	1	1580	31.9	6	R.TGPAATTLPDGAAAESLVESSEVAVIGFFK.D
*	HsFLAG-p53-DNA-D	3.9054	0.2971	1965.58	1966.244	6118.4	1	461.8	46.9	3	K.HNQLPLVIEFTEQTAPK.I
*	HsFLAG-p53-DNA-D	4.7819	0.2705	1966.39	1966.244	6162.4	1	1118.8	42.2	1	K.HNQLPLVIEFTEQTAPK.I
*	HsFLAG-BC014022_	2.7465	0.1518	1081.95	1082.374	4933.9	1	942.1	81.2	1	K.THILLFLPK.S
*	HsFlag-VPS71_Ti_1	3.6736	0.2682	1835.95	1835.026	7873.2	1	1021.3	60.7	1	K.ILFIFIDSDHTDNQR.I
gi|19913432|r	2	3	14.00%	351	40329	5	ATPase, H+ transporting, lysosomal, V0 subunit D isoform 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	5.104	0.4975	2479.54	2480.741	9060.4	1	1652.6	54.8	1	K.AGVLSQADYLNLVQCETLEDLK.L

*	HsFLAG-ARP6_Ti_1	5.0435	0.4094	2975.5	2977.257	8105.8	1	795.5	29.8	2	K.LHLQSTDYGNFLANEASPLTVSVIDDR.L
gi|4506619|re	3	13	14.00%	157	17779	11.3	ribosomal protein L24 [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1(	2.8606	0.126	1193.59	1193.391	4808.5	1	584.5	87.5	2	R.QINWTVLYR.R
*	HsYL1_Ti_102.2003.	3.4261	0.3289	1261.63	1262.507	9858.5	3	813.8	58.3	5	R.AITGASLADIMAK.R
*	HsFLAG-ARP6_Ti_1	4.3862	0.362	1263.45	1262.507	7589.3	1	2066	87.5	6	R.AITGASLADIMAK.R
gi|33469968|r	6	13	13.90%	719	81308	6.5	minichromosome maintenance protein 7 isoform 1 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	2.8816	0.2971	1635.6	1635.901	7067.7	1	776.3	61.5	1	K.LFADAVQELLPQYK.E
	HsFlag-VPS71_Ti_1(	4.2939	0.467	2034.39	2034.409	7484.1	1	1482.1	61.1	3	R.IAQPGDHVSVTGIFLPILR.T
	HsFLAG-TCF3_Ti_1(	2.6046	0.1236	1553.37	1551.87	7035.3	1	592.5	53.6	1	K.ALLLLLLVGGVDQSPR.G
	HsFLAG-p53-DNA-D	3.9488	0.3654	1590.36	1590.785	6462.5	1	1447.4	79.2	2	R.LAQHITYVHQHSR.Q
	HsFlag-VPS71_Ti_1(	3.4384	0.2839	1475.76	1474.703	6085.5	1	814.1	66.7	5	R.TQRPADVIFATVR.E
	HsSrcap_Ti_203.428	3.5219	0.4177	2986.92	2985.239	8074.5	1	648.5	36	1	R.GFTPAQFQAALDEYEELNVWQVNASR.T
gi|5453994|re	6	14	13.90%	631	71690	4.7	RAD21 homolog [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	2.9608	0.194	1141.31	1140.33	4801.3	3	873.2	87.5	1	K.IWLAAHWDK.K
*	HsFlag-VPS71_Ti_1(	3.6304	0.3959	2147.78	2147.356	6714.1	1	518.3	52.8	1	K.AHVFECNLESSVESIISPK.V
*	HsARP6-FLAG_Ti_1	3.495	0.1284	1458.06	1457.632	6555	1	1434.3	86.4	1	K.YLLADCNEAFIK.I
*	HsFLAG-p53-DNA-D	3.2491	0.1851	1730.12	1730.979	5111.1	2	865.8	60.7	3	K.MAFRPGVVDLPEENR.E
*	HsFLAG-ARP6_Ti_2	4.8318	0.3119	2148.44	2149.403	6600.7	1	1301.2	57.9	3	R.AQLSDYSDIVTTLDLAPPTK.K
*	HsFlag-VPS71_Ti_1(	3.4153	0.1762	1557.79	1556.808	4076.2	1	801.6	79.2	5	K.LFSLPAQPLWNNR.L
gi|20270371|r	2	4	13.90%	245	28048	7.2	hypothetical protein LOC134147 [Homo sapiens]				
*	HsFLAG-RPB5MP_2	3.6158	0.2275	1970.46	1971.31	5222.1	1	778.1	56.2	2	K.AVIVIQDIFGWQLPNTR.Y
*	HsFLAG-RPB5MP_2	4.2714	0.3228	1929.45	1931.282	6129.1	1	987.8	59.4	2	K.NPTLFIFAENDVVIPLK.D
gi|40254978|r	4	11	13.80%	594	66526	5.6	FIP1-like 1 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.2339	0.4654	1951.99	1952.174	6018.1	1	474.2	47.2	3	K.TGAPQYGSYGTAPVNLNIK.T
*	HsFlag-VPS71_Ti_1(	3.6543	0.4653	1811.82	1811.135	4788.7	1	861.7	65.6	6	R.RLPGAIDVIGQTITISR.V
*	HsFLAG-p53-DNA-D	4.3964	0.3826	2843.18	2844.199	4540.5	1	792.8	34.6	1	R.AFPYGNVAFPHLPGSAPSWPSLVDTSK.Q
*	HsFlag-VPS71_Ti_1(	2.8091	0.2709	1931.31	1930.931	6144	2	362	44.4	1	K.EAGSEPAPEQESTEATPAE.-
gi|27545326|r	3	4	13.80%	385	44141	6.2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1 isoform a				
gi|55956801|r	3	4	14.10%	376	43158	5.7	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1 isoform b				
	HsARP6-FLAG_Ti_1	3.1243	0.2982	1548.26	1548.601	7771.4	1	846.7	61.5	1	K.ASEVEEILDGNDEK.Y
	HsFLAG-p53-DNA-D	3.4103	0.3483	1921.73	1922.188	6776.6	1	897.8	59.4	1	K.TYAFSENPLPTVEIAIR.N
	HsFLAG-p53-DNA-D	3.6227	0.2844	2539.61	2538.708	7624.6	1	498.2	38.1	2	R.NTGDADQWCPLLETLTDAEMEK.K
gi|33350932|r	42	124	13.70%	4646	532412	6.4	dynein, cytoplasmic, heavy polypeptide 1 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.8392	0.2055	2477.32	2477.858	7986.8	1	1456.8	34.8	1	R.KLVPLLLEDGGEAPAALEAALEEK.S
*	HsFLAG-p53-DNA-D	6.1956	0.5032	2477.91	2477.858	7211.2	1	1725.4	58.7	2	R.KLVPLLLEDGGEAPAALEAALEEK.S
*	HsFlag-VPS71_Ti_1(	5.98	0.4768	2349.13	2349.684	5858.7	1	1618.4	63.6	9	K.LVPLLLEDGGEAPAALEAALEEK.S
*	HsFlag-VPS71_Ti_1(	5.8743	0.4095	2349.93	2349.684	7900.2	1	2049.7	42	10	K.LVPLLLEDGGEAPAALEAALEEK.S
*	HsFLAG-p53-DNA-D	3.9172	0.4392	1640.59	1640.88	6419.8	1	1278.6	76.9	4	K.FLSDPQVHTVLVER.S
*	HsFLAG-p53-DNA-D	4.1226	0.2288	2914.17	2914.284	7034.1	1	608.6	27	4	R.VLTLSEDSPYETLHSFISNAVAPFFK.S
*	HsFlag-VPS71_Ti_1(	3.429	0.3841	2914.69	2914.284	8926.5	1	680.9	34	2	R.VLTLSEDSPYETLHSFISNAVAPFFK.S
*	HsFLAG-FLJ20729_	4.3532	0.335	1816.94	1817.996	8835	1	1037.4	56.7	2	K.VEDPTFLNQLQSGVNR.W
*	HsARP6-FLAG_Ti_1	3.023	0.3218	1692.23	1691.876	4260.8	1	517.4	64.3	1	K.DFPLNDLLSATELDK.I
*	HsFLAG-ARP6_Ti_1	3.411	0.2694	1375.17	1374.663	3458.5	2	702.6	81.8	2	K.VNFLPEIITLSK.E

*	HsFLAG-ARP6_Ti_1	4.4457	0.3093	2159.26	2158.465	10315.4	4	1023.2	34.7	2	K.AHQANQLYPFAISLIESVR.T
*	HsFLAG-ARP6_Ti_2	3.4182	0.128	1462.37	1459.642	7472.8	1	1651.6	83.3	1	R.AWTQVLLGQAEDK.A
*	HsFLAG-p53-DNA-D	3.6596	0.1792	2530.45	2529.896	7779.2	1	495	38.6	2	K.TKPVTGNLRPEEALQALTIYEGK.F
*	HsFlag-VPS71_Ti_1	4.382	0.38	1961.25	1960.191	8313	1	1419.3	62.5	8	R.FYFVGDEDLLEIIGNSK.N
*	HsARP6-FLAG_Ti_1	2.8558	0.1634	1580.42	1580.737	5911.8	1	710.2	66.7	1	K.FNYGFEYLGVQDK.L
*	HsFLAG-ARP6_Ti_1	2.7048	0.2264	1690.3	1690.894	7643.5	2	478.1	41.2	1	R.LGGSPFGPAGTGKTESVK.A
*	HsFLAG-ARP6_Ti_1	4.2429	0.3506	1962.82	1962.238	9057.5	1	1429.8	59.4	1	R.MLSAVSQQVQCIQEALR.E
*	HsFLAG-p53-DNA-D	4.1418	0.3839	1801.57	1801.997	4611.1	1	779.2	63.3	2	K.AISKDHLYGTLDPNTR.E
*	HsFLAG-p53-DNA-D	2.9145	0.278	1474.99	1474.659	7165.8	1	618.4	63.6	1	R.EWTDGLFTHVLR.K
*	HsFLAG-p53-DNA-D	4.7099	0.3353	1924.91	1925.213	10018.9	1	1662.6	63.3	2	K.ALEHAFQLEHIMDLTR.L
*	HsARP6-FLAG_Ti_1	3.0491	0.2639	1552.53	1552.811	6248.9	1	700.8	57.1	1	K.VAAPDVVVPTLDTVR.H
*	HsFlag-VPS71_Ti_1	5.4016	0.4642	2448.24	2446.862	8597	1	1924.9	56.8	9	R.ALPDMEVVGLNFSSATTPELLLK.T
*	HsFlag-VPS71_Ti_1	2.6604	0.3272	2339.57	2339.64	8922.8	1	705.4	44.7	1	R.TYAEPLTAAMVEFYTMSQER.F
*	HsFLAG-p53-DNA-D	4.9853	0.4186	1753.62	1753.911	4715.9	1	1064.6	76.9	3	R.FTQDTQPHYIYSPR.E
*	HsFlag-VPS71_Ti_1	3.617	0.2814	2123.92	2124.531	5691.5	1	847.5	52.8	7	R.GIFEALRPLETLPVEGLIR.I
*	HsFlag-VPS71_Ti_1	3.6049	0.1695	2125.05	2124.531	4090.4	1	1218.8	50	1	R.GIFEALRPLETLPVEGLIR.I
*	HsFlag-VPS71_Ti_1	4.3667	0.4185	2789.49	2789.2	3642.4	1	450.9	45.5	1	K.VFYEEELDVPLVLFNEVLDHVLR.I
*	HsFlag-VPS71_Ti_1	4.6268	0.3369	2789.53	2789.2	6066.5	2	887.6	31.8	3	K.VFYEEELDVPLVLFNEVLDHVLR.I
*	HsFLAG-ARP6_Ti_1	3.7456	0.4084	1774.2	1774.045	6601.1	1	745.7	53.3	2	R.NLHVVFTMNPSSEGLK.D
*	HsFLAG-p53-DNA-D	5.2047	0.3916	2062.42	2062.294	10806.3	1	2368.2	70	1	R.HYLDFINHYANLFHEK.R
*	HsFLAG-p53-DNA-D	4.1367	0.399	2267.75	2266.513	5503	1	676.8	52.6	2	R.ENFIPTIVNFSAEEISDAIR.E
*	HsFlag-VPS71_Ti_1	2.7636	0.2347	2264.44	2264.521	3337.2	8	181.5	39.5	1	R.WQASSLPADDLCTENAIMLK.R
*	HsFlag-VPS71_Ti_1	5.1705	0.3061	2330.76	2330.658	3514.7	1	832.1	65.8	3	R.YPLIIDPSGQATEFIMNEYK.D
*	HsFlag-VPS71_Ti_1	5.5741	0.4447	2599.11	2599.946	8198.2	1	997.9	45.5	13	R.FGNPLLVQDVESYDPVLNPVLNR.E
*	HsFLAG-ARP6_Ti_2	3.2835	0.1147	1115.67	1115.315	6332.8	2	1154.3	83.3	2	K.SLLQALNEVK.G
*	HsFLAG-p53-DNA-D	5.0016	0.3061	1717.95	1717.954	7032.8	1	1570.2	75	6	R.ILDDDTIITTLENLK.R
*	HsFLAG-p53-DNA-D	3.136	0.2345	1967.09	1968.133	7684.1	1	677.6	53.1	2	K.GTVGEPTYDAEFQHFLR.G
*	HsFLAG-p53-DNA-D	3.7042	0.2481	3326.17	3326.693	8684.6	1	718.4	26.9	1	R.REEFVQWVELLPDTQTPSWLGLPNNAER.V
*	HsFLAG-ARP6_Ti_2	2.8805	0.3887	1406.64	1405.693	8533.1	1	849	62.5	1	R.VLLTTQGVDMISK.M
*	HsFLAG-Lin9_Ti_20	3.7048	0.3701	2411.73	2412.797	6416.5	1	577.5	45	1	R.TLHTTASNWLHLIPQTLSHLK.R
*	HsFLAG-ARP6_Ti_1	3.9316	0.3699	1798.8	1799.121	5775.6	1	655.9	56.2	2	K.LSLSNAISTALPLTQLR.W
*	HsFLAG-p53-DNA-D	3.5696	0.3172	1581.21	1580.867	3759.4	2	424.1	61.5	3	K.ASVVTLPVYLNFTR.A
gi|7661686|re	12	35	13.70%	1717	194190	7.2	polymerase (RNA) I polypeptide A, 194kDa [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	4.0452	0.2257	3953.33	3952.308	9161.1	3	476.9	18.2	1	K.EVCSTCVQDFSNCSGHLGHIELPLTVYNPLLFDK.L
*	HsFlag-NUFIP_Ti_1	3.2139	0.2119	1286.02	1286.578	5232.6	1	644.7	75	4	K.LTITFPAMVHR.T
*	HsFlag-NUFIP_Ti_11	4.3107	0.3608	1981.82	1982.332	4131.7	1	815.4	68.8	6	R.FNPSVFFLDFLVVPPSR.S
*	HsFlag-NUFIP_Ti_1	3.1855	0.1813	2616.34	2615.041	9181.7	2	629	36.4	1	R.SVICPDMYINTNEIGIPMVFATK.L
*	HsFLAG-p53-DNA-D	2.5614	0.2064	1941.15	1942.225	5995.4	1	414.5	53.3	1	K.LTYPQPVTPWNVQELR.Q
*	HsFlag-NUFIP_Ti_11	3.0019	0.2774	1608.09	1608.878	5051.1	3	393.7	50	1	K.QLLTPATGAPKPQGTK.I
*	HsFLAG-TIP49b_Ti_	4.3758	0.3602	1596.62	1597.734	9156.4	1	1468.2	69.2	9	R.IIEESTHCGPQAVR.A
*	HsFLAG-ARP6_Ti_1	3.2805	0.3149	2153.96	2155.323	7799.9	1	731	44.7	3	R.DSDGSVVQFLYGEDGLDIPK.T
*	HsFlag-NUFIP_Ti_1	3.8875	0.2814	3591.45	3591.984	5738.3	1	547.2	25.8	2	R.SLCEPGEAVGLLAAQSIGEPSTQMTLNTFHFAGR.G
*	HsFlag-NUFIP_Ti_1	4.6338	0.1619	1700.8	1699.906	4620.8	1	1552.6	91.7	5	R.FQFLPHAYYQQEK.C

*	HsFlag-NUFIP_Ti_1	4.4921	0.4859	2337.21	2337.739	7350.6	1	797.9	45.2	1	K.INFDMSSLVVSLAHGAVIYATK.G
*	HsFLAG-p53-DNA-D	4.0694	0.3755	1830.58	1830.131	8369.2	1	1449	66.7	1	K.ELVLNTEGINLPELFK.Y
gi|4504715|re	6	13	13.70%	644	70783	9.3	poly A binding protein, cytoplasmic 4 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.0589	0.308	1929.23	1930.084	9460.6	1	1041	53.1	1	R.SLGYAYVNFQQPADAER.A
	HsFLAG-ARP6_Ti_1	3.0592	0.2797	1267.66	1267.483	5025.5	1	890.6	80	1	R.ALDTMNFDVIK.G
	HsFLAG-ARP6_Ti_1	4.5583	0.3978	1807.79	1808.007	7833.5	1	1601.2	70	1	K.ALYDTFSAFGNILSCK.V
	HsFLAG-ARP6_Ti_1	3.6131	0.4405	1663.85	1663.79	5123.3	1	681.7	57.1	3	K.GFGFVCFSSPEEATK.A
*	HsFLAG-ARP6_Ti_1	4.0483	0.2689	1515.47	1515.839	3303.3	1	807.6	76.9	2	R.IVGSKPLYVALAQR.K
*	HsFlag-NUFIP_Ti_1	4.9939	0.3372	1670.28	1671.01	6146.3	1	1228.5	78.6	5	R.LFPLIQTMHSNLAGK.I
gi|5729933|re	4	5	13.70%	568	63634	8.4	septin 9 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_2	3.0652	0.2609	1464.18	1464.659	3609.8	3	418.4	60.7	1	K.VPEVPTAPATDAAPK.R
*	HsFLAG-p53-DNA-D	4.5514	0.3161	3856.92	3857.331	8521.4	1	1128.3	26.4	1	K.RVEIQMPKPAEAPTAPSPAQTLENSEPAPVSQLQSR.L
*	HsFlag-VPS71_Ti_1	4.8074	0.4573	2011.87	2011.3	4940.8	1	1033.9	64.7	2	K.APVDFGYVGIDSILEQMR.R
*	HsFlag-VPS71_Ti_1	2.744	0.2445	1072.26	1072.16	6670.9	4	832.1	75	1	K.SITHDIEEK.G
gi|48526509|r	5	14	13.60%	456	50465	9.4	translocase of inner mitochondrial membrane 50 homolog [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.7608	0.3119	1271.28	1271.376	5987.8	3	699.2	68.2	2	R.RAPDQAAEIGSR.G
*	HsFLAG-ARP6_Ti_1	4.2024	0.3399	1730.46	1730.831	4434.2	1	580.1	59.4	2	K.AQGPQQQPGSEGPSYAK.K
*	HsFLAG-ARP6_Ti_1	4.5545	0.3793	1913.42	1913.138	5884.5	1	1149.9	66.7	3	K.IPDEFDNDPILVQQLR.R
*	HsFLAG-ARP6_Ti_1	5.2204	0.4623	1932.47	1933.168	7497.3	1	1683	68.8	5	R.TVLEHYALEDDPLAAFK.Q
*	HsFLAG-ARP6_Ti_1	4.2129	0.2971	1933.42	1933.168	5600.8	1	1160.3	48.4	2	R.TVLEHYALEDDPLAAFK.Q
gi|4504191|re	12	30	13.50%	1360	152785	6.9	mutS homolog 6 [Homo sapiens]				
*	HsYL1_Ti_102.2326.	4.0417	0.248	2179.09	2177.384	4783.6	1	377.3	45	4	R.SVAPAAPTSCDFSPGDLVWAK.M
*	HsSrcap_Ti_206.229	3.2839	0.2406	1476.24	1475.69	7781.2	1	1159.7	66.7	1	K.GGHFYSAKPEILR.A
*	HsFLAG-FLJ20729_	3.049	0.4167	1647.22	1646.805	8690.7	1	811.1	53.6	2	K.GNWAHSGFPEIAFGR.Y
*	HsYL1_Ti_101.1990.	3.9848	0.38	1975.9	1976.061	6663.4	1	1107.7	61.8	3	K.GTQTYSVLEGDPSENYSK.Y
*	HsYL1_Ti_105.2258.	3.5717	0.2676	1741.09	1742.071	2981.9	1	530.7	67.9	2	R.TLVAHYPPVQVLFEK.G
*	HsYL1_Ti_102.2854.	3.1207	0.2416	2398.86	2398.598	3292.2	1	380.7	47.6	1	K.SSLSCSLQEGLIPGSQFWDASK.T
*	HsYL1_Ti_106.1906.	2.5503	0.2711	964.68	965.14	4175.2	1	452.4	75	4	K.IHNVGSPLK.S
*	HsYL1_Ti_101.1780.	2.9954	0.2882	1336.44	1336.499	4819.6	1	769.3	75	1	R.AIMYEETTYSK.K
*	HsYL1_Ti_102.3516.	2.0271	0.2293	1352.63	1353.601	7107.7	1	799.2	68.2	1	K.IIDFLSALEGFK.V
*	HsYL1_Ti_102.3506.	4.6855	0.1471	1355.07	1353.601	5026.3	1	1348.4	86.4	4	K.IIDFLSALEGFK.V
*	HsFLAG-FLJ20729_	5.2726	0.4174	3134.89	3134.337	8735.5	1	1836.3	33.7	6	K.AGFDSDYDQALADIRENEQSLLEYLEK.Q
*	HsFLAG-Lin9_Ti_20	3.5035	0.3395	2465.89	2467.7	14045.7	1	1280.2	45	1	R.TLFSTHYHSLVEDYSQNVAVR.L
gi|47271406|r	4	12	13.50%	689	74355	9.6	bin3, bicoid-interacting 3 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.2264	0.4027	4019.7	4021.396	6804.2	1	760.9	25.7	2	R.RVNSDCDSVLPSNFLLGGNIFDPLNLNSLLDEEVSR.T
*	HsSrcap_Ti_202.550	3.5765	0.2061	3864.99	3865.209	6055.2	2	445.2	20.6	1	R.VNSDCDSVLPSNFLLGGNIFDPLNLNSLLDEEVSR.T
*	HsFlag-NUFIP_Ti_1	4.9469	0.3648	2596.45	2596.86	7261.6	1	947.2	47.8	2	K.DITDPLSLNTCTDEGHVVLASPLK.T
*	HsFlag-NUFIP_Ti_1	5.97	0.3965	3671.92	3673.07	9624.9	1	1526.5	28.9	7	R.IQLKPEQFSSYLTSPDVGFSSYELVATPHNTSK.G
gi|13676857|r	13	176	13.50%	639	70021	5.7	heat shock 70kDa protein 2 [Homo sapiens]				
	HsFlag-FLJ90652_2	3.6517	0.3726	1487.89	1488.594	3812.9	1	610.4	75	34	R.TTPSYVAFTDTER.L
	Hs293Flag-Ies2_Ti_1	3.2174	0.4318	1488.58	1488.594	3710.2	1	167.1	54.2	6	R.TTPSYVAFTDTER.L
	HsYL1_Ti_103.1140.	2.546	0.195	1180.57	1181.331	4585.1	2	464.2	66.7	2	K.VQVEYKGETK.T
	HsFLAG-ARP6_Ti_1	3.2097	0.268	1181.78	1181.331	4772.1	4	814.9	83.3	12	K.VQVEYKGETK.T

*	HsFLAG-ARP6_Ti_1	3.4481	0.2614	1904.56	1905.12	4323.4	1	568.5	56.2	2	K.VHSAVITVPAYFNDSQR.Q
	HsFLAG-Lin9_Ti_20	5.2508	0.4465	1660.49	1660.908	5331.5	1	1768.4	80	50	R.IINEPTAAAIAYGLDK.K
	HsFLAG-ARP5_Ti_1	3.8699	0.1778	1788.62	1789.082	4190.7	1	571.2	59.4	2	R.IINEPTAAAIAYGLDKK.G
	HsFlag-FLJ90652_2	2.0904	0.2727	1480.7	1481.651	2330.8	4	142.3	59.1	1	R.ARFEELNADLFR.G
	HsFLAG-ARP6_Ti_1	4.2068	0.2215	1481.81	1481.651	6808.7	1	1830.4	59.1	3	R.ARFEELNADLFR.G
	HsYL1_Ti_103.1942.	4.6423	0.2622	1483.93	1481.651	4875.6	1	1115	86.4	58	R.ARFEELNADLFR.G
	HsFlag-FLJ90652_2	3.6003	0.2919	1254.46	1254.385	7777.4	2	1585.6	88.9	3	R.FEELNADLFR.G
	HsTIP60_Ti_105.226	2.8115	0.2224	1082.24	1082.244	4474.4	5	672.9	87.5	2	K.LLQDFFNGK.E
	HsFlag-FLJ90652_2	2.5343	0.1365	931.17	931.08	5013.8	4	875.8	100	1	K.RNTTIPTK.Q
gi|89038196|r	22	65	13.40%	2855	315119	6.8	PREDICTED: MAX dimerization protein 5 isoform 1 [Homo sapiens]				
gi|89038895|r	22	65	13.40%	2855	315105	6.8	PREDICTED: similar to MAX-interacting protein isoform 6 [Homo sapiens]				
gi|89038893|r	22	65	13.40%	2855	315105	6.8	PREDICTED: similar to MAX-interacting protein isoform 5 [Homo sapiens]				
gi|89038198|r	22	65	13.40%	2855	315119	6.8	PREDICTED: MAX dimerization protein 5 isoform 2 [Homo sapiens]				
	HsFlag-DPCD_Ti_20	3.7048	0.2784	2012.31	2013.169	5622.3	3	553.1	47.2	1	R.LTEGQGSEIQPGDLDPLSR.G
	HsFlag-DPCD_Ti_20	4.2623	0.3371	1992.36	1993.187	8815.1	1	1444.7	70	2	K.KLEYTICETEPEQPVR.H
	HsFlag-VPS71_Ti_1	4.2291	0.3244	4039.19	4039.757	5720.9	1	592.2	24.3	1	K.VEGEVDPEPVYIPTPSVIEPMKPLLLPQPEVLSPTVK.G
	HsH2AZ-FLAG_293_	3.0861	0.3167	1278.2	1278.494	4331.2	1	552.1	66.7	1	K.GLPFYAGLSPAGK.L
	HsFlag-DPCD_Ti_20	4.7908	0.3411	3218.29	3217.69	6179.1	1	873	30.6	5	K.ITYSSGGQPVGTASLIPLQSGSFALLQLPGQK.P
	HsARP6-FLAG_Ti_1	4.4752	0.484	1735.4	1736.083	5389.2	1	1033.7	70	4	K.PVPSSILQHVASLQMK.R
	HsFlag-DPCD_Ti_20	4.5004	0.3473	1926.62	1927.162	5482	1	1173.8	67.6	3	K.KVLQSEGEAVDPEANVIK.Q
	HsFlag-DPCD_Ti_20	5.0603	0.4001	1798.41	1798.988	6776.8	1	1803.8	75	2	K.VLQSEGEAVDPEANVIK.Q
	HsH2AZ-FLAG_293_	4.963	0.4677	2396.97	2397.524	6338.3	1	1158.1	57.5	5	K.TCQENSDVFQQEQGISDLLGK.S
	HsH2AZ-FLAG_293_	3.6255	0.2295	1287.91	1288.489	5396.3	1	1255.3	81.8	4	R.ISNPSAFSIVPR.R
	HsFLAG-p53-DNA-D	2.8884	0.2818	1091.5	1092.197	5707	1	578.2	72.2	2	K.TTAAHTQSFK.Q
	HsH2AZ-FLAG_293_	5.1181	0.3302	1523.49	1523.64	5411.6	1	1693.6	84.6	3	R.AFSEIQGLTDQADK.L
	HsFLAG-p53-DNA-D	5.2647	0.3378	3578.65	3579.063	9328.8	1	1555.7	29.7	1	R.KKDQATENTSPLNTPHTSANLVMTPQGQLLTLK.G
	HsFlag-DPCD_Ti_20	3.8662	0.2702	3321.09	3322.715	8532.9	1	670.3	23.3	3	K.DQATENTSPLNTPHTSANLVMTPQGQLLTLK.G
	HsFlag-DPCD_Ti_20	3.5515	0.3308	2140.78	2141.469	6821.2	1	579	42.5	2	K.GPLFSGPVVAVSPDLLESDLK.P
	HsFlag-NUFIP_Ti_1	5.5706	0.4292	4381.26	4382.046	8363.8	1	1141.3	23.2	2	MPR.I
	HsFlag-DPCD_Ti_20	3.4058	0.4872	1947.54	1949.227	10467.8	1	963.4	47.4	2	R.IVNVTSLATEGGLVDMGGSK.Y
	HsFlag-DPCD_Ti_20	3.0496	0.2944	1749.43	1749.921	6818.8	1	820.4	64.3	2	K.YPHEVPDSKPSDHLK.D
	HsARP6-FLAG_Ti_1	3.7748	0.364	1388.3	1388.65	6527.4	1	1029.5	70.8	5	R.VTLGPTQVFLANK.D
	HsFlag-DPCD_Ti_20	3.6222	0.2564	1401.6	1401.605	7175.6	1	1228.3	75	8	R.ATFQVEHLGTGLK.E
	HsFlag-DPCD_Ti_20	4.1994	0.4007	2179.52	2180.438	4964.3	1	1069.2	62.5	5	K.NTSGLPAEPESVSSPPTLHMK.T
	HsFlag-DPCD_Ti_20	3.3924	0.1149	2047.02	2048.278	9380.6	1	977.2	52.9	2	K.TGLENSNSTDTLWRPMPK.L
gi|21237805|r	11	49	13.40%	1214	132879	5.7	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c2 isoform a [Homo sapiens]				
gi|21237808|r	11	49	14.40%	1130	124841	5.6	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c2 isoform b [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.1114	0.4749	1792.84	1792.899	7272.8	1	1239.1	71.4	1	K.YYEAADTVTQFDNVR.L
	HsFLAG-p53-DNA-D	3.7352	0.2449	1289.6	1289.474	6709.3	2	861	75	1	K.KYIQAEPPTNK.S
	HsFLAG-p53-DNA-D	5.9718	0.4547	2152.04	2152.496	8061.2	1	2200.4	69.4	22	K.SLSSLVVQLLQFQEEVFGK.H
	HsFLAG-p53-DNA-D	2.0841	0.2953	966.51	967.113	4711.4	1	402.8	62.5	2	K.HVSNAPLTK.L
	HsFLAG-Lin9_Ti_20	4.1184	0.4231	1432.23	1432.629	9494.1	1	1366.4	61.5	2	K.AGGSLCHILAAAYK.F
	HsFLAG-p53-DNA-D	5.5115	0.4502	2894.72	2895.262	7963.5	1	1160	32.3	4	K.NNASHVVYPVPGNLEEEEWVRPVMK.R

	HsFlag-VPS71_Ti_10	3.4336	0.1859	2240.34	2240.573	8004.4	1	732.2	50	1	R.EWTEQETLLLLEALEMYK.D
	HsFlag-VPS71_Ti_10	4.0724	0.2671	1432.39	1432.585	6575.7	1	1169.4	80	6	R.TQDECILHFLR.L
	HsFLAG-p53-DNA-D	6.743	0.4825	1885.3	1886.112	9907.1	1	2725.6	67.5	5	R.DIGEGNLSTAAAAALAAAAVK.A
	HsFLAG-p53-DNA-D	2.1902	0.198	924.5	925.032	4939.2	1	519.1	78.6	1	K.HLAAVEER.K
	HsARP6-FLAG_Ti_1	4.2653	0.3252	1332.08	1332.642	7108.5	1	1762	86.4	4	K.SLVALLVETQMK.K
gi|24415383|r	11	27	13.40%	1130	119624	4.3	proline-, glutamic acid-, leucine-rich protein 1 [Homo sapiens]				
*	HsH2AZ-FLAG_293_	3.7257	0.2665	1538.65	1538.871	8385.3	1	1896.7	55.8	1	R.LLLLESVSGLLQPR.T
*	HsH2AZ-FLAG_293_	4.0044	0.1993	1539.54	1538.871	6318.4	1	998.9	69.2	5	R.LLLLESVSGLLQPR.T
*	HsH2AZ-FLAG_293_	2.8642	0.3242	1303.26	1303.464	4898.2	1	829.4	70.8	2	R.TGSAVAPVHPPNR.S
*	HsH2AZ-FLAG_293_	4.1615	0.5634	2294.25	2293.588	7597	1	1098	54.3	1	R.LHGSVGGAQNLSALGALVSLSNAR.L
*	HsH2AZ-FLAG_293_	2.8692	0.1078	941.19	941.118	4288.8	1	778.5	92.9	1	K.LASFFLSR.V
*	HsH2AZ-FLAG_293_	4.7807	0.4205	2138.3	2139.302	6881.8	1	1428.3	64.7	2	R.VDALSPQLQQLACECYSR.L
*	HsH2AZ-FLAG_293_	3.8216	0.271	1275.4	1275.491	4574.4	1	1236.8	87.5	1	R.LPSLGAGFSQGLK.H
*	HsH2AZ-FLAG_293_	2.8555	0.1851	1179.56	1179.321	7575.8	1	930.3	70	2	K.NISLHGDGPLR.L
*	HsH2AZ-FLAG_293_	3.3703	0.2726	1483.42	1483.754	3018.2	1	548.7	79.2	2	R.LLPQVLNSWSIGR.D
*	HsH2AZ-FLAG_293_	4.0638	0.3574	1528.32	1527.674	6764.2	1	990	63.3	8	R.GSPDGSLQTGKPSAPK.K
*	HsH2AZ-FLAG_293_	3.6783	0.4085	2109.53	2110.285	4611.5	1	475.2	47.5	2	R.GADTAPTLAPEALPSQGEVER.E
gi|42558250|r	4	10	13.40%	709	78366	5.2	membrane component chromosome 11 surface marker 1 isoform 1 [Homo sapiens]				
gi|42734503|r	4	10	13.70%	694	76862	5.1	membrane component chromosome 11 surface marker 1 isoform 2 [Homo sapiens]				
	HsFlag-VPS71_Ti_10	5.4964	0.3812	3704	3705.949	6633.7	1	1124.2	28	2	EAMK.Q
	HsFlag-VPS71_Ti_10	3.7015	0.2464	1456.72	1456.595	5638.3	1	1092.5	81.8	1	K.YQEVTNNLEFAK.E
	HsFlag-VPS71_Ti_10	4.4994	0.3328	2495.78	2494.801	3404	1	418.9	47.6	4	K.QGLNGVPILSEEELSLLDEFYK.L
	HsFlag-VPS71_Ti_10	3.7922	0.3854	2294.84	2296.544	9590.3	1	1179.6	52.8	3	R.LNEQYEHASIHLWDLLEGK.E
gi|24308207|r	4	7	13.40%	583	63473	8.3	leucine rich repeat containing 47 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_204	5.2652	0.4912	4159.06	4159.661	8523.5	1	1319.9	26.4	3	R.LQSLNLTGNCLDSFPAELFRPGALPLLSELAAADNCLR.E
*	HsFLAG-FLJ20729_	3.1777	0.1806	1561.45	1560.837	8740.1	2	886	57.7	1	R.VLHVSENPVPLTVR.V
*	HsFLAG-FLJ20729_	2.7799	0.2243	1340.52	1340.525	6708	1	685.9	68.2	2	K.RTAATLATHELR.A
*	HsFLAG-Lin9_Ti_205	3.1397	0.3507	1628.1	1628.878	7755.4	1	639.1	53.8	1	K.GPLLYCARPPQDLK.I
gi|19913408|r	16	36	13.30%	1621	182661	8.1	DNA topoisomerase II, beta isozyme [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	3.9805	0.1768	1462.4	1462.643	8120.4	1	1780.5	79.2	3	K.IFDEILVNAADNK.Q
*	HsFLAG-FLJ20729_	3.385	0.3389	1886.51	1887.1	7747.4	1	628.1	50	1	K.VSIDPESNIISIWNNGK.G
	HsFLAG-FLJ20729_	2.6641	0.3413	1234.61	1235.469	4339	5	421.9	70	1	K.GIPVVEHKVEK.V
*	HsFLAG-p53-DNA-D	5.6512	0.3568	2489.31	2488.753	8527.4	1	1891.8	59.5	8	K.VYVPALIFGQLLTSSNYDDDEK.K
*	HsFLAG-Lin9_Ti_203	4.0216	0.3752	2176.93	2174.294	9774.2	1	932.5	50	1	K.HFDGEDYTCITFQPDLSK.F
*	HsFLAG-Lin9_Ti_205	2.9967	0.185	1160.24	1160.402	6083.8	8	707.7	70	1	K.AGVSVKPFQVK.N
*	HsFLAG-FLJ20729_	3.567	0.2872	1761.17	1761.982	8557.9	1	1041	56.7	3	K.AASNCGIVESILNWVK.F
*	HsFLAG-p53-DNA-D	4.8623	0.3512	1530.64	1530.807	6922.6	1	1633.3	79.2	3	K.HGFLEEFITPIVK.A
*	HsFLAG-FLJ20729_	4.8096	0.4538	1833	1832.112	10496.5	1	1252.4	60	2	R.RLHGLPEQFLYGTATK.H
*	HsFLAG-FLJ20729_	2.5229	0.1398	1675.1	1675.925	4644.9	1	397.3	50	1	R.LHGLPEQFLYGTATK.H
*	HsFLAG-Lin9_Ti_204	2.7382	0.1771	1264.85	1265.411	6432.9	1	659.6	72.2	1	K.HLTYNDFINK.E
*	HsFLAG-p53-DNA-D	3.105	0.3473	1501.44	1501.726	4375.4	2	378	57.7	2	R.SIPSLVDGFKPGQR.K
*	HsFLAG-p53-DNA-D	3.773	0.2148	1109.02	1109.271	6445.4	1	1425	90	5	K.LAQAEAAGLHK.V
*	HsFLAG-p53-DNA-D	3.1166	0.315	1982.57	1981.172	7037.8	1	578.7	50	1	K.KSQDFGNLFSFPSYSQK.S

*	HsFLAG-FLJ20729_	3.8123	0.3829	1852.71	1852.998	7395.9	1	708.4	53.3	2	K.SQDFGNLFSFPSYSQK.S
*	HsFLAG-Lin9_Ti_20	3.8954	0.1256	2939.52	2939.161	9149.9	5	784.9	27	1	K.KTSFDQDSDVDIFPSDFPTEPPSLPR.T
gi|40807485|r	10	18	13.30%	941	106925	8.3	U5 snRNP-associated 102 kDa protein [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.9817	0.4477	1591.53	1591.68	3162.8	1	464.8	69.2	4	K.HLQTGENHTSVDPR.Q
*	HsFlag-DPCD_Ti_20	4.5338	0.4349	1746.33	1746.912	7189	1	1291.9	65.6	1	R.LSQVSDSVSGQTVVDPK.G
*	HsFlag-ZnF-HIT2_Ti_	3.0227	0.3073	1123.55	1122.269	4137.7	1	555.7	77.8	1	K.ALEHVPNSVR.L
*	HsFLAG-Lin9_Ti_20	3.3061	0.4114	1977.47	1976.212	8326.1	1	569.8	46.9	1	R.AVECCPTSVELWLALAR.L
*	HsFlag-ZnF-HIT2_Ti_	2.6143	0.0976	1071.89	1072.166	5207.4	1	599	81.2	1	K.ARENIPTDR.H
	HsFLAG-Lin9_Ti_20	3.565	0.2948	1599.41	1599.913	9168	1	1175.8	61.5	2	R.AIYAYALQVFPSKK.S
	HsFlag-ZnF-HIT2_Ti_	3.0571	0.1797	1150.29	1150.28	6214.9	2	919.8	83.3	1	K.AREAYNQGLK.K
	HsARP6-FLAG_Ti_1	3.6791	0.3541	1171.23	1171.341	7113.9	1	1479.4	94.4	4	K.NPGLWLESVR.L
	HsSrcap_Ti_202.386	3.5181	0.3417	1648.26	1648.812	10176.3	2	920.5	57.7	2	K.IDSDLGDAWAFFYK.F
	HsFlag-ZnF-HIT2_Ti_	3.5196	0.2513	1187.28	1187.307	7173.9	1	1400.9	88.9	1	R.HGELWCAVSK.D
gi|4758860|re	11	85	13.30%	699	73720	9.5	nucleolar and coiled-body phosphoprotein 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.8651	0.4637	1844.45	1845.238	4225.6	1	769.1	66.7	11	R.RVVPSDLYPLVLGFLR.D
*	HsFLAG-Lin9_Ti_20	3.4007	0.4776	1688.52	1689.051	3147.3	1	476.3	67.9	14	R.VVPSDLYPLVLGFLR.D
*	HsFLAG-Lin9_Ti_20	3.9874	0.3468	1688.94	1689.051	6240.7	1	1108.5	46.4	3	R.VVPSDLYPLVLGFLR.D
*	HsVPS71-FLAG_Ti_	3.0778	0.1649	1118.97	1118.189	6636.1	2	806.5	77.8	3	R.DNQLSEVANK.F
*	HsFLAG-ARP6_Ti_1	6.184	0.4492	2502.23	2501.755	9030.3	1	2299.4	59.1	40	K.ATGATQQDANASSLLDIYSFWLK.S
*	HsFlag-DPCD_Ti_20	1.9876	0.098	1025.47	1026.224	5491	1	428.5	66.7	1	R.KLQANGPVAK.K
*	HsFlag-DPCD_Ti_20	2.5952	0.1175	1025.96	1026.224	7821.6	4	760.1	72.2	1	R.KLQANGPVAK.K
*	HsFLAG-p53-DNA-D	2.1379	0.1437	1036.64	1037.247	4644.9	9	428.7	60	5	K.SPAVKPAAAPK.Q
*	HsFlag-DPCD_Ti_20	3.0715	0.2046	1037.29	1037.247	6216.7	8	976.1	80	3	K.SPAVKPAAAPK.Q
*	HsFLAG-p53-DNA-D	2.7928	0.1491	1212.49	1212.392	5106.1	8	628.9	65.4	2	K.VAGGAAPSKPASAK.K
*	HsFLAG-p53-DNA-D	2.4384	0.3294	966.31	967.023	7857.7	1	726.7	75	2	R.VADNSFDAK.R
gi|4758140|re	3	6	13.30%	472	53216	8.7	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6 [Homo sapiens]				
*	HsFLAG-FLJ20729_	4.2051	0.2296	2366.7	2367.642	10094.8	4	987.9	29.3	1	R.GPVKPTGGPGGGGTQTQQQMNQLK.N
*	HsFLAG-Lin9_Ti_20	3.2994	0.2376	2218.46	2217.669	8206.6	1	881	50	1	K.LLSQDFVQIMEDIILTLPK.N
*	HsFLAG-FLJ20729_	5.4062	0.3618	2320.18	2321.684	11052.6	1	2478.2	63.2	4	R.FGHLGLAINLITYDDRFNLK.S
gi|56237027|r	5	8	13.20%	577	63481	9.2	insulin-like growth factor 2 mRNA binding protein 1 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.6698	0.3298	1876.13	1877.101	7266.6	1	1466.6	71.9	2	K.LYIGNLNESVTPADLEK.V
*	HsFLAG-p53-DNA-D	3.3702	0.2837	1472.34	1472.811	4125.6	1	620	69.2	2	R.LLVPTQYVGAIIGK.E
*	HsFLAG-p53-DNA-D	3.3998	0.3254	1692.24	1691.768	6286.7	2	561.6	53.3	2	K.AISVHSTPEGCSSACK.M
*	HsFLAG-p53-DNA-D	2.8913	0.2637	1865.64	1864.106	9978.3	3	610.1	46.7	1	K.ITISSLQDLTLYNPER.T
*	HsFLAG-ARP6_Ti_1	3.3671	0.1713	1500.73	1501.59	3865.7	1	691.1	75	1	R.DQTPDENDQVIVK.I
gi|4557493|re	4	15	13.20%	577	60959	6.8	cleavage stimulation factor subunit 2 [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.1486	0.4401	1923.83	1925.145	4061.6	1	467.9	56.2	7	R.SVFVGNIPYEATEEQLK.D
*	HsFlag-VPS71_Ti_1	4.3527	0.2865	1453.1	1452.65	5353.7	1	1243.4	79.2	5	K.DIFSEVGPVVSFR.L
	HsFLAG-p53-DNA-D	3.2359	0.2699	2129.84	2127.256	7974.2	1	882.3	50	1	K.GYGFCEYQDQETALSAMR.N
*	HsFlag-VPS71_Ti_1	4.31	0.3491	2832.99	2833.075	7363.7	1	557.4	31.5	2	K.SLGTGAPVIESPYGETISPEDAPESISK.A
gi|4503513|re	3	4	13.20%	325	36502	5.6	eukaryotic translation initiation factor 3, subunit 2 beta, 36kDa [Homo sapiens]				
*	HsFlag-FLJ90652_2	2.7573	0.2517	1317.26	1317.367	5281.3	2	730.4	72.7	1	K.HVLTGSADNSCR.L
*	HsFLAG-p53-DNA-D	4.1694	0.4099	1680.01	1680.863	8116.1	1	1318.6	66.7	2	K.GHFGPINSVAFHPDGK.S

*	HsFLAG-Lin9_Ti_20	3.1779	0.3139	1983.63	1983.143	7677.5	1	766.8	57.1	1	R.IHYFDPQYFEFEFEA.-
gi|NTAP-BHD	11	95	13.10%	651	72628	6.2	N-terminal TAP-tagged BHD Mutant [Homo sapiens]				
gi|NTAP-BHD	11	95	11.10%	768	85705	6.4	N-terminal TAP-tagged BHD WT [Homo sapiens]				
	HsSrcap_Ti_202.368	4.3431	0.2429	2382.86	2382.61	6572.8	1	956.2	55.3	13	K.DQQSAFYEILNMPNLNEAQR.N
	HsScrap_Ti_102.366	6.3388	0.3791	2384.55	2382.61	5229	1	1447.2	47.4	8	K.DQQSAFYEILNMPNLNEAQR.N
	HsScrap_Ti_102.185	2.7054	0.1778	908.26	907.057	3615.2	8	763.3	92.9	2	R.NGFIQSLK.D
	HsScrap_Ti_103.247	5.2468	0.2521	2347.83	2349.56	7562.3	1	1687.4	41.7	15	R.NGFIQSLKDDPSQSTNVLGEAK.K
	HsSrcap_Ti_202.220	5.1087	0.3311	2348.56	2349.56	4724.8	1	914.2	57.1	8	R.NGFIQSLKDDPSQSTNVLGEAK.K
	HsScrap_Ti_102.167	3.9226	0.2787	1461.51	1461.525	4346.8	1	912.3	76.9	3	K.DDPSQSTNVLGEAK.K
	HsScrap_Ti_102.362	4.0728	0.2988	2480.5	2481.699	4673.1	1	521.5	50	11	K.EQQNAFYEILNMPNLNEEQR.N
	HsSrcap_Ti_203.237	5.0704	0.3913	2362.75	2363.587	4433.1	3	505.7	47.6	16	R.NGFIQSLKDDPSQSANLLSEAK.K
	HsScrap_Ti_104.246	5.6128	0.3933	2363.48	2363.587	6885.7	1	1475.4	41.7	16	R.NGFIQSLKDDPSQSANLLSEAK.K
	HsSrcap_Ti_203.215	5.381	0.2702	2492.09	2491.761	8946.3	1	1419.6	35.2	1	R.NGFIQSLKDDPSQSANLLSEAKK.L
	HsScrap_Ti_102.182	2.8932	0.1625	1477.91	1475.552	7373.3	1	1128.3	73.1	2	K.DDPSQSANLLSEAK.K
gi|14249500|r	1	2	13.10%	260	29157	6.9	transforming growth factor beta regulator 1 [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	3.924	0.3051	3666.3	3666.903	4210.7	1	385.8	22.7	2	K.DGGVQPQFEIVPEDDPQNAIVSSSADACHAELLR.T
gi|47271443|r	3	15	13.10%	221	25476	11.9	splicing factor, arginine/serine-rich 2 [Homo sapiens]				
*	HsFLAG-FLJ20729_	3.0934	0.2926	1909.6	1909.053	7729.5	4	729.6	50	1	K.RDAEDAMDAMDGAVLDGR.E
*	HsFLAG-p53-DNA-D	5.3012	0.3851	1753.24	1752.865	9310.6	1	2028.3	68.8	4	R.DAEDAMDAMDGAVLDGR.E
*	HsFLAG-ARP5_Ti_1	3.1604	0.2464	1309.53	1309.387	4568.6	1	584	70	10	R.YGRPPDSHHSR.R
gi|13904866|r	3	8	13.10%	137	15747	12	ribosomal protein L28 [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	1.9584	0.1619	872.54	873.002	4124.9	9	244.9	83.3	1	R.YNGLIHR.K
*	HsFLAG-ARP6_Ti_1	3.032	0.2917	873.81	873.002	5590	2	733.8	91.7	2	R.YNGLIHR.K
*	HsFLAG-ARP6_Ti_1	2.4184	0.1679	1043.38	1044.15	4775.2	1	609.4	70	5	K.TVGVEPAADGK.G
gi|4505257|re	6	11	13.00%	577	67820	6.4	moesin [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.5815	0.3698	2082.51	2083.259	6009.5	1	804.4	59.4	1	K.FYPEDVSEELIQDITQR.L
*	HsFlag-VPS71_Ti_1	3.7341	0.3523	2868.55	2868.176	3637.9	1	495.1	44	2	K.EGILNDDIYCPPETAVLLASYAVQSK.Y
	HsFLAG-p53-DNA-D	2.5927	0.1817	1105.13	1105.282	3983.4	2	598.4	87.5	1	K.IGFPWSEIR.N
	HsFLAG-p53-DNA-D	3.082	0.2462	1310.92	1311.526	4859.6	1	673.5	75	2	K.KAPDFVFYAPR.L
	HsFlag-VPS71_Ti_1	4.0952	0.4189	1184.54	1183.352	5649.2	1	979.7	83.3	2	K.APDFVFYAPR.L
	HsFlag-VPS71_Ti_1	3.4434	0.2393	1473.57	1473.731	4190	1	702.4	81.8	3	R.RKPDTIEVQQMK.A
gi|4557809|re	5	13	13.00%	439	48535	7	ornithine aminotransferase precursor [Homo sapiens]				
*	Hs293Flag-Ies2_Ti_1	3.8204	0.2535	1956.4	1954.143	5945.2	1	699.8	60	3	R.AFYNNVLGEYEEYITK.L
*	HsFLAG-KIAA0515_	3.4431	0.2104	1238.41	1238.434	6204	1	1387.8	90	1	K.IVFAAGNFWGR.T
*	HsFLAG-TCF3_Ti_1	5.4684	0.4567	2142.27	2142.368	12061.5	1	2744.9	63.2	7	R.VAIAALEVLEEENLAENADK.L
*	HsFLAG-KIAA0515_	1.8843	0.1341	1056.45	1057.235	4284.5	8	247.3	61.1	1	K.LPSDVVTAVR.G
*	HsFLAG-KIAA0515_	3.2529	0.2732	1057.52	1057.235	4965.6	2	1041.2	88.9	1	K.LPSDVVTAVR.G
gi|23238211|r	2	2	13.00%	300	34333	7.3	actin related protein 2/3 complex subunit 2 [Homo sapiens]				
gi|5031599|re	2	2	13.00%	300	34333	7.3	actin related protein 2/3 complex subunit 2 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	4.2315	0.3375	3249.05	3246.644	8090.3	1	1213.1	30.4	1	K.RVYGSFLVNPESGYNVSLLYDLENLPASK.D
	HsFLAG-ARP6_Ti_1	2.5474	0.1901	1217.27	1217.29	5897.8	1	662.2	72.2	1	R.DDETMYVESK.K
gi|5031931|re	2	7	13.00%	215	23384	4.6	nascent-polypeptide-associated complex alpha polypeptide [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.3592	0.2101	1551.64	1550.882	6937.8	1	1249.4	75	6	K.NILFVITKPDVYK.S

*	HsFLAG-FLJ20729_	4.7271	0.2213	1614.55	1615.781	9896.9	2	2393.6	78.6	1	K.IEDLSQQAQLAAAEK.F
gi|7706499|re	1	2	13.00%	108	12320	7.8	DNA directed RNA polymerase III polypeptide K [Homo sapiens]				
*	HsSrcap_Ti_205.181	4.2586	0.4263	1753.59	1753.887	4974.9	1	835	73.1	2	R.FACNTCPYVHNITR.K
gi|4885399|re	11	27	12.90%	1217	141541	7.2	chondroitin sulfate proteoglycan 6 (bamacan) [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	2.0702	0.2147	794.68	794.932	5149.3	2	537.9	83.3	1	K.HNVIVGR.N
*	HsFLAG-ARP6_Ti_1	3.1646	0.274	1164.31	1164.35	4976.6	1	787.6	75	3	R.LALLHEGTGPR.V
*	HsARP6-FLAG_Ti_1	3.8063	0.3542	1553.34	1553.73	10954	1	1330	65.4	2	K.NDVMNLLESAGFSR.S
*	HsFlag-DPCD_Ti_20	3.7853	0.3442	1857.69	1858.015	7505.8	1	1006.7	64.3	1	R.ALEYTIYNQELNETR.A
*	HsFLAG-FLJ20729_	3.9217	0.4006	1760.27	1760.96	8004.6	1	997.2	63.3	3	R.SLQSLEASLHAMESTR.E
*	HsFLAG-FLJ20729_	5.7336	0.4593	1860.4	1861.056	7445.3	1	1980.5	75	8	K.AELGTDLLSQLSLEDQK.R
*	HsFlag-VPS71_Ti_1	3.6769	0.2906	2064.89	2065.239	8466.3	1	621.1	42.1	2	R.ETEGGTVLTATTSELEAINK.R
*	HsFlag-VPS71_Ti_1	3.713	0.2668	1619.55	1617.842	8351.5	1	806.5	57.7	2	K.IRELGSLPQEAFEK.Y
*	HsFLAG-Lin9_Ti_20	3.6988	0.3818	1966.42	1966.115	3926	1	359.2	50	2	R.GSGSQSSVPSVDQFTGVGIR.V
*	HsARP6-FLAG_Ti_1	3.2402	0.2558	1387.93	1387.749	8489.5	1	1155.8	66.7	1	K.SLVALALIFAIQK.C
*	HsFLAG-ARP6_Ti_1	2.2757	0.2002	1135.22	1136.117	6053.2	4	454.8	61.1	2	K.DFVEDDTTHG.-
gi|4758410|re	6	18	12.90%	673	74128	6.1	fragile X mental retardation syndrome related protein 2 [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	3.4906	0.313	1320.42	1320.578	7604.2	1	1124.5	72.7	6	R.LRPVNPNPLATK.G
	HsFLAG-ARP6_Ti_1	4.8261	0.3789	1996.31	1996.249	5795.8	1	945.8	58.3	3	R.EDLMGLAIGTHGANIQQAR.K
*	HsFLAG-ARP6_Ti_1	4.9606	0.4353	1879.36	1880.071	6191.9	1	1232.5	68.8	4	K.VPGVTAIELGEETCTFR.I
*	HsFLAG-ARP6_Ti_1	3.1526	0.3306	1656.28	1656.789	4783.8	1	818.4	73.1	2	R.SYLEFSEDSVQVPR.N
	HsFLAG-FLJ20309_	2.4912	0.0894	944.53	944.116	6753.9	7	655	71.4	1	K.VIQEIVDK.S
*	HsFLAG-ARP6_Ti_1	4.767	0.5311	1756.51	1756.78	8282.4	1	1279.1	59.4	2	K.AGYSTDESSSSSLHATR.T
gi|4503607|re	2	3	12.90%	333	35080	8.4	electron transfer flavoprotein, alpha polypeptide [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.8034	0.2288	2352.15	2352.841	6949.8	1	1213.8	50	1	K.IVAPELYIAVGISGAIQHLAGMK.D
*	HsFLAG-ARP6_Ti_1	3.988	0.3608	2209.92	2209.503	8357.4	1	905.3	47.4	2	K.DPEAPIFQVADYGIVADLFK.V
gi|5454052|re	2	3	12.90%	248	27774	4.7	stratifin [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.0381	0.3033	2441.1	2440.763	6228	1	857.4	33.3	1	K.VETELQGVCDTVLGLLDSHLIK.E
	HsFLAG-FLJ20729_	3.7624	0.1371	1189.5	1190.444	6163.6	5	1616.1	88.9	2	K.DSTLIMQLLR.D
gi|11321591|r	3	6	12.90%	209	24034	7.8	high-mobility group box 2 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.7878	0.3699	1553.62	1553.756	4959.5	1	762.2	67.9	3	K.IKSEHPGLSIGDTAK.K
*	HsFLAG-Lin9_Ti_20	3.5049	0.3665	1312.32	1312.422	4348.1	1	715.5	75	1	K.SEHPGLSIGDTAK.K
*	HsFLAG-p53-DNA-D	3.6653	0.3346	1394.37	1394.585	7357.2	1	1304.4	77.3	2	K.KLGEMWSEQSAK.D
gi|24432106|r	8	22	12.80%	923	102902	5.2	p30 DBC protein [Homo sapiens]				
gi|40548408|r	8	22	12.80%	923	102902	5.2	p30 DBC protein [Homo sapiens]				
	HsFLAG-FLJ20729_	4.2135	0.4765	1499.51	1499.797	4189.3	1	860.1	78.6	7	K.SPAPPLLHVAALGQK.Q
	HsYL1_Ti_101.1814.	4.9035	0.4677	2165.02	2164.244	4871.6	1	1556.6	71.4	2	K.EAAPDAGAEPITADSDPAYSSK.V
	HsYL1_Ti_102.2591.	2.5197	0.1255	1589.92	1589.872	4617.7	1	484.5	61.5	1	K.VLLLSSPGLEELYR.C
	HsFLAG-FLJ20729_	3.2922	0.4352	1610.04	1610.694	5217.9	1	503.5	64.3	2	R.CAQAQTGIDLSGCTK.W
	HsFLAG-UTX1_Ti_2	3.7896	0.3791	1550.62	1550.757	4657.2	1	937	75	6	R.FAEFQYLQPGPPR.R
	HsYL1_Ti_102.3568.	3.9246	0.3942	2605.13	2605.948	4489.8	1	519.4	43.8	2	R.QEGLDGGLPEEVLFGNLDLLPPPGK.S
	HsFLAG-FLJ20729_	3.5073	0.2648	2606.25	2605.948	7435.3	6	600.9	27.1	1	R.QEGLDGGLPEEVLFGNLDLLPPPGK.S
	HsYL1_Ti_101.1751.	3.046	0.2123	1560.17	1559.629	4590.5	1	666.8	61.5	1	K.ADSWVEKEEPAPSN.-
gi|11225260|r	7	21	12.80%	765	90726	9.3	DNA topoisomerase I [Homo sapiens]				

*	HsFLAG-p53-DNA-D	3.4593	0.2418	1318.4	1318.467	7134.3	1	1356.9	90	1	R.KLEEEEDGKLK.K
*	HsFLAG-p53-DNA-D	3.3553	0.26	1755.63	1755.023	4133.4	1	683.2	66.7	6	K.GPVFAPPYEPLPENVK.F
*	HsFLAG-p53-DNA-D	4.607	0.1481	2831.56	2829.138	9953.5	1	1560.6	34.8	1	R.VEHINLHPELDGQEYVVEFDFLGK.D
*	HsFlag-VPS71_Ti_1	3.9785	0.2856	1356.96	1356.58	5593.8	1	1143.2	81.8	3	K.HLQDLMEGLTAK.V
*	HsFLAG-Lin9_Ti_20	3.6993	0.3266	1508.51	1508.715	7117.3	1	1006.5	70.8	1	R.TYNASITLQQQLK.E
*	HsFLAG-Lin9_Ti_20	3.6144	0.3025	1181.54	1182.334	6800.5	1	1354.7	88.9	7	R.AVAILCNHQR.A
*	HsFLAG-p53-DNA-D	3.5534	0.1797	1432.28	1432.53	7327.7	3	853.3	72.7	2	K.LEVQATDREENK.Q
gi|7662645|re	1	2	12.80%	258	29396	9.4	mitochondrial ribosomal protein S18B [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	4.9038	0.357	3663.77	3665.012	5470.6	1	541.9	25.8	2	R.DLDFSTSHGAVSATPPAPTLVSGDPWYPWYNWK.Q
gi|4506903|re	2	3	12.70%	221	25542	8.6	splicing factor, arginine/serine-rich 9 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.2952	0.4021	1683.57	1683.945	2902.6	2	368.5	63.3	1	R.VLVSGLPPSGSWQDLK.D
*	HsFlag-NUFIP_Ti_1	2.9403	0.2444	1455.36	1455.615	6035.7	1	812.8	72.7	2	R.GSPHYFSPFRPY.-
gi|19923217|r	23	56	12.60%	3256	358747	9.4	antigen identified by monoclonal antibody Ki-67 [Homo sapiens]				
*	HsYL1_Ti_101.1210.	2.9658	0.1927	1090.38	1090.175	4521.3	2	1023.2	77.8	2	R.DVESVQTPSK.A
*	HsFLAG-ARP6_Ti_2	3.5275	0.3165	1632.45	1633.758	6615.4	1	894.2	69.2	4	K.TPVQYSQQQNSPQK.H
*	HsFLAG-FLJ20729_	3.7808	0.2431	2159.8	2160.343	8498.1	5	847.8	31.2	1	R.TPAKVEDAADSATKPENLSSK.T
*	HsYL1_Ti_102.3015.	3.5812	0.2457	3681.24	3681.029	5219.1	4	365.2	22.9	1	K.LGTTAGQMCSGLPGLSSVDINNFGDSINESEGIPLK.R
*	HsFlag-DPCD_Ti_20	3.7879	0.1938	1420.15	1420.652	5446.5	1	708	65.4	9	K.AQSLVISPPAPSPR.K
*	HsFLAG-FLJ20729_	5.0021	0.4042	2664.91	2665.975	10393	1	1273.5	32.3	2	K.KPVGEVHSQFSTGHANSPCTIIIGK.A
*	HsFLAG-FLJ20309_	3.9919	0.3157	1666.27	1665.801	8430.6	1	1505.7	73.1	3	K.SEETNTEIVECILK.R
*	HsFLAG-FLJ20309_	3.2404	0.1184	1353.14	1353.478	8088.8	9	706.4	63.6	2	R.GQNLLQTQDHAK.A
	HsFLAG-UTX1_Ti_2	4.246	0.4207	1764.02	1763.942	5102.3	1	991.6	66.7	6	R.TPKEEAQSLEDLAGFK.E
*	HsFlag-VPS71_Ti_1	2.6802	0.1899	1316.37	1315.527	5072.2	2	570.1	70.8	1	K.AMLTPKPAGGDEK.D
*	HsFLAG-p53-DNA-D	4.1285	0.3245	2973.74	2972.324	7598.5	1	711.4	27.8	1	K.AQALEDLAGFKELFQTPGHTEELVAAGK.T
*	HsFLAG-UTX1_Ti_2	3.4576	0.3892	1828.04	1828.032	3310.8	1	419.6	59.4	2	K.ELFQTPGHTEELVAAGK.T
*	HsFLAG-Lin9_Ti_20	4.4054	0.3397	1945.69	1946.041	6898.2	1	1043.9	58.8	1	K.IPCDSPQSDPVDTPTSTK.Q
*	HsFLAG-Lin9_Ti_20	3.901	0.3992	1785.42	1785.951	4586.1	1	687.2	62.5	4	K.ELFQTPGHTEEAVAAGK.T
*	HsFlag-DPCD_Ti_20	3.3972	0.3806	1798.69	1799.932	6032.2	1	591.1	53.1	2	R.SQPDPVDTPTSSKPQSK.R
*	HsFLAG-p53-DNA-D	3.8382	0.332	2098.6	2099.175	10253.5	1	995.4	50	3	K.LTQTSGETTHTHTEPTGDGK.S
*	HsFlag-VPS71_Ti_1	4.4211	0.4381	2347.59	2346.599	7295.6	1	1038.9	52.5	2	K.SEVPEDLAGFIELFQTPSHTK.E
*	HsFLAG-UTX1_Ti_2	2.9756	0.2722	1897.3	1897.092	7006.9	4	470.2	44.1	3	R.ASQPDLVDTPTSSKPQPK.R
*	HsFLAG-BC014022_	3.1056	0.2983	1395.16	1395.617	6301.2	1	718	66.7	1	K.AMHTPKPAVGEEK.D
*	HsFlag-DPCD_Ti_20	2.9315	0.2745	1268.11	1268.372	5240.7	4	707.7	72.7	1	K.LDQPGNLPGSNR.R
*	HsYL1_Ti_105.1662.	3.2944	0.4554	1925.15	1925.192	5127.1	1	606.9	55.9	2	R.SPQPDPVGTPTIFKPQSK.R
*	HsFlag-DPCD_Ti_20	3.403	0.2715	1945.82	1945.14	5223	1	534.6	50	1	K.IPCESPPLEVVDTTASTK.R
*	HsFLAG-Lin9_Ti_20	4.5761	0.3445	3758.12	3760.019	10225.4	1	905.5	22.1	2	K.AQPLEDLASFQELSQTPGHTEELANGAADSFTSAPK.Q
gi|4503337|re	5	22	12.60%	514	57674	9.4	dyskerin [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	3.9701	0.2446	2469	2468.775	6702.9	1	581.4	45.2	1	R.TGFINLDKPSNPSSHEVVAWIR.R
*	HsFLAG-ARP6_Ti_1	2.9046	0.2578	1579.61	1579.756	10413.2	2	672.9	53.8	1	K.PSNPSSHEVVAWIR.R
*	HsFLAG-Lin9_Ti_20	3.7466	0.1229	1396.33	1396.546	7255.8	1	1244.5	75	6	R.LHNAIEGGTQLSR.A
*	HsFlag-NUFIP_Ti_11	5.5776	0.4127	2109.35	2110.548	6564.7	1	1121.7	57.9	10	R.ALETLTGALFQRPPLIAAVK.R
*	HsFlag-VPS71_Ti_1	2.7651	0.3213	983.52	984.14	7434.2	1	844.3	72.2	4	K.APQVVAEAAK.T
gi|55741709|r	6	15	12.50%	843	100186	6.3	RNA binding motif protein 25 [Homo sapiens]				

*	HsFlag-VPS71_Ti_1	3.6605	0.3787	2076.76	2076.279	7962.2	1	547.3	46.9	2	K.LQAFGFCEYKEPESTLR.A
*	HsFlag-VPS71_Ti_1	2.6884	0.1083	1165.65	1166.363	5916.1	7	638.2	66.7	1	R.LLHDLQIGEK.K
*	HsFLAG-Lin9_Ti_20	3.4653	0.314	2032.55	2034.06	5734.4	1	441	47.1	3	R.EYSSELNAPSQESDSHPR.K
*	HsFlag-VPS71_Ti_1	3.3072	0.2638	1356.43	1356.478	5036.6	1	559.1	61.5	4	K.LGASNSPGQPNSVK.R
*	HsFLAG-p53-DNA-D	5.1448	0.4694	2451.73	2452.637	8096.2	1	1189.2	55	1	K.KLPVDSVFNKFEDEDSDDVPR.K
*	HsFlag-VPS71_Ti_1	4.4809	0.2976	2909.37	2906.41	7395.1	1	1120.7	33.3	4	K.IPTAKPELFAYPLDWSIVDSILMER.R
gi|5031957|re	1	3	12.50%	265	30472	6.3	polyglutamine binding protein 1 isoform 1 [Homo sapiens]				
gi|74027259|r	1	3	22.10%	149	17183	5.5	polyglutamine binding protein 1 isoform 2 [Homo sapiens]				
gi|74027257|r	1	3	12.50%	265	30472	6.3	polyglutamine binding protein 1 isoform 1 [Homo sapiens]				
gi|74027255|r	1	3	12.50%	265	30472	6.3	polyglutamine binding protein 1 isoform 1 [Homo sapiens]				
gi|74027253|r	1	3	12.50%	265	30472	6.3	polyglutamine binding protein 1 isoform 1 [Homo sapiens]				
gi|74027247|r	1	3	12.50%	265	30472	6.3	polyglutamine binding protein 1 isoform 1 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	4.3117	0.397	3782.01	3782.123	4239.3	1	479.9	25	3	K.VFDPSCGLPYYWNADTDLVSWLSPHDPNSVVTK.S
gi|5453555|re	2	5	12.50%	216	24423	7.5	ras-related nuclear protein [Homo sapiens]				
*	HsFLAG-FLJ20729_	2.7472	0.082	1516.42	1516.71	5103.3	7	536.8	62.5	1	R.VCENIPIVLCGNK.V
*	HsFLAG-p53-DNA-D	3.6988	0.3978	1785.53	1786.043	4801.9	1	599.4	61.5	4	K.SNYNFEKPFLWLAR.K
gi|18702323|r	1	2	12.50%	96	10855	7.5	dynein, cytoplasmic, light polypeptide 2B [Homo sapiens]				
gi|7661822|re	1	2	12.50%	96	10922	7.2	Roadblock-1 [Homo sapiens]				
gi|29570775|r	1	2	19.00%	63	7342	7.3	cytoplasmic dynein light chain 2A isoform b [Homo sapiens]				
	HsARP6-FLAG_Ti_1	3.7978	0.3437	1447.38	1447.588	5986.7	1	969.6	81.8	2	R.DIDPQNDLTFLR.I
gi|11321601|r	6	14	12.40%	784	85596	7.6	phosphofructokinase, platelet [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.7781	0.2675	1822.05	1821.123	7523.2	1	810.2	60.7	1	R.LPLMECVQMTQDVQK.A
*	HsFLAG-FLJ20729_	3.9618	0.4113	2120.44	2120.326	9280.5	1	821.6	45	2	K.EIGWTDVGGWTGQGGSILGTK.R
*	HsFLAG-ARP6_Ti_1	3.0837	0.1155	1255.04	1254.444	6935.5	1	1535.8	88.9	1	K.YLEEIATQMR.T
*	HsFLAG-ARP6_Ti_1	5.3953	0.4058	2677.21	2678.745	8130.8	1	1119	47.6	1	R.NESCSENYTTDFIYQLYSEEGK.G
*	HsFLAG-ARP6_Ti_1	4.7619	0.4345	1812.42	1812.013	8706.6	1	1546	68.8	5	K.NVLGHMQQGGAPSPFDR.N
*	HsFLAG-Lin9_Ti_20	3.9006	0.2864	1413.96	1414.691	5869.5	1	841	72.7	4	K.RNVIFQPVAELK.K
gi|13654270|r	4	7	12.40%	734	83065	4.7	LAS1-like [Homo sapiens]				
*	HsH2AZ-FLAG_293_	2.7013	0.3055	1955.94	1957.185	9728.2	1	697.8	50	1	R.ELLVSYEEEQFTVLEK.F
*	HsFLAG-Lin9_Ti_20	3.8275	0.3536	1614.53	1614.801	8692.4	1	1491.1	73.1	3	R.GLHSQNFTQALLER.M
*	HsH2AZ-FLAG_293_	4.322	0.3785	2607.79	2608.864	6608.8	1	1189.5	35.9	2	K.SPYTLDSLYWSVKPASSSFGSEAK.A
*	HsH2AZ-FLAG_293_	4.2068	0.3121	3857.65	3857.071	7984.2	1	994.8	24.3	1	K.TDTLGLSCGVGSGNCSNSSSSNFEGLLWSQGQLHGLK.T
gi|38195084|r	3	7	12.40%	347	39899	5.7	HMT1 hnRNP methyltransferase-like 2 isoform 2 [Homo sapiens]				
gi|38195089|r	3	7	11.90%	361	41486	5.5	HMT1 hnRNP methyltransferase-like 2 isoform 1 [Homo sapiens]				
gi|38195087|r	3	7	12.50%	343	39572	5.7	HMT1 hnRNP methyltransferase-like 2 isoform 3 [Homo sapiens]				
	HsFLAG-p53-DNA-D	2.7019	0.195	1402.84	1400.62	6116.5	8	426	59.1	1	K.WLAPDGLIFPDR.A
	HsFLAG-TCF3_Ti_1	2.9158	0.3156	1725.53	1725.855	4082	1	321.8	50	2	R.TGFSTSPESPYTHWK.Q
	HsFLAG-ARP6_Ti_1	3.5727	0.3344	1721.25	1721.969	6598.3	1	906.6	60	4	K.TGEEIFGTIGMRPNAK.N
gi|14141157|r	2	7	12.40%	346	36926	6.9	heterogeneous nuclear ribonucleoprotein H3 isoform a [Homo sapiens]				
gi|14141159|r	2	7	13.00%	331	35239	6.9	heterogeneous nuclear ribonucleoprotein H3 isoform b [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.6244	0.4565	1919.66	1920.132	8182.3	1	1280.7	62.5	6	R.ATENDIANFFSPLNPIR.V
	HsFLAG-p53-DNA-D	5.4823	0.4491	2522.46	2523.797	6810.8	1	1315.9	54	1	R.YIELFLNSTPGGGSGMGGSGMGGYGR.D
gi|8923444|re	1	4	12.40%	153	17201	8.2	nucleolar protein family A, member 2 isoform a [Homo sapiens]				

*	HsFLAG-p53-DNA-D	5.4911	0.4021	2156.77	2156.447	10017.4	1	1863.1	61.1	4	R.TYQELLVNQNPIAQPLASR.R
gi|51479152|r	1	2	12.40%	137	15773	7.2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d isoform b [Homo sapiens]				
gi|5453559|re	1	2	10.60%	161	18491	5.3	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d isoform a [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	2.6956	0.2604	1931.61	1933.214	3938	1	625.6	62.5	2	R.LAALPENPPAIDWAYYK.A
gi|50592994|r	2	6	12.40%	105	11737	4.9	thioredoxin [Homo sapiens]				
*	HsTIP60_Ti_103.196	3.1076	0.3549	1336.53	1337.429	10489.5	1	1192.9	62.5	2	K.TAFQEALDAAGDK.L
*	HsFLAG-RPB5MP_2	3.9899	0.2844	1337.06	1337.429	6833.5	1	1977.6	83.3	4	K.TAFQEALDAAGDK.L
gi|48762920|r	5	10	12.30%	780	85018	7.5	liver phosphofructokinase isoform b [Homo sapiens]				
gi|50346005|r	5	10	11.60%	827	90203	7.8	liver phosphofructokinase isoform a [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.8002	0.2464	3103.5	3104.459	10889.2	1	1062.1	27.6	1	R.AAAYNLVQHGITNLCVIGGDGSLTGANIFR.S
	HsFLAG-ARP6_Ti_1	4.6352	0.0801	1914.8	1915.172	7827.4	1	996.2	56.2	1	R.IMEVIDAITTTAQSHQR.T
	HsFLAG-ARP6_Ti_1	3.1065	0.2496	1008.67	1009.197	4599.2	1	1146.6	93.8	2	R.VTVLGHVQR.G
	HsFLAG-ARP6_Ti_1	4.3465	0.4415	2145.32	2145.485	5533.2	1	1207.5	57.1	1	K.SNFSLAILNVGAPAAGMNAAVR.S
	HsFLAG-ARP6_Ti_1	5.4219	0.3913	1908.42	1909.112	9832.4	1	2147.3	67.6	5	R.TNVLGHLQQGGAPTPFDR.N
gi|13236583|r	3	4	12.30%	316	36072	5.9	BRCA1/BRCA2-containing complex subunit 36 isoform 1 [Homo sapiens]				
gi|64762484|r	3	4	13.40%	291	33150	6	BRCA1/BRCA2-containing complex subunit 36 isoform 2 [Homo sapiens]				
	HsScrap_Ti_103.204	3.7511	0.3638	1588.4	1586.794	7656.7	1	1317.4	75	2	R.VLYTCFQSIQAQK.S
	HsSrcap_Ti_206.262	4.5524	0.3616	1667.46	1667.048	7992.3	1	1034.5	64.3	1	R.IEIPIHIVPHVTIGK.V
	HsScrap_Ti_102.212	2.1343	0.1282	1244.44	1245.425	7918.6	1	840.1	70	1	K.VCLESAVELPK.I
gi|89058472|r	2	183	12.30%	106	11497	4.6	PREDICTED: similar to Ig kappa chain V-II region RPMI 6410 precursor [Homo sapiens]				
gi|89066978|r	2	183	10.20%	127	13922	4.6	PREDICTED: similar to Ig kappa chain V-II region Cum [Homo sapiens]				
gi|89062133|r	2	183	10.30%	126	13837	8	PREDICTED: similar to Ig kappa chain V-II region RPMI 6410 precursor [Homo sapiens]				
gi|89059101|r	2	183	12.30%	106	11497	4.6	PREDICTED: similar to Ig kappa chain V-II region RPMI 6410 precursor [Homo sapiens]				
	HsFlag-FLJ90652_2	4.4294	0.3826	1303.92	1304.399	8509.6	1	1977.6	87.5	127	R.FSGSGSGTDFTLK.I
	Hs293Flag-Ies2_Ti_1	3.2749	0.2984	1305.45	1304.399	4352.7	1	464.6	66.7	56	R.FSGSGSGTDFTLK.I
gi|4503765|re	5	14	12.20%	632	71175	7.4	fragile X mental retardation 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.4716	0.2715	1555.15	1555.595	8853.2	1	2105.4	83.3	2	K.DINESDEVEVYSR.A
	HsFLAG-ARP6_Ti_1	4.8261	0.3789	1996.31	1996.249	5795.8	1	945.8	58.3	3	R.EDLMGLAIGTHGANIQQAR.K
*	HsFLAG-p53-DNA-D	3.5632	0.3059	1650.54	1650.872	5775.1	2	641.6	57.7	4	R.SFLEFAEDVIQVPR.N
*	HsFLAG-p53-DNA-D	3.8648	0.3693	1477.58	1477.53	8417.3	1	1243.5	75	3	K.ENSTHFSQPNSTK.V
*	HsFLAG-UTX1_Ti_2	4.9636	0.4512	1841.45	1842.143	6901.7	1	1545.9	67.6	2	R.VLVASSVVAGESQKPELK.A
gi|49472822|r	2	3	12.20%	320	35611	6.1	eukaryotic translation initiation factor 3, subunit 4 delta, 44kDa [Homo sapiens]				
*	HsScrap_Ti_103.276	3.9344	0.3721	2464.53	2465.849	6146.5	1	595	41.7	2	K.GIPLATGDTSPEPELLPGAPLPPPK.E
*	HsFLAG-ARP6_Ti_1	2.9167	0.1744	1526.03	1524.714	7471.5	2	761.4	65.4	1	K.LPGELEPVQATQNK.T
gi|4502847|re	1	4	12.20%	172	18648	9.5	cold inducible RNA binding protein [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	5.1081	0.4066	2349.46	2346.599	7480.6	1	1541.5	60	4	K.LFVGGLSFDTNEQSLEQVFSK.Y
gi|5174659|re	1	2	12.20%	98	11471	6.2	S100 calcium binding protein A13 [Homo sapiens]				
gi|66737374|r	1	2	12.20%	98	11471	6.2	S100 calcium binding protein A13 [Homo sapiens]				
gi|66737372|r	1	2	12.20%	98	11471	6.2	S100 calcium binding protein A13 [Homo sapiens]				
gi|66737370|r	1	2	12.20%	98	11471	6.2	S100 calcium binding protein A13 [Homo sapiens]				
gi|66737368|r	1	2	12.20%	98	11471	6.2	S100 calcium binding protein A13 [Homo sapiens]				
	HsFlag-VPS71_Ti_1	4.1083	0.1933	1419.61	1419.707	5686	1	958.4	77.3	2	K.ELVTQQLPHLLK.D
gi|54607053|r	26	86	12.10%	2671	292708	7.4	GCN1 general control of amino-acid synthesis 1-like 1 [Homo sapiens]				

*	HsFLAG-ARP6_Ti_1	3.7636	0.287	1441.9	1441.627	6158.7	1	1164.7	76.9	2	K.NLLHSLQSSGIGSK.A
*	HsFlag-VPS71_Ti_1	3.6074	0.2277	2193.63	2194.617	6393.6	2	1021.5	36.8	1	R.GDTLLQALDLLPLLIQTVEK.A
*	HsFLAG-FLJ20729_	3.1576	0.2072	2193.96	2194.617	4390.8	1	920.9	57.9	2	R.GDTLLQALDLLPLLIQTVEK.A
*	HsFLAG-Lin9_Ti_20	4.2783	0.3673	2021.58	2022.396	7362.8	5	748.9	36.1	2	R.VLPQLISTITASVQNPALR.L
*	HsFLAG-Lin9_Ti_20	4.5855	0.4092	2021.82	2022.396	8676.2	1	1245.9	61.1	4	R.VLPQLISTITASVQNPALR.L
*	HsFLAG-Lin9_Ti_20	4.2037	0.2772	2240.34	2238.627	8375.1	1	1478.6	55	8	R.LQELDGELEAALGLLDIILAK.N
*	HsFLAG-FLJ20729_	4.3144	0.2571	2314.6	2315.758	8659.8	1	1227.9	35	5	K.NPSGLTQYIPVLVDSFLPLLK.S
*	HsFLAG-TCF3_Ti_1	4.9102	0.3186	2315.9	2315.758	4286	1	981.8	62.5	21	K.NPSGLTQYIPVLVDSFLPLLK.S
*	HsYL1_Ti_106.2927.	3.1428	0.4294	2401.36	2401.854	4020.4	1	374.5	41.3	1	R.VGKGEPGAAPLSAPAFSLVFPFLK.M
*	HsYL1_Ti_103.3774.	3.7	0.2882	2118.88	2117.496	3998.2	1	723.3	62.5	6	K.GEPGAAPLSAPAFSLVFPFLK.M
*	HsFLAG-Lin9_Ti_20	3.5205	0.2633	1300.41	1300.544	11475.7	1	1522.2	72.7	1	R.LLTWVIGTGSPR.L
*	HsFLAG-Lin9_Ti_20	2.8545	0.3068	1467.79	1467.754	4782.1	1	510.4	58.3	2	K.LYRPPPVLDALGR.V
*	HsFLAG-FLJ20729_	3.5258	0.2451	1268.37	1268.409	7022.1	1	1496.7	90	1	K.LSQYLDSSQVK.P
*	HsFlag-VPS71_Ti_1	3.4651	0.1899	1780.19	1779.043	3831.3	1	602.8	71.4	3	K.ENVNSLLPVFEEFLK.N
*	HsFLAG-FLJ20729_	4.3467	0.3733	1826.58	1827.131	8682.8	1	1978.3	73.3	9	K.LVLPSLLAALEEESWR.T
*	HsFLAG-p53-DNA-D	3.5406	0.3927	2118.98	2119.466	7014.5	1	1136.7	60.5	1	R.NPEILAIAPVLLDALTDPSR.K
*	HsFLAG-FLJ20729_	3.7037	0.1072	2246.81	2247.64	6003.5	1	789.5	35	2	R.NPEILAIAPVLLDALTDPSRK.T
*	HsFlag-DPCD_Ti_20	2.6567	0.1996	2249.7	2247.64	6438.7	2	455.7	42.5	1	R.NPEILAIAPVLLDALTDPSRK.T
*	HsYL1_Ti_101.1623.	4.2758	0.4694	2047.56	2048.099	7256.7	1	1867.3	66.7	2	K.MTTETASEDDNFGTAQSNK.A
*	HsFlag-VPS71_Ti_1	2.9965	0.1762	2652.07	2652.065	8815.2	2	379.6	31.8	1	K.TFEQLHSTIGHQALEDILPFLLK.Q
*	HsFlag-VPS71_Ti_1	4.561	0.3614	2652.34	2652.065	8462.7	1	2503.9	42	3	K.TFEQLHSTIGHQALEDILPFLLK.Q
*	HsFLAG-Lin9_Ti_20	2.8798	0.1809	1520.52	1520.769	10260.5	1	1017.3	57.1	1	R.VLAFLSSVAGDALTR.H
*	HsFLAG-p53-DNA-D	4.0377	0.2675	1475.42	1475.919	5578.6	1	1331.7	76.9	4	R.HLGVILPAVMLALK.E
*	HsFlag-VPS71_Ti_1	3.051	0.3251	2449.67	2449.72	6334.2	1	542.5	40.5	1	R.LFNDSSPVVLEESWDALNAITK.K
*	HsYL1_Ti_106.2280.	2.9577	0.1977	1184.5	1183.48	5766.3	1	1541.3	85	1	K.KGVTSILPVLR.E
*	HsFLAG-Lin9_Ti_20	3.368	0.1119	1487.07	1487.739	7752	2	1188.9	70.8	1	K.VDPLFTELLNGIR.A
gi|40807496|	7	15	12.10%	1048	116954	6.7	OTU domain containing 4 protein isoform 1 [Homo sapiens]				
	HsFLAG-ARP6_Ti_2	3.5371	0.1745	2724.98	2724.987	9547.3	1	1109.1	34.1	1	K.DFIIYREPNVSPSQVTENNFPEK.V
*	HsFlag-FLJ90652_2	3.7187	0.3675	1838.24	1838.931	5823	1	823.6	66.7	1	K.KPSTSGQNFHSDVDYR.G
*	HsFlag-FLJ20643_Ti	5.3679	0.3936	3912.47	3913.172	6736.1	1	928.7	27.2	3	R.LLYEIQNRDEQAFPALSSSSVNQSASQSSNPCVQR.K
*	HsFlag-FLJ20643_Ti	4.9147	0.3666	1616.66	1615.737	7780.4	1	1739.4	80.8	4	K.RPEPSTLENITDDK.Y
*	HsFlag-FLJ20643_Ti	2.2174	0.1993	940.54	940.041	5867.5	1	490.1	68.8	1	K.YATVSSPSK.S
*	HsFlag-FLJ20643_Ti	3.3562	0.2142	1547.28	1546.715	9321.3	8	739.5	57.7	1	K.GELDLSLENLDLSK.D
*	HsFlag-FLJ20643_Ti	5.0941	0.3317	1568.86	1568.811	5847.6	1	1694.6	80	4	R.KADTALASIPPVAEGK.A
gi|27765083|	3	3	12.10%	708	76573	5.1	calpastatin isoform a [Homo sapiens]				
gi|27765085|	3	3	12.50%	686	74067	5	calpastatin isoform b [Homo sapiens]				
	HsFlag-VPS71_Ti_1	3.2066	0.3847	1838.62	1838.111	3972.7	4	263.6	44.1	1	K.SLTPAVPVESKPDKPSGK.S
	HsFlag-VPS71_Ti_1	3.5517	0.1312	3605.56	3604.826	4251	1	465.3	23.6	1	K.EGITGPPADSSKPIGPDDAIDALSSDFTCGSPTAAGK.K
	HsFlag-VPS71_Ti_1	3.8147	0.2048	3281.34	3279.372	5426.2	1	682.6	26.7	1	K.KPADDQDPIDALSGDLDSCPSTTETSQNTAK.D
gi|8922712|re	3	4	12.10%	429	49398	6.8	septin 11 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.5914	0.3774	2142.47	2141.389	8638.6	3	467.7	42.1	1	R.NLSLSGHVGFDSLPDQLVNK.S
*	HsFLAG-p53-DNA-D	4.1531	0.3229	1635.06	1635.814	9118.5	1	2129.3	83.3	1	K.KKELEEEVNNFQK.K
*	HsFLAG-p53-DNA-D	4.813	0.2983	1957.7	1958.139	9289.3	1	1682.6	61.1	2	K.AAAQLLQSQAQQSGAQQTK.K

gi|4758356|re	2	2	12.10%	380	42593	8.6	flap structure-specific endonuclease 1 [Homo sapiens]				
*	HsFLAG-FLJ20729_	3.55	0.2862	2757.06	2758.168	9991	1	788.6	26	1	K.HLLSLMGIPYLDAPSEAEASCAALVK.A
*	HsFLAG-FLJ20729_	2.9426	0.2892	2322.57	2323.605	5904.8	3	486.7	44.7	1	K.EAHQLFLEPEVLDPESVELK.W
gi|15147337|r	19	43	12.00%	2799	309352	5.8	E3 ubiquitin protein ligase, HECT domain containing, 1 [Homo sapiens]				
*	HsSrcap_Ti_204.245	3.609	0.3907	2051.94	2052.338	3834.2	1	486.8	58.8	2	K.YNLNSHPPLNVLEQATIK.Q
	HsSrcap_Ti_204.211	3.8332	0.3508	1883.47	1884.068	4965	1	375.2	50	3	K.QCVVGPNHAAFLLEDGR.V
	HsSrcap_Ti_203.201	3.5332	0.2232	2387.73	2387.611	5265.6	1	711.3	47.6	1	R.IGFSVQPDRLELGKPDNNDGSK.L
	HsSrcap_Ti_205.516	6.8965	0.5039	3614.41	3613.149	7666.4	1	1397.4	28.7	7	R.DRGSGLLGSQPQPVIPASVIPEELISQAQVVLQGK.S
	HsSrcap_Ti_202.526	5.1069	0.3006	3341.77	3341.873	8312.7	1	1114.1	28.9	3	R.GSGLLGSQPQPVIPASVIPEELISQAQVVLQGK.S
	HsSrcap_Ti_203.298	4.273	0.4006	2425.7	2425.703	8905.7	1	926	47.5	1	K.KNTPVQSPVSLGEDLQWWPDK.D
	HsSrcap_Ti_203.155	4.2959	0.4652	1762.11	1762.874	9669.8	1	2341.3	82.1	2	K.LEHTAQTYSELQGER.I
	HsSrcap_Ti_205.226	2.5641	0.2152	2058.3	2058.389	7384.2	2	344.9	44.1	1	K.KLCIPEKTEILAVNVDSK.G
	HsSrcap_Ti_203.357	5.4116	0.4112	3424.81	3422.698	8341.6	1	1029.2	29.3	1	R.YCIFDLATGKAEQENNFPTSSIAFLGQNER.N
	HsScrap_Ti_103.279	3.5567	0.3784	1730.44	1730.017	7546.2	1	1000.9	60	3	R.NVAIFTAGQESPIILR.D
	HsSrcap_Ti_204.167	4.007	0.3901	1674.2	1674.739	5898.3	1	952.3	70.8	1	K.RTSPTAYCDCWEK.C
	HsScrap_Ti_103.240	3.2398	0.2866	1513.8	1513.778	6677.3	1	751.8	65.4	1	R.LLTATNLVTLPNSR.G
	HsSrcap_Ti_202.556	2.6525	0.2554	1860.02	1860.208	7917	2	700.1	56.2	1	K.CTADILLLDTLLGTLVK.E
	HsSrcap_Ti_205.199	4.032	0.3372	1604.5	1603.861	6594.7	1	1028.3	65.4	4	K.YNHLVYSQIPAAVK.L
	HsSrcap_Ti_202.271	4.0855	0.2292	1927.94	1928.106	6450.3	1	1220.7	66.7	1	K.LTYQDAVNLQNYVEEK.L
	HsYL1_Ti_102.3468.	4.3753	0.2905	2426	2425.756	2886.1	1	844.9	59.1	2	R.VFMEDVGAEPGSILTELGGFEVK.E
	HsSrcap_Ti_203.405	3.0423	0.3143	1690.42	1690.893	10272	2	999.6	53.6	1	R.SFYTAIAQAFLSNEK.L
	HsSrcap_Ti_203.411	4.7715	0.4124	2140.56	2141.491	7771.8	1	2004.9	70.6	4	R.ILGLCLLQNELCPITLNR.H
	HsSrcap_Ti_204.201	4.2297	0.2878	1495.32	1495.841	7061.5	1	1651.8	79.2	4	R.MLVVAEQPLHAMR.K
gi|4757900|re	2	6	12.00%	417	48142	4.4	calreticulin precursor [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.5843	0.4158	1609.48	1608.791	7310.6	1	2392.3	88.5	2	R.FYALSASFEPFSNK.G
*	HsFLAG-p53-DNA-D	5.8593	0.4664	4150.76	4151.577	9567.9	1	1686.8	28.6	4	K.GTWIHPEIDNPEYSPDPSIYAYDNFGVLGLDLWQVK.S
gi|8923092|re	2	3	12.00%	382	42864	9.8	glutaminyl-peptide cyclotransferase-like [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	3.0057	0.2471	1126.41	1126.258	4874.2	2	564.2	75	2	R.TPGSPGNLQVR.K
*	HsFLAG-TCF3_Ti_1	3.6705	0.3221	3670.97	3671.191	9957.3	1	836.4	22.1	1	K.LFPPGSTPFVGATDSAVPCALLLELAQALDLELSR.A
gi|27735029|r	2	3	12.00%	216	25091	6.7	MOB1, Mps One Binder kinase activator-like 1A [Homo sapiens]				
gi|8922671|re	2	3	12.00%	216	25008	7.2	Mob4B protein [Homo sapiens]				
	HsFLAG-ARP5_Ti_1	2.8115	0.1609	1656.33	1656.879	6674.2	9	422	50	2	K.KNIPEGSHQYELLK.H
	HsARP6-FLAG_Ti_1	2.7569	0.2679	1498.54	1497.607	8868.5	1	730.9	59.1	1	K.YEYHWADGTNIK.K
gi|4758950|re	2	2	12.00%	216	23743	9.4	peptidylprolyl isomerase B precursor [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	3.9357	0.2889	1365.04	1365.526	7713.5	1	1308	75	1	K.TVDNFVALATGEK.G
*	HsFLAG-ARP6_Ti_1	3.0073	0.2494	1459.62	1458.611	8178.6	1	1012.3	66.7	1	K.DTNGSQFFITTVK.T
gi|6912292|re	3	29	12.00%	191	22225	5.9	chromobox homolog 5 (HP1 alpha homolog, Drosophila) [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.6836	0.1469	1189.35	1190.293	7178.7	3	697.2	65	2	K.DTDEADLVLAK.E
*	HsFLAG-ARP6_Ti_1	3.3583	0.2407	1190.32	1190.293	5953.4	1	1341.5	80	1	K.DTDEADLVLAK.E
	HsFlag-NUFIP_Ti_1	4.4119	0.1679	1525.57	1525.711	7777.5	1	1543.6	77.3	26	K.CPQIVIAFYEER.L
gi|8923269|re	8	29	11.90%	929	105693	9.4	testis expressed sequence 10 [Homo sapiens]				
*	HsH2AZ-FLAG_293_	3.7081	0.1847	1412.26	1412.759	4455.4	2	740	70.8	6	R.LAAVQLLQFLAPK.I
*	HsH2AZ-FLAG_293_	4.7019	0.3986	1815.31	1815.163	7220	1	1713.6	73.3	5	K.VLDILLEQYPALITGR.S

*	HsH2AZ-FLAG_293_	5.4766	0.44	1963.42	1964.229	9465.8	1	2214.6	70.6	7	R.NPELSTQLIDIIHTAAAR.A
*	HsH2AZ-FLAG_293_	4.1533	0.2691	1964.35	1964.229	6666.6	1	1427.9	48.5	1	R.NPELSTQLIDIIHTAAAR.A
*	HsH2AZ-FLAG_293_	4.6345	0.3726	2084.78	2086.309	5643.1	1	1593.9	66.7	3	R.IYDPQEGAVVVLPADSQQR.L
*	HsH2AZ-FLAG_293_	5.0445	0.3827	2045.49	2045.473	5093.5	1	888	58.8	4	R.LVQLVYFLPSLPADLLSR.L
*	HsH2AZ-FLAG_293_	4.6912	0.2428	1451.32	1451.619	7752.5	1	2170.2	87.5	1	R.SQNFDILQSAISK.H
*	HsH2AZ-FLAG_293_	3.295	0.3049	1506.23	1506.786	3942	1	584.7	65.4	2	R.VGPEELPVVGQLLR.L
gi|4758556|re	3	4	11.90%	683	77529	9.5	PRP3 pre-mRNA processing factor 3 homolog [Homo sapiens]				
*	HsFLAG-p53-DNA-D	2.6611	0.1396	1699.47	1699.904	4688.1	3	496.4	53.6	1	K.AADHLKPFLDDSTLR.F
*	HsFlag-VPS71_Ti_1	5.5478	0.3682	3332.15	3330.694	5433.2	1	1138	33.3	2	K.TPSSSQPERLPIGNTIQPSQAATFMNDAIEK.A
*	HsFLAG-p53-DNA-D	5.2182	0.3488	3926.42	3928.39	8670.2	1	722.2	24.3	1	K.REDYFGITNLVEHPAQLNPPVDNDTPVTLGVYLTK.K
gi|5031571|re	2	6	11.90%	394	44761	6.7	actin-related protein 2 isoform b [Homo sapiens]				
gi|53692187|r	2	6	11.80%	399	45377	7.2	actin-related protein 2 isoform a [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.7812	0.4132	1392.85	1393.541	4341.2	1	743.3	80	2	K.HLWDYTFGPEK.L
	HsFLAG-Lin9_Ti_20	6.3159	0.4039	3939.67	3940.445	7999.4	1	1432.5	27.9	4	R.FEAPEALFQPHLINVEGVGVAELLFNTIQAADIDTR.S
gi|25777711|r	1	4	11.90%	160	18063	4.5	S-phase kinase-associated protein 1A isoform a [Homo sapiens]				
gi|25777713|r	1	4	11.70%	163	18658	4.5	S-phase kinase-associated protein 1A isoform b [Homo sapiens]				
	HsSrcap_Ti_204.523	4.8198	0.4189	2137.19	2137.481	8285.5	1	1576.1	61.1	4	K.VDQGTLFELILAANYLDIK.G
gi|4505941|re	10	24	11.80%	1174	133896	6.9	PolII_Rpb2 {DNA directed RNA polymerase II polypeptide B; polymerase (RNA) II (DNA directed) polypeptide				
*	HsFlag-NUFIP_Ti_1	4.2966	0.4476	2798.3	2799.023	7184.3	1	791.9	42	2	R.IVEDAPPIDLQAEAQHASGEVEEPPR.Y
*	HsFlag-NUFIP_Ti_11	3.7306	0.237	1834.91	1835.072	6140.5	1	611.4	57.7	3	K.FEQIYLSKPTHWER.D
*	HsFlag-NUFIP_Ti_11	3.4021	0.2651	1246.58	1246.452	7864.9	2	1086.2	80	4	R.LTFASTLSHLR.R
*	HsFlag-NUFIP_Ti_1	3.0466	0.1179	1242.83	1241.526	6762.1	4	1056	77.8	2	R.ICRPLLIVEK.Q
*	HsFlag-NUFIP_Ti_11	4.7095	0.4135	2245.99	2247.66	8615.8	1	1093	52.8	1	R.MDTLAHVLYYPQKPLVTTR.S
*	HsFlag-NUFIP_Ti_11	5.7943	0.4581	2247.31	2247.66	7905.4	1	2564.4	51.4	3	R.MDTLAHVLYYPQKPLVTTR.S
*	HsFlag-NUFIP_Ti_1	4.0032	0.3678	2212.99	2213.464	9209.3	1	554.1	42.1	1	R.TSETGIVDQVMVTLNQEGYK.F
*	HsSrcap_Ti_205.314	3.9709	0.2457	1501.15	1500.763	7472	1	982.3	66.7	2	R.MTIGHLIECLQGK.V
*	HsFlag-NUFIP_Ti_1	4.2248	0.3757	1550.67	1551.742	6581.7	1	1224.2	75	2	K.ISNLLSDYGYHLR.G
*	HsFlag-NUFIP_Ti_1	3.9146	0.2907	1486.66	1487.624	7689.6	1	1786.4	83.3	4	R.DCQIAHGAAQFLR.E
gi|4759196|re	5	14	11.80%	1142	126500	6.4	symplekin [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.0245	0.3013	2499.34	2498.946	8810.6	1	1121.1	47.8	1	K.FMVHPAISSINLTTALGSLANIAR.Q
*	HsARP6-FLAG_Ti_1	2.6268	0.2173	1838.3	1839.183	6892.4	1	958.5	62.5	2	K.VVLEAPLITESALEVVR.K
*	HsFLAG-p53-DNA-D	4.5986	0.2819	3308.67	3309.747	9572.4	1	1070.7	26.6	2	R.LLGTQHGEGNSALSPLNPGELLIALHNIDSVK.C
*	HsFLAG-p53-DNA-D	3.8976	0.2419	3191.03	3191.586	8611.4	1	966.2	27.7	2	R.SFTPHQQAHIPNSIMTILEASGKQEPEAK.E
*	HsFLAG-p53-DNA-D	4.5966	0.3784	3460.19	3460.909	4404.3	1	368.9	23.4	7	K.EAPAGPLEEDDLEPLTLAPAPAPRPPQDLIGLR.L
gi|5031579|re	4	8	11.80%	692	76108	5.1	A-kinase anchor protein 8 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	4.5848	0.3459	3292.1	3291.555	7658.1	1	625.5	23.4	1	K.ANDGGLAAGAPAMHMASYGPEPCTDNSDSLIAK.I
*	HsYL1_Ti_101.1566.	2.8748	0.1914	1111.68	1111.15	2884.3	4	561.7	87.5	2	R.SFDDEEIQK.H
*	HsFLAG-TCF3_Ti_1	4.0209	0.2485	2084.12	2084.331	10386.1	4	1273.8	34.2	1	K.ETPEEVAADVLAEVITAAVR.A
*	HsMRGBP-FLAG_Ti_	4.3245	0.4559	1970.77	1971.085	5464.4	1	837.5	57.9	4	R.VAPAPAAADAEVEQTDAESK.D
gi|21450832|r	1	3	11.80%	255	29484	7.1	hypothetical protein LOC220134 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	5.9662	0.3993	3516.16	3515.983	8283.4	1	1416.9	31	3	K.IGDEIIVINELLNKLELEIQYQEQTNNSLK.E
gi|21361361|r	5	7	11.70%	632	67868	8.1	ilvB (bacterial acetolactate synthase)-like isoform 1 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	5.183	0.4269	2104.19	2102.491	6786.1	1	1758.1	63.9	1	R.FIFTLVGGHISPLLVACEK.L

*	HsSrcap_Ti_204.315	5.0971	0.4304	1916.43	1917.225	8734.6	1	1421.1	62.5	2	R.GALQAVDQLSLFRPLCK.F
*	HsSrcap_Ti_204.316	4.1846	0.2955	1917.67	1917.225	6731.8	2	978.7	43.8	1	R.GALQAVDQLSLFRPLCK.F
*	HsSrcap_Ti_206.261	4.7	0.3836	1998.88	1999.376	6283.1	1	897.5	61.1	1	K.RPLMVLGSQALLTPTSADK.L
*	HsSrcap_Ti_202.360	4.3714	0.4305	2227.8	2227.481	6425.4	1	952.6	58.3	2	K.LVEGLQGQTWAPDWVEELR.E
gi|41281398|r	3	3	11.70%	582	64888	8.5	soc-2 suppressor of clear homolog [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	3.8361	0.1966	3696.96	3696.029	9228.8	1	715.6	22.7	1	K.EIGNCTQITNLDLQHNELLDLPDTIGNLSSLSR.L
*	HsFLAG-Lin9_Ti_20	3.2133	0.274	2367.41	2366.801	12034.1	1	810.4	40.5	1	K.IPEDVSGLVSLEVLILSNNLLK.K
*	HsFLAG-Lin9_Ti_20	3.1098	0.3462	1482.74	1483.751	9412.5	1	936.7	66.7	1	K.LVLTNNQLTTLPR.G
gi|24307981|r	2	2	11.70%	291	31835	5.2	exosome component 7 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.8873	0.3883	1597.53	1595.706	10626.8	1	1282.2	64.3	1	R.GGDDLGTEIANTLYR.I
*	HsFLAG-p53-DNA-D	3.5833	0.3958	2074.91	2073.4	9838.8	1	721.8	47.2	1	K.VLHASLQSVLHKEESLGPK.R
gi|44955910|r	9	24	11.60%	911	99854	8.2	E2F transcription factor 7 [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	3.2526	0.378	1870.38	1871.187	7903.1	1	803	53.3	2	R.IYDIVNVLESLHLVSR.V
*	HsARP6-FLAG_Ti_1	4.0318	0.3371	1870.74	1871.187	3534.2	1	555.5	43.3	2	R.IYDIVNVLESLHLVSR.V
*	HsFLAG-FLJ20729_	4.8109	0.4281	1647.47	1647.996	6734.7	1	2028.3	82.1	4	R.LYDIANVLTSLALIK.K
*	HsFlag-VPS71_Ti_1	3.738	0.4118	1333.8	1333.403	7335.2	1	1667.2	86.4	2	R.HGSFNTVQASER.I
*	HsH2AZ-FLAG_293_	3.2687	0.3104	1760.51	1760.896	6603.9	1	626.8	47.1	1	R.SSEAPATVELSSAPSAQK.R
*	HsFlag-FLJ90652_2	3.5788	0.2118	1246.09	1246.36	5654.5	1	1159.4	81.8	5	K.KPSDSTDLASPK.T
*	HsFlag-VPS71_Ti_1	6.297	0.5171	2362.7	2360.675	10168.4	1	2343.9	41.7	6	R.SHSVVQQPESPVYVGHPVSVVK.L
*	HsFlag-VPS71_Ti_1	3.0403	0.3334	1202.66	1203.427	6454.7	1	745.7	75	1	K.LHQSPVPVTPK.S
*	HsFlag-VPS71_Ti_1	2.5445	0.3077	1203.54	1203.427	6906.1	1	792.6	75	1	K.LHQSPVPVTPK.S
gi|21218438|r	5	10	11.60%	593	65261	9.7	GATA zinc finger domain containing 2B [Homo sapiens]				
*	HsSrcap_Ti_205.196	4.7382	0.4169	2513.55	2514.844	5762.1	1	763.3	45.8	2	K.TPVVQNAASIVQPSPAHVGQQGLSK.L
*	HsSrcap_Ti_205.196	5.032	0.4057	2514.7	2514.844	7956.2	1	1450.2	35.4	3	K.TPVVQNAASIVQPSPAHVGQQGLSK.L
*	HsSrcap_Ti_206.220	3.2522	0.2238	1720.67	1719.941	5502.3	5	533	53.3	1	K.LPSRPGAQGVEPQNLR.T
*	HsSrcap_Ti_205.209	3.7031	0.3211	1687.92	1688.957	5017.5	1	505.3	57.1	3	R.SATNTTLPHMLMSQR.V
*	HsFlag-VPS71_Ti_1	3.4226	0.3602	1394.04	1392.601	3523.5	1	831.7	83.3	1	R.VIAPNPAQLQGQR.G
gi|16905526|r	4	17	11.60%	398	45566	8.9	death-associated protein 3 [Homo sapiens]				
gi|4758118|re	4	17	11.60%	398	45566	8.9	death-associated protein 3 [Homo sapiens]				
	HsFlag-NUFIP_Ti_11	3.9547	0.2409	1326.33	1325.637	8395.2	1	1223.2	80	2	R.KPALELLHYLK.N
	HsFlag-NUFIP_Ti_1	4.5676	0.2974	1659.95	1659.926	5497.8	1	1157.5	50	3	K.SPIAPEELALVHNLR.K
	HsFlag-NUFIP_Ti_1	5.4356	0.3554	1660.73	1659.926	6210.5	1	1596.9	78.6	7	K.SPIAPEELALVHNLR.K
	HsFlag-NUFIP_Ti_1	4.4259	0.3438	2251.23	2250.556	4962.6	1	650.4	52.6	5	K.EGFDALDPFIPILVSNYNPK.E
gi|56181387|r	3	3	11.60%	303	34856	5.9	STIP1 homology and U-box containing protein 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.5835	0.4053	1309.63	1310.495	8063.2	1	1253.7	75	1	R.NPLVAVYYTNR.A
*	HsFLAG-ARP6_Ti_1	2.5645	0.2842	1028.59	1028.156	5016.3	1	717.2	81.2	1	R.VGHFDPVTR.S
*	HsFLAG-ARP6_Ti_1	4.4706	0.3069	1684.51	1684.004	4466.4	1	1086	75	1	R.SPLTQEQLIPNLAMK.E
gi|5453880|re	2	4	11.60%	249	28585	4.1	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A [Homo sapiens]				
*	HsH2AZ-FLAG_293_	3.4269	0.3083	1467.96	1468.619	5410.5	1	553.6	66.7	1	K.CPNLTHLNLSGNK.I
	HsFLAG-p53-DNA-D	4.483	0.4382	1973.2	1974.1	7741.8	1	1183.4	63.3	3	K.SLDLFNCEVTNLNDYR.E
gi|4758638|re	2	4	11.60%	224	25035	6.4	peroxiredoxin 6 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.8603	0.4294	2030.86	2032.268	9333	1	1795.8	68.8	1	R.FHDFLGDSWGILFSHPR.D
*	HsFlag-VPS71_Ti_1	2.4564	0.2461	1008.68	1008.205	5464.9	2	760.1	75	3	R.VVFVFGPDK.K

gi|27436901|r	2	5	11.60%	198	21348	8.9	mitochondrial ribosomal protein L12 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.0092	0.2609	1361.55	1361.584	8009.3	1	1799	86.4	3	K.NYIQGINLVQAK.K
*	HsFLAG-ARP6_Ti_1	3.9966	0.2321	1284.41	1284.539	5903.3	3	1116.7	80	2	K.KLVESLPQEIK.A
gi|4502313|re	1	2	11.60%	155	15736	8.5	ATPase, H+ transporting, lysosomal, V0 subunit c [Homo sapiens]				
gi|89040630|r	1	2	11.20%	160	16129	9.5	PREDICTED: similar to Vacuolar ATP synthase 16 kDa proteolipid subunit [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	4.6228	0.4292	1907.59	1908.3	8264.8	1	1013.9	52.9	2	K.SGTGIAAMSVMRPEQIMK.S
gi|31377595|r	7	18	11.50%	953	106359	8.2	conserved nuclear protein NHN1 [Homo sapiens]				
*	HsYL1_Ti_101.1551.	3.2058	0.3527	1508.01	1507.511	7048	1	727	58.3	1	K.SQDQDSEVNELSR.G
*	HsFlag-DPCD_Ti_20	3.7106	0.295	3255.96	3256.325	5729.6	1	648.7	30.6	1	R.ELDEHELDYDEEVPEEPAPAVQEDEAEK.A
*	HsH2AZ-FLAG_293_	4.7191	0.391	2252.98	2252.395	4374.4	1	1076.9	70.6	6	R.DTVLEPYADPYYDYEIER.F
*	HsFLAG-FLJ20729_	3.1674	0.2794	1699.99	1700.805	7741.3	1	635.8	58.3	2	R.VQYTETEPYHNYR.E
*	HsFLAG-Lin9_Ti_20	2.9046	0.3215	1299.51	1300.544	4252.6	1	700.3	70.8	2	K.KPAPPPAPPQATK.T
*	HsFLAG-Lin9_Ti_20	3.4249	0.2661	1301.1	1300.544	6887.9	1	1245.9	79.2	3	K.KPAPPPAPPQATK.T
*	HsFlag-NUFIP_Ti_2	3.8242	0.3092	2632.56	2632.852	4404.7	1	563.5	34.4	3	K.SSQQPSTPQQAPPGQPQQGTFVAHK.E
gi|4885281|re	4	11	11.50%	558	61398	7.8	glutamate dehydrogenase 1 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.953	0.2706	1426.22	1426.482	8910	1	1560.1	77.3	1	R.DDGSWEVIEGYR.A
*	HsFLAG-ARP6_Ti_1	4.5743	0.433	2046.29	2045.318	6833	1	969.8	55.3	4	K.KGFIGPGIDVPAPDMSTGER.E
	HsFLAG-ARP6_Ti_1	4.2461	0.4415	1749.2	1750.028	7602.2	1	1450.8	70	2	K.TFVVQGFGNVGLHSMR.Y
*	HsFLAG-p53-DNA-D	3.7078	0.2532	1738.78	1738.941	4320	1	407.9	53.3	4	K.HGGTIPIVPTAEFQDR.I
gi|13375656|r	2	2	11.50%	244	27949	8	UL16 binding protein 3 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.8543	0.4642	2148.78	2149.426	8924.7	1	1642.9	61.1	1	K.VLSMGHLEEQLYATDAWGK.Q
*	HsFLAG-ARP6_Ti_1	2.8578	0.212	997.34	997.145	5629.9	1	1019.1	93.8	1	K.WTVVHAGAR.R
gi|5454106|re	1	2	11.50%	218	21711	6.5	TBP-related factor 10 [Homo sapiens]				
*	HsFLAG-FLJ20309_	5.9292	0.5396	1964.63	1965.133	6924.2	1	1831.7	62.5	2	K.ASPAGTAGGPGAGAAAGGTGPLAAR.A
gi|61835148|r	7	29	11.40%	621	69721	6.2	fragile X mental retardation-related protein 1 isoform a [Homo sapiens]				
gi|61835172|r	7	29	13.20%	536	59920	6.8	fragile X mental retardation-related protein 1 isoform c [Homo sapiens]				
gi|61835164|r	7	29	13.20%	539	60792	6.4	fragile X mental retardation-related protein 1 isoform b [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.8108	0.1985	2379.89	2380.761	6520.1	1	831.9	50	2	R.IFYHPETTQLMILSASEATVK.R
	HsARP6-FLAG_Ti_1	3.6123	0.136	2380.18	2380.761	10599.4	2	1270.3	32.5	1	R.IFYHPETTQLMILSASEATVK.R
	HsFLAG-ARP6_Ti_1	3.0669	0.2374	1198.45	1198.426	5967.6	7	925.6	77.8	1	R.VNILSDMHLR.S
	HsFLAG-p53-DNA-D	4.2427	0.3276	1948.77	1949.168	5801	1	1338.1	67.6	3	R.KVPGVTAIELDEDTGTFR.I
	HsFLAG-ARP6_Ti_1	4.5911	0.5043	1820.16	1820.994	6369.1	1	1261.9	65.6	5	K.VPGVTAIELDEDTGTFR.I
	HsFLAG-FLJ20309_	4.1942	0.371	1697.19	1696.943	5158.4	1	1126.5	73.1	16	R.GFLEFVEDFIQVPR.N
	HsFLAG-FLJ20309_	2.4912	0.0894	944.53	944.116	6753.9	7	655	71.4	1	K.VIQEIVDK.S
gi|7657611|re	2	7	11.40%	264	30987	9.2	DnaJ (Hsp40) homolog, subfamily C, member 8 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	5.5124	0.2211	3351.44	3352.722	9723.9	4	812.7	24.1	5	R.LTRPGSSYFNLNPFEVLQIDPEVTDEEIK.K
*	HsFlag-VPS71_Ti_1	4.9312	0.2823	3480.35	3480.896	5948.5	1	599.1	25	2	R.LTRPGSSYFNLNPFEVLQIDPEVTDEEIKK.R
gi|4826898|re	1	10	11.40%	140	15054	8.3	profilin 1 [Homo sapiens]				
*	HsFLAG-FLJ20729_	4.2004	0.2074	1643.99	1644.952	5501.7	1	1377.8	73.3	10	K.TFVNITPAEVGVLVGK.D
gi|7661966|re	12	23	11.30%	2089	226690	5.5	mediator of DNA damage checkpoint 1 [Homo sapiens]				
*	HsFlag-DPCD_Ti_20	3.1934	0.3629	1656.42	1656.846	9086.1	1	1071.4	64.3	2	R.DCGSLNGTQILRPPK.V
*	HsFLAG-FLJ20729_	3.532	0.3919	1884.33	1885.084	5835.1	1	490.8	50	2	K.SQLPAEGDAGAEWAAAVLK.Q
*	HsFLAG-Lin9_Ti_20	4.1791	0.2302	2357.18	2356.6	10120.6	1	1454.4	35.2	2	R.AHEVGAQGGPPVAQVEQDLPISR.E

*	HsFLAG-p53-DNA-D	3.7728	0.3051	3391.81	3391.78	6963.6	1	765.5	27.3	1	R.MTPFPATSAAPEPHPSTSTAQPVTPKPTSQATR.S
*	HsFlag-DPCD_Ti_20	4.0577	0.3719	3376.77	3378.715	6042.3	1	531.8	25.8	1	K.TPETLVPTAPKLEPSTSTDQPVTPEPTSQATR.G
*	HsSrcap_Ti_201.075	3.6944	0.215	2242.76	2243.389	6109.4	1	616.9	47.5	1	K.LEPSTSTDQPVTPEPTSQATR.G
*	HsFLAG-UTX1_Ti_2	3.1948	0.2633	1922.28	1923.174	3318.3	1	236.1	44.1	2	K.TPESIVPIAPELQPSTSR.N
*	HsFLAG-Lin9_Ti_20	3.89	0.29	2624.67	2624.907	6275.6	1	681.5	31.2	1	K.TPEPVVPTAPEPHPTTSTDQPVTPK.L
*	HsFlag-VPS71_Ti_1	4.2337	0.492	2166.73	2167.427	8265.8	1	890.2	47.7	3	R.AVLALGGSLAGSAAEASHLVTDR.I
*	HsARP6-FLAG_Ti_1	3.1146	0.4148	1635.25	1635.907	5053	1	622.7	65.4	2	R.GIPILSLDWLHQSR.K
*	HsFLAG-FLJ20729_	3.3034	0.3498	2039.12	2040.302	6317.3	1	543.3	50	1	R.VVITCPQDFPHCSIPLR.V
*	HsFLAG-Lin9_Ti_20	3.5457	0.2972	1796.64	1797.232	5440.9	9	380.6	46.9	5	R.VGLPLLSPEFLLTGVLK.Q
gi|5174559|re	5	8	11.20%	738	80242	6	melanoma-associated antigen p97 isoform 1, precursor [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.8415	0.4239	1733.44	1733.965	3700.6	1	889.7	73.3	1	R.TVGWNVPVGYLVESGR.L
*	HsFLAG-ARP6_Ti_1	5.33	0.4516	2234.79	2235.511	5229.2	1	1340.4	72.2	4	K.TLPSWGQALLSQDFELLCR.D
*	HsFLAG-ARP6_Ti_1	2.6872	0.1463	1273.52	1273.482	2480.8	1	434.5	80	1	R.LKPEIQCVSAK.S
*	HsFLAG-ARP6_Ti_1	4.1853	0.1778	2283.47	2283.517	4857.5	1	694	35.7	1	R.SCHAGFGSPAGWDVPVGALIQR.G
*	HsFLAG-ARP6_Ti_1	3.7065	0.3582	1802.05	1802.999	9257.8	1	1186.6	64.3	1	K.MFDSSNYHGQDLLFK.D
gi|47174861|r	2	6	11.20%	473	53194	10.1	peter pan homolog [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.2431	0.2263	1838.38	1838.032	5723.7	1	1207.6	73.3	4	R.NLEAYAANPHSFVFTR.G
*	HsFlag-NUFIP_Ti_1	5.7895	0.4874	3804.64	3806.089	9108.7	1	1432.8	27.1	2	R.LQDISELLATGAGLSESEAEPDGDHNITELPQAVAGR.G
gi|21264355|r	3	6	11.20%	411	46649	4.9	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin e1 [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	2.5838	0.2819	1833.22	1834.166	6364.4	1	372.2	41.2	1	R.VTASSGITIPKPPKPPDK.P
*	HsFLAG-Lin9_Ti_20	3.7274	0.3553	1696.32	1696.903	7874.5	1	1347.7	71.4	2	K.AYHNSPAYLAYINAK.S
*	HsFLAG-FLJ20729_	4.1894	0.2755	1400.14	1400.531	8209.4	1	1396.7	70.8	3	K.IAAEIAQAEEQAR.K
gi|5902078|re	2	3	11.20%	107	12528	10.1	splicing factor, arginine/serine-rich 5 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.9489	0.1783	1310.34	1311.345	6552.4	2	794	68.2	1	R.DADDAVYELDGK.E
*	HsFLAG-ARP6_Ti_1	4.2602	0.2114	1311.16	1311.345	4880.4	1	1357.3	86.4	2	R.DADDAVYELDGK.E
gi|11559929|r	5	7	11.10%	874	97718	5.5	coatomer protein complex, subunit gamma 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.7627	0.3119	1847.87	1847.128	10363.1	1	812.4	50	2	K.ELAPAVSVLQLFCSSPK.A
*	HsFLAG-Lin9_Ti_20	4.1204	0.2722	1245.36	1245.546	7097.9	1	1806.1	86.4	2	R.SIATLAITTLLK.T
*	HsFLAG-p53-DNA-D	3.0689	0.155	1903.46	1903.287	9626.6	1	766.3	50	1	K.FGAQNEEMLPSILVLLK.R
*	HsFLAG-Lin9_Ti_20	3.5468	0.3106	2023.94	2023.303	4220.1	1	359.1	52.9	1	R.SLPYNQPGTCYTLVALPK.E
*	HsFLAG-Lin9_Ti_20	3.7251	0.2514	3800.83	3802.869	6642.5	3	372.9	21.1	1	K.DCDPTTGETDDEGYEDEYVLEDLEVTVADHIQK.V
gi|19923485|r	3	8	11.10%	432	51466	9.8	cisplatin resistance-associated overexpressed protein [Homo sapiens]				
gi|52426743|r	3	8	11.10%	432	51466	9.8	cisplatin resistance-associated overexpressed protein [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	4.2332	0.3618	2014.85	2013.189	6166.4	1	997.2	63.3	4	K.YYLCGFCPAELFTNTR.S
	HsFLAG-FLJ20309_	4.2281	0.4551	1715.66	1715.861	8625.2	1	1222.8	58.8	2	R.LALSQNQQSSGAAGPTGK.N
	HsFLAG-Lin9_Ti_20	3.6864	0.3633	1500.12	1500.602	7477.6	1	1088.2	65.4	2	R.STTSTIESFAAQEK.Q
gi|39930469|r	2	2	11.10%	306	35583	10	brix domain containing 1 [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	2.9287	0.2152	2061.1	2060.271	5801.7	1	355.4	46.9	1	K.NITRPFEDQTSLEFFSK.K
*	HsFlag-FLJ20643_Ti	2.9509	0.1536	2002.29	2005.206	7701.1	1	1002.2	59.4	1	K.PMLIFAGDDFDVTEDYR.R
gi|27764863|r	5	10	11.10%	298	32926	9.7	solute carrier family 25, member A6 [Homo sapiens]				
gi|4502099|re	5	10	11.10%	298	32895	9.7	solute carrier family 25, member 5 [Homo sapiens]				
	HsFLAG-TIP49b_Ti_	2.5219	0.292	1136.57	1137.368	5845.8	9	464.8	66.7	2	K.LLLQVQHASK.Q
	HsFLAG-ARP6_Ti_1	2.6013	0.2171	1122.3	1122.269	4917	1	646.5	81.2	1	K.EQGVLSFWR.G

	HsFLAG-TCF3_Ti_1	2.9251	0.3102	1447.57	1447.676	5723.7	1	451.2	54.5	2	R.YFPTQALNFAFK.D
	HsFLAG-ARP6_Ti_1	3.3748	0.2596	1448.12	1447.676	4592.9	1	871.3	81.8	4	R.YFPTQALNFAFK.D
	HsSrcap_Ti_204.285	3.3103	0.3503	1691.17	1690.939	4362.7	1	527.1	65.4	1	R.YFPTQALNFAFKDK.Y
gi|38490531|r	4	6	11.00%	1082	120237	7.3	splicing factor, arginine/serine-rich 14 [Homo sapiens]				
gi|62859987|r	4	6	11.00%	1082	120237	7.3	splicing factor, arginine/serine-rich 14 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	6.2315	0.5049	3936.37	3937.1	10082.2	1	1695.6	28.6	1	R.GSWEQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSR.L
	HsFLAG-ARP6_Ti_1	3.1168	0.1477	2203.51	2203.464	7629.2	2	593.2	42.1	1	K.TLSNPLDLALALETTNSLCR.K
	HsFlag-NUFIP_Ti_1	4.6603	0.4006	2978.15	2977.343	5235.1	1	485.9	37	2	K.ILEAVGLQDIAPSPAAFPNFEDSTLFGR.E
	HsFLAG-Lin9_Ti_20	3.5337	0.1825	4013.1	4012.337	4841.5	1	278.1	19.1	2	R.FVAQVGPEIEQFSIENSTDNPDLWFLHDQNSSAFK.F
gi|6912478|re	4	6	11.00%	536	60030	5	karyopherin alpha 6 [Homo sapiens]				
*	HsFlag-FLJ90652_2	5.0192	0.4673	2090.83	2091.462	7644.9	1	1685.7	67.6	2	R.DYVLNCSILNPLLTLLTK.S
	HsFLAG-TIP49a_Ti_	3.4162	0.2619	1393.24	1392.617	5742.1	1	859.8	72.7	1	K.PLCDLLTVMDSK.I
	HsFLAG-Lin9_Ti_20	5.0013	0.2717	1553.05	1552.858	10861.1	1	2767	80.8	2	K.IVQVALNGLENILR.L
	HsFlag-FLJ90652_2	4.8161	0.3707	1909.07	1907.09	9756.6	1	2054.1	75	1	K.IEFLQSHENQEIYQK.A
gi|25777602|r	7	18	10.90%	908	100200	5.2	proteasome 26S non-ATPase subunit 2 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.8778	0.2656	2218.74	2219.416	7186.5	1	1252.9	36.4	2	K.APVQPQQSPAAAPGGTDEKPSGK.E
*	HsFLAG-TIP49b_Ti_	4.4283	0.3958	2218.85	2219.416	7381.6	1	888.5	47.7	1	K.APVQPQQSPAAAPGGTDEKPSGK.E
*	HsFlag-VPS71_Ti_1	2.9699	0.3226	1960.86	1961.141	7346.4	1	576.8	43.8	2	R.LVGSQEELASWGHEYVR.H
*	HsFlag-FLJ90652_2	2.841	0.2702	1167.66	1168.208	7256	1	986.2	77.3	2	R.FGGSGSQVDSAR.M
*	HsFLAG-ARP6_Ti_1	3.5258	0.2868	1038.01	1038.235	5466.4	1	1302.7	94.4	2	R.LAQGLTHLGK.G
*	HsFlag-FLJ90652_2	4.8218	0.3492	1453.26	1453.682	7097	1	1679.9	78.6	7	R.VGQAVDVVGQAGKPK.T
*	HsFlag-VPS71_Ti_1	3.7639	0.3148	2460.21	2458.901	3355.5	4	245.1	38.1	2	R.AELATEEFLPVTPILEGFVILR.K
gi|21614499|r	6	14	10.90%	586	69413	6.3	villin 2 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	5.1741	0.4016	2038.17	2039.246	6427.1	1	1579.1	75	5	K.FYPEDVAEELIQDITQK.L
	HsFLAG-p53-DNA-D	2.5927	0.1817	1105.13	1105.282	3983.4	2	598.4	87.5	1	K.IGFPWSEIR.N
	HsFLAG-p53-DNA-D	3.082	0.2462	1310.92	1311.526	4859.6	1	673.5	75	2	K.KAPDFVFYAPR.L
	HsFlag-VPS71_Ti_1	4.0952	0.4189	1184.54	1183.352	5649.2	1	979.7	83.3	2	K.APDFVFYAPR.L
	HsFlag-VPS71_Ti_1	3.4434	0.2393	1473.57	1473.731	4190	1	702.4	81.8	3	R.RKPDTIEVQQMK.A
*	HsFLAG-FLJ20729_	4.2273	0.4108	1652.6	1652.799	6881.1	1	1491.1	71.4	1	K.SQEQLAAELAEYTAK.I
gi|5729842|re	1	2	10.90%	184	20720	5.5	glyoxalase I [Homo sapiens]				
*	HsFLAG-FLJ20729_	3.6793	0.325	2303.61	2304.607	5769.4	1	652.9	52.6	2	K.GLAFIQDPDGYWIEILNPNK.M
gi|23308577|r	3	5	10.70%	533	56651	6.7	phosphoglycerate dehydrogenase [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	3.2663	0.3423	2048.02	2049.257	8832.2	1	901.2	50	1	R.ALVDHENVISCPHLGASTK.E
*	HsFLAG-ARP6_Ti_1	3.9403	0.3677	1627.69	1626.903	5242.6	2	722.8	60	3	K.NAGNCLSPAVIVGLLK.E
*	HsFLAG-p53-DNA-D	3.4955	0.2113	2275.91	2273.668	8091	1	729.7	47.6	1	R.TQTSDPAMLPTMIGLLAEAGVR.L
gi|21264351|r	3	5	10.70%	475	54184	9.5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin d2 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.1559	0.3608	2733.76	2734.128	8505.9	1	750.5	28.1	1	K.LAGLLQHPDPIVINHVISVDPNDQK.K
*	HsFLAG-p53-DNA-D	3.5408	0.2051	1731.99	1731.911	4628.8	2	696.1	64.3	2	R.AAFYHQPWAQEAVGR.H
*	HsFLAG-Lin9_Ti_20	3.2849	0.2464	1341.14	1341.553	9785.7	2	852.1	65	2	R.RQELEQVLGIR.L
gi|4759100|re	4	13	10.70%	484	53542	10.5	splicing factor p54 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.9985	0.1503	2370.14	2369.599	9159.2	1	745.2	45	1	K.FHDPDSAVVAQHLTNTVFVDR.A
*	HsFlag-VPS71_Ti_1	3.8541	0.2992	1786.93	1785.09	3940.2	1	724.7	62.5	3	R.ALIVVPYAEGVIPDEAK.A
*	HsFlag-VPS71_Ti_1	3.8824	0.3346	1406.66	1406.668	5113.4	1	900.5	73.1	2	K.LNHVAAGLVSPSLK.S

*	HsFlag-NUFIP_Ti_11	4.0343	0.3136	1407.28	1406.668	6103.1	1	1007.4	69.2	7	K.LNHVAAGLVSPSLK.S
gi|23397429|r	3	5	10.70%	374	42503	5.6	B5 receptor [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	2.8413	0.2224	1517.38	1516.799	8786.1	2	677.6	58.3	1	R.LQLLSNLFHGMDK.N
*	HsFLAG-Lin9_Ti_20	5.0311	0.4646	2047	2046.414	6561.5	1	1223.2	61.8	3	K.FLEGELIHDLLTIFVSAK.L
*	HsFlag-VPS71_Ti_1	2.539	0.2525	1022.45	1022.152	4907.7	1	779.9	81.2	1	K.VVVSHSTHR.T
gi|51479192|r	3	5	10.60%	406	42429	5.6	ring finger protein 1 [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.5612	0.1582	1573.08	1573.789	5002.7	4	434.1	53.8	3	R.SLRPDPNFDALISK.I
*	HsFLAG-TCF3_Ti_1	3.4395	0.3901	1783.22	1782.951	7154.1	1	805.3	63.3	1	R.LHNQQALSSSIEEGLR.M
*	HsFLAG-TCF3_Ti_1	3.1131	0.1647	1534.15	1534.762	4224	1	427	58.3	1	K.VSRPLELCYAPTK.D
gi|22547136|r	2	4	10.60%	311	34919	9.7	mitochondrial ribosomal protein L4 isoform a [Homo sapiens]				
gi|22547138|r	2	4	10.60%	311	34919	9.7	mitochondrial ribosomal protein L4 isoform a [Homo sapiens]				
	HsFlag-NUFIP_Ti_1	4.0413	0.3419	1679.57	1679.916	4102	1	1045	73.3	2	R.VGLADLHPDVFATAPR.L
	HsFLAG-ARP6_Ti_1	3.7272	0.2904	1926.02	1926.263	7065.9	1	830.8	56.2	2	K.HQTLVLTLPTVAFLEDK.L
gi|21265084|r	2	2	10.60%	303	34453	8.1	mitochondrial ribosomal protein L1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.7848	0.2105	1325.01	1324.563	7324.2	3	674.8	65	1	K.KFQILDFTSPK.Q
*	HsFLAG-ARP6_Ti_1	3.0728	0.3147	2352.34	2353.677	5739.8	1	383.7	40	1	K.NVEPFTSVLSLPYPFASEINK.V
gi|4758788|re	2	2	10.60%	264	30242	7.5	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase) [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.2611	0.4394	1554.03	1552.729	8127.5	1	1180.8	66.7	1	R.ILTDYGFEGHPFR.K
*	HsSrcap_Ti_204.327	2.9432	0.2699	1869.92	1870.117	8607.7	3	476.1	46.4	1	R.KFDLNSPWEAFPVYR.Q
gi|56549119|r	6	12	10.50%	866	97652	7.6	dynamin 2 isoform 3 [Homo sapiens]				
gi|56549121|r	6	12	10.50%	870	98064	7.5	dynamin 2 isoform 1 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	5.4719	0.3074	2984.84	2985.29	9993.2	1	1890.9	33	3	K.LQDAFSSIGQSCHLDLPQIAVVGGQSAGK.S
	HsFLAG-Lin9_Ti_20	3.1219	0.3454	1271.87	1272.369	6897.2	1	779.9	72.2	1	K.TEHAEFLHCK.S
	HsFLAG-Lin9_Ti_20	3.0938	0.3188	1698.37	1698.913	5841.8	1	1047.5	67.9	1	K.VPVGDQPPDIEYQIK.D
	HsFLAG-Lin9_Ti_20	3.2367	0.3029	1337.8	1338.509	7309.4	1	873.8	75	2	K.TLNQQLTNHIR.E
	HsFLAG-Lin9_Ti_20	3.0271	0.3096	1623.38	1622.902	4172	1	538.5	64.3	1	R.TGLFTPDLAFEAIVK.K
	HsFLAG-Lin9_Ti_20	3.6557	0.2565	1362.44	1362.531	5007.3	1	953.8	85	4	K.HVFAIFNTEQR.N
gi|5032067|re	1	2	10.50%	153	17561	9.4	Sin3A-associated protein, 18kDa [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	3.6432	0.2977	1834.21	1834.082	7663.6	1	1053.3	60	2	K.FQIGDYLDIAITPPNR.A
gi|27597090|r	8	12	10.40%	1726	199071	4.9	suppressor of Ty 6 homolog [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.3536	0.3686	2586	2586.725	10965.5	1	1218.7	45.2	1	R.TSFDDRLEDDDFDLIEENLGVK.V
*	HsFlag-NUFIP_Ti_1	2.5463	0.2336	3113.07	3112.33	9215.6	3	315.2	25	1	K.LPGYTDAALQEAQEIFGVDFDYDEFEK.Y
*	HsFlag-NUFIP_Ti_1	3.2416	0.3497	1668.09	1668.895	7421.2	1	1238.2	75	2	R.NQHFEVPFIAFYR.K
*	HsARP6-FLAG_Ti_1	4.807	0.4113	1537.35	1536.635	7420.4	1	2171.2	87.5	2	K.DLDLDAFAEELER.Q
*	HsFlag-NUFIP_Ti_1	3.1889	0.3412	1366.97	1367.601	8603.5	1	1028.4	68.2	2	K.LIICNVTGIAHR.R
*	HsFlag-NUFIP_Ti_1	5.2543	0.3866	4654.92	4656.877	8960.6	1	960.8	23.1	2	VK.T
*	HsFLAG-UTX1_Ti_2	3.8119	0.373	2211.56	2211.483	6055.4	1	713	55	1	R.TRTPASINATPANINLADLTR.A
*	HsFlag-NUFIP_Ti_1	4.6752	0.3239	3327.81	3327.807	8406.3	1	881.9	26.7	1	R.LTPRPSPSPMIESTPMSIAGDATPLLDEMDR.-
gi|21361368|r	5	9	10.40%	795	87302	7.1	pyrroline-5-carboxylate synthetase isoform 1 [Homo sapiens]				
gi|62912457|r	5	9	10.50%	793	87089	7.1	pyrroline-5-carboxylate synthetase isoform 2 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	4.4247	0.3317	2505.98	2504.75	8116.8	1	938.5	43.5	4	K.TDLLIVLSDVEGLFDSPPGSDDAK.L
	HsFLAG-FLJ20729_	3.5756	0.3643	2029.78	2030.285	4087.7	1	626.3	58.8	2	K.LIDIFYPGDQQSVTFGTK.S
	HsFLAG-Lin9_Ti_20	3.1775	0.3066	1355.72	1354.546	9254.3	1	1029.9	62.5	1	K.VSGHVITDIVEGK.K

	HsFLAG-FLJ20729_	5.0129	0.4178	1772.64	1773.129	7509.3	1	1724.2	73.3	1	R.ILHLLTQEALSIHGVK.E
	HsFLAG-FLJ20729_	3.1173	0.1932	1462.41	1462.747	6377.1	1	677.3	63.6	1	R.TPLFDQIIDMLR.V
gi|4757790|re	4	5	10.40%	628	68683	5.7	ash2 (absent, small, or homeotic)-like [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	2.8687	0.3707	2108.31	2109.3	5086.2	1	379.7	44.4	1	K.FGLLDQDLSNIGPAYDNQK.Q
*	HsFLAG-FLJ20729_	3.8066	0.2217	1474.36	1474.79	9276.4	1	1051.3	66.7	1	R.VLLALHDRAPQLK.I
*	HsScrap_Ti_103.290	3.6102	0.3697	1957.87	1958.224	4645.6	1	525.8	52.9	2	R.LGWSQPLGNLQAPLGYDK.F
*	HsFLAG-FLJ20729_	2.5013	0.3651	1762.41	1763.043	5665.6	1	594	57.1	1	K.DIFEGVYFPAISLYK.S
gi|18201905|r	4	10	10.40%	558	63147	8.3	glucose phosphate isomerase [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	5.11	0.4322	1833.97	1833.135	4104	1	1038.3	71.9	4	K.TLAQLNPESSLFIIASK.T
*	HsFlag-VPS71_Ti_1	3.2089	0.2735	1219.47	1219.383	6166.6	1	1195.5	85	3	K.HFVALSTNTTK.V
*	HsFlag-VPS71_Ti_1	4.2453	0.4023	1706.09	1705.069	7340.7	1	1211.6	67.9	1	K.ILLANFLAQTEALMR.G
*	HsFLAG-p53-DNA-D	3.1696	0.2595	1709.56	1709.943	6618.9	1	849.2	64.3	2	K.VFEGNRPTNSIVFTK.L
gi|8923900|re	3	14	10.40%	434	48379	7.9	cytidine 5'-monophosphate N-acetylneuraminic acid synthetase [Homo sapiens]				
*	HsFLAG-FLJ20729_	2.9876	0.2139	1585.09	1585.933	3559.5	1	470.6	60.7	3	R.GVEKPPHLAALILAR.G
*	HsFLAG-p53-DNA-D	3.8234	0.3455	1431.76	1431.767	4996.3	1	1207.5	87.5	4	K.HLAGVPLIGWVLR.A
*	HsFLAG-FLJ20729_	4.8034	0.4211	1690.26	1689.832	6784.4	1	1409.3	71.9	7	K.RVGLSGAPADACSTAQK.A
gi|17158023|r	1	2	10.40%	230	25456	11.1	hypothetical protein LOC85395 [Homo sapiens]				
*	HsYL1-FLAG_Ti_20	3.4849	0.4636	2109.96	2110.331	5062.1	1	434.9	43.5	2	K.GEAAPGPAPPAPEATPPPASAAGK.D
gi|4503747|re	17	42	10.30%	2602	278193	5.7	filamin B, beta (actin binding protein 278) [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.3406	0.3465	1227.4	1227.53	5275.5	1	1365.1	90	13	R.LIALLEVLSQK.R
	HsFLAG-p53-DNA-D	3.4629	0.0813	972.27	972.175	2910.7	4	584.7	92.9	2	R.LLGWIQNK.I
*	HsFlag-VPS71_Ti_1	4.6192	0.4871	2048.22	2049.293	4304.6	1	1004.8	71.9	3	K.IPYLPITNFNQNWQDGK.A
*	HsFlag-VPS71_Ti_1	3.3623	0.2905	1657.69	1657.654	8924	1	1444.5	69.2	1	K.IEYNDQNDGSCDVK.Y
*	HsARP6-FLAG_Ti_1	2.829	0.115	1563.24	1562.809	5048.8	1	458.6	53.8	2	K.VLFASQEIPASPFR.V
*	HsFlag-VPS71_Ti_1	3.5127	0.333	1502.89	1502.751	5467.9	1	762.8	60.7	1	K.SPFTVGVAAPLDLSK.I
*	HsFlag-VPS71_Ti_1	2.6752	0.2912	1150.65	1151.308	4981.9	1	374	59.1	1	K.VVASGPGLEHGK.V
*	HsFlag-VPS71_Ti_1	3.0844	0.2722	1151.54	1151.308	7903.2	1	1634.3	86.4	2	K.VVASGPGLEHGK.V
*	HsFlag-VPS71_Ti_1	4.3539	0.3557	2228.7	2227.522	7038.4	1	1346.9	57.9	2	K.GLHVVEVTYDDVPIPNSPFK.V
*	HsFlag-VPS71_Ti_1	3.9396	0.2999	2548.87	2548.855	4019.7	1	463.2	42	2	K.VTASGPGLSSYGVPASLPVDFAIDAR.D
*	HsFLAG-ARP6_Ti_1	3.15	0.4221	1342.99	1343.476	7496	1	1011.6	68.2	2	K.DGTYAVTYIPDK.T
*	HsFlag-VPS71_Ti_1	2.6776	0.1757	2314.72	2314.604	4237.4	3	240.8	35	1	K.DGTCTVTYLPTLPGDYSILVK.Y
*	HsFlag-VPS71_Ti_1	4.1548	0.3337	2470.41	2468.761	6202.5	1	610.8	41.3	3	K.LGSAADFLLDISETDLSSLTASIK.A
*	HsFLAG-Lin9_Ti_20	3.5078	0.2965	1634.51	1634.925	9134.3	1	2127.1	84.6	2	K.RLPNNHIGISFIPR.E
*	HsFLAG-Lin9_Ti_20	4.715	0.4717	1645.64	1645.86	4993.5	1	797.2	63.3	1	R.APSVATVGSICDLNLK.I
*	HsFLAG-p53-DNA-D	5.2767	0.364	2309.51	2309.546	6714.6	1	1231.1	38.6	2	R.GQHVTGSPFQFTVGPLGEGGAHK.V
*	HsFLAG-ARP6_Ti_1	3.0376	0.2058	2273.29	2273.427	6012.1	1	690.3	45	2	K.NGSCGVSYIAQEPGNYEVSIK.F
gi|7656991|re	2	7	10.30%	474	53249	7.1	coronin, actin binding protein, 1C [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.2331	0.3686	2441.98	2441.656	6578.1	1	683.5	47.4	1	R.YFEITDESPYVHYLNTFSSK.E
*	HsFLAG-p53-DNA-D	5.6925	0.3589	3272.05	3273.49	9159.8	1	1679.5	33	6	R.KSDLFQDDLYPDTAGPEAALEAEEWFEGK.N
gi|7657647|re	1	3	10.30%	351	39595	5.3	tropomodulin 2 (neuronal) [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	5.2422	0.2601	3835.86	3837.273	6833.1	1	653.7	22.1	3	K.VTLDPELEEALASASDTELYDLAAVLGVHNLLNNPK.F
gi|8923405|re	2	4	10.30%	252	29591	9.2	RNA (guanine-9-) methyltransferase domain containing 1 [Homo sapiens]				
*	HsSrcap_Ti_204.301	2.8934	0.4203	1667.29	1667.871	7709.3	1	1093.9	66.7	1	R.NVDPFHIYFCNLK.I

*	HsSrcap_Ti_204.205	4.2104	0.2913	1543.53	1543.77	5382.2	1	1226.7	83.3	3	K.RLNLATECLPLDK.Y
gi|4502787|re	1	2	10.30%	116	13075	8.2	glycoprotein hormones, alpha polypeptide precursor [Homo sapiens]				
*	HsYL1_Ti_101.1286.	3.1348	0.274	1357.36	1356.405	5565.1	1	1438.8	86.4	2	K.NVTSESTCCVAK.S
gi|18034690|r	2	4	10.20%	384	43472	6	hypothetical protein LOC25980 [Homo sapiens]				
*	HsFlag-ZnF-HIT2_Ti_	5.9212	0.3971	2182.14	2182.481	5452.5	1	920.6	61.1	2	R.ANLQELDQFLGPYPYATLK.K
*	HsFlag-ZnF-HIT2_Ti_	4.7579	0.512	2194.86	2195.492	5376.2	1	884	57.9	2	R.FSELPTQMFPEGATPAEITK.H
gi|4505753|re	3	4	10.20%	254	28804	7.2	phosphoglycerate mutase 1 (brain) [Homo sapiens]				
gi|89036296|r	3	4	11.40%	228	25881	6.3	PREDICTED: similar to Phosphoglycerate mutase 1 (Phosphoglycerate mutase isozyme B) (PGAM-B) (BPG-				
gi|89036292|r	3	4	10.20%	254	28804	7.2	PREDICTED: similar to Phosphoglycerate mutase 1 (Phosphoglycerate mutase isozyme B) (PGAM-B) (BPG-				
gi|89035672|r	3	4	10.20%	254	28850	7.2	PREDICTED: similar to Phosphoglycerate mutase 1 (Phosphoglycerate mutase isozyme B) (PGAM-B) (BPG-				
gi|89035650|r	3	4	11.40%	228	25881	6.3	PREDICTED: similar to Phosphoglycerate mutase 1 (Phosphoglycerate mutase isozyme B) (PGAM-B) (BPG-				
gi|89035644|r	3	4	10.20%	254	28804	7.2	PREDICTED: similar to Phosphoglycerate mutase 1 (Phosphoglycerate mutase isozyme B) (PGAM-B) (BPG-				
gi|50593010|r	3	4	10.30%	253	28766	8.9	phosphoglycerate mutase 2 (muscle) [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.1016	0.2069	1685.17	1684.976	5090.6	3	621	65.4	2	R.ALPFWNEEIVPQIK.E
	HsFLAG-FLJ20729_	3.2529	0.3346	1306.89	1307.542	7976.6	1	874.5	68.2	1	K.RVLIAAHGNSLR.G
	HsH2AZ-FLAG_293_	3.2734	0.2751	1151.29	1151.354	5397.7	1	1002.2	80	1	R.VLIAAHGNSLR.G
gi|54112390|r	6	14	10.10%	1091	123183	5.2	calcium channel, voltage-dependent, alpha 2/delta subunit 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.7728	0.3476	1537.77	1537.71	8588.7	1	1112.7	65.4	1	K.TASGVNQLVDIYEK.Y
*	HsFLAG-ARP6_Ti_1	3.325	0.3491	1506.25	1506.745	3505.4	1	754.7	79.2	3	R.IKPVFIEDANFGR.Q
*	HsFLAG-ARP6_Ti_1	3.5043	0.2891	2231.35	2233.588	11501.2	1	913.5	47.4	1	R.INTQEYLDVLGRPMVLAGDK.A
*	HsFLAG-ARP6_Ti_1	3.3679	0.4651	1943.74	1944.294	9898.9	1	797.6	50	1	K.NQLILGVMGVDVSLEDIK.R
*	HsFLAG-ARP6_Ti_1	4.1009	0.2399	3153.52	3153.573	5077.8	1	444.6	25	2	R.FTLCPNGYYFAIDPNGYVLLHPNLQPK.N
*	HsFLAG-ARP6_Ti_1	5.1105	0.3739	2098.03	2098.363	9210.6	1	1783.3	64.7	6	R.VLLDAGFTNELVQNYWSK.Q
gi|33457332|r	2	3	10.10%	606	63877	8.5	RAVER1 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	3.8915	0.2974	4425.41	4425.992	6146.5	1	521.5	21.7	2	C
*	HsFLAG-Lin9_Ti_20	5.3801	0.3446	2388.41	2389.603	8862.8	1	1938.1	41.7	1	R.ALSAVHSPTFCQLACGQDGQLK.G
gi|7705284|re	4	6	10.10%	565	63177	5.8	anaphase-promoting complex subunit 7 [Homo sapiens]				
*	HsSrcap_Ti_204.177	2.6163	0.217	2572.71	2573.786	8789.6	2	564.6	34.8	1	K.VRPSTGNSASTPQSQCLPSEIEVK.Y
*	HsFlag-VPS71_Ti_1	5.0016	0.1834	2573.29	2573.786	6478	1	920.1	31.5	2	K.VRPSTGNSASTPQSQCLPSEIEVK.Y
*	HsFlag-VPS71_Ti_1	3.2714	0.3953	1912.02	1912.287	8108.2	1	799.9	52.9	1	R.QCPLALDAILGLLSLSVK.G
*	HsFLAG-FLJ20729_	5.0869	0.4424	1711.52	1711.912	8616.3	1	2445.6	82.1	2	R.DNVDLLGSLADLYFR.A
gi|38570081|r	2	3	10.10%	483	51617	8.5	CUG triplet repeat, RNA-binding protein 1 isoform 2 [Homo sapiens]				
gi|71164871|r	2	3	10.10%	486	52063	8.5	CUG triplet repeat, RNA-binding protein 1 isoform 3 [Homo sapiens]				
gi|5729794|re	2	3	10.20%	482	51546	8.5	CUG triplet repeat, RNA-binding protein 1 isoform 1 [Homo sapiens]				
	HsFlag-VPS71_Ti_1	3.5842	0.2416	1411.36	1411.619	7731	1	1263.3	70.8	1	K.AALEAQNALHNMK.V
	HsFlag-VPS71_Ti_1	5.9255	0.3702	4040.47	4041.585	8185.6	1	1364.5	27.9	2	K.EGPEGANLFIYHLPQEFGDQDLLQMFMPFGNVVSAK.V
gi|13899231|r	2	3	10.10%	267	30243	10.1	mitochondrial ribosomal protein L9 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.2047	0.3236	1601.13	1600.855	4270.2	1	570.2	67.9	1	R.LLPQGLAVYASPENK.K
*	HsFLAG-ARP6_Ti_1	3.5868	0.2441	1248.16	1248.511	5754	1	1038.5	77.3	2	K.NLGVVVAPHTLK.L
gi|4505317|re	6	11	10.00%	1030	115281	5.4	protein phosphatase 1, regulatory (inhibitor) subunit 12A [Homo sapiens]				
*	HsSrcap_Ti_204.180	2.9233	0.2736	1440.02	1439.574	4992.9	1	519.7	68.2	1	R.QWLNSGHINDVR.H
*	HsFLAG-Lin9_Ti_20	2.7263	0.2685	1826.31	1825.98	7058.3	1	779.7	56.7	1	K.DYDGWTPLHAAAHWGK.E
*	HsSrcap_Ti_202.497	6.5588	0.4051	2453.38	2454.693	8262.1	1	2419.8	64.3	4	K.VGQTAFDVADEDILGYLEELQK.K

*	HsSrcap_Ti_202.497	5.2552	0.279	2454.42	2454.693	7914.3	1	1139.2	34.5	2	K.VGQTAFDVADEDILGYLEELQK.K
*	HsSrcap_Ti_205.202	5.2302	0.3044	3782.98	3784.213	6212.4	1	1063.9	27.6	2	K.TKPLASVTNANTSSTQAAPVAVTTPTVSSGQATPTSPIK.K
*	HsSrcap_Ti_202.007	2.1395	0.2403	1368.44	1369.514	6462.5	1	628.7	61.5	1	K.TGSYGALAEITASK.E
gi|21361734|r	4	14	10.00%	791	83296	9.4	hypothetical protein LOC55683 [Homo sapiens]				
*	HsFLAG-FLJ20436_	3.5147	0.3112	1315.32	1315.553	6041.2	1	1373.6	80.8	8	K.TGAAGAEALSLLLK.R
*	HsFLAG-FLJ20436_	3.705	0.2601	2270.77	2271.619	6473.6	1	721.9	43.2	2	K.LPGSPLILIASSGPSSSVFPTSR.R
*	HsFLAG-FLJ20436_	5.5572	0.5482	2205.39	2205.337	7538	1	1539.2	56.8	1	K.LPASPSGSEDLSSVSSSPTSSPK.T
*	HsFLAG-FLJ20436_	2.637	0.2502	1856.57	1856.13	4010.5	2	311	44.4	3	K.LASSLPGLAQISNQASGLK.V
gi|4826686|re	6	27	10.00%	740	82432	7.2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1 [Homo sapiens]				
*	HsFLAG-FLJ20309_	2.7305	0.2501	1881.44	1880.235	3573.5	1	405	56.2	2	K.TGAFSIPVIQIVYETLK.D
*	HsFLAG-FLJ20729_	6.0273	0.4328	2372.56	2373.624	9257.3	1	2296.6	43.8	3	R.FLVLDEADGLLSQGYSDFINR.M
*	HsFLAG-p53-DNA-D	5.1215	0.5067	2373.13	2373.624	9600.9	1	1580.2	57.5	12	R.FLVLDEADGLLSQGYSDFINR.M
*	HsFlag-VPS71_Ti_1	3.9975	0.2691	1907.36	1905.202	3758.5	1	576.9	58.8	5	K.GHVDILAPTVQELAALEK.E
*	HsFLAG-p53-DNA-D	4.0412	0.2181	2135.5	2135.43	5529.7	1	1107.3	44.1	1	K.EAQTSFLHLGYLPNQLFR.T
*	HsFLAG-p53-DNA-D	4.6455	0.4424	2135.66	2135.43	7262	1	982.3	50	4	K.EAQTSFLHLGYLPNQLFR.T
gi|19923502|r	3	4	10.00%	490	52513	10.5	GATA zinc finger domain containing 2A [Homo sapiens]				
*	HsSrcap_Ti_202.006	3.1678	0.2142	2738.13	2737.894	7971.4	2	421.3	32.1	1	K.GTTATSAQANSTPTSVASVVTSAESPASR.Q
*	HsSrcap_Ti_205.267	4.064	0.4234	1983.77	1984.303	8272.6	1	870.8	47.4	2	K.TPLSTGGTLAFVSPSLAVHK.S
*	HsSrcap_Ti_205.266	5.3011	0.3645	1984.84	1984.303	6197.3	1	1146.3	40.8	1	K.TPLSTGGTLAFVSPSLAVHK.S
gi|5453682|re	1	2	10.00%	359	40623	4.9	HMBA-inducible [Homo sapiens]				
*	HsSrcap_Ti_204.224	4.8487	0.3027	3836.48	3837.127	6109.4	1	1001.1	28.6	2	R.AFPQLGGRPGPEGEGSLESQPPPLQTQACPESSCLR.E
gi|16751921|r	1	2	10.00%	110	11284	6.5	dermcidin precursor [Homo sapiens]				
*	HsH2AZ-FLAG_293_	2.7978	0.2124	1129.3	1129.172	5168.7	1	895.4	80	2	K.ENAGEDPGLAR.Q
gi|24308085|r	3	7	9.90%	545	62717	6.1	monooxygenase, DBH-like 1 isoform 2 [Homo sapiens]				
gi|72534688|r	3	7	8.80%	613	69653	6.3	monooxygenase, DBH-like 1 isoform 1 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	5.0148	0.4776	2532.23	2532.896	3968.1	1	700.2	54.5	2	K.TSVLSTALPYFDLVNQDVPIPNK.D
	HsFLAG-ARP6_Ti_1	2.9767	0.2319	1949.88	1950.267	3622.2	1	493.7	59.4	1	R.CASIPDIMEQLQFIGVK.E
	HsFLAG-ARP6_Ti_1	3.8403	0.2483	1764.11	1764.12	7029	1	1054	65.4	4	K.EIYRPVTTWPFIIK.S
gi|24308009|r	2	3	9.90%	272	30369	6.6	methionyl aminopeptidase 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.697	0.3306	1777.13	1777.94	4005.4	1	525.4	61.5	1	R.NCYPSPLNYYNFPK.S
*	HsFLAG-ARP6_Ti_1	2.8307	0.13	1495.28	1495.724	5589.3	2	643.3	66.7	2	K.LFHTAPNVPHYAK.N
gi|37544743|r	1	2	9.90%	101	11741	11.3	PREDICTED: similar to 60S ribosomal protein L35 [Homo sapiens]				
gi|89057079|r	1	2	7.40%	136	15556	10.6	PREDICTED: similar to 60S ribosomal protein L35 [Homo sapiens]				
gi|89050566|r	1	2	7.40%	136	15556	10.6	PREDICTED: similar to 60S ribosomal protein L35 [Homo sapiens]				
gi|89037172|r	1	2	9.90%	101	11741	11.3	PREDICTED: similar to 60S ribosomal protein L35 [Homo sapiens]				
gi|6005860|re	1	2	8.10%	123	14551	11	ribosomal protein L35 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.3496	0.1776	1144.39	1144.357	7264.4	1	1285.3	88.9	2	R.VLTVINQTQK.E
gi|4507943|re	6	10	9.80%	1071	123386	6.1	exportin 1 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.0457	0.2733	2542.52	2542.777	5392.4	1	1422.9	44	1	K.LDINLLDNVVNCLYHGEGAQQR.M
*	HsFlag-FLJ90652_2	3.1333	0.2112	1170.76	1170.412	8248.7	1	1459.1	88.9	1	R.MAQEVLTHLK.E
*	HsFlag-VPS71_Ti_1	4.7147	0.4991	2149.99	2149.513	3904.1	1	738.3	64.7	4	K.YMLLPNQVWDSIIQQATK.N
*	HsFlag-VPS71_Ti_1	3.8225	0.303	2888.82	2888.293	6917.4	2	499.5	34	2	K.ISTSLNPGNPVNNQIFLQEYVANLLK.S
*	HsFlag-VPS71_Ti_1	3.1547	0.1972	1341.67	1341.509	6439.3	1	980	72.7	1	K.SAFPHLQDAQVK.L

*	HsFLAG-p53-DNA-D	3.2159	0.3267	1911.28	1911.251	6247.9	1	902.3	59.4	1	K.LFVTGLFSLNQDIPAFK.E
gi|21361181|r	8	13	9.80%	1023	112896	5.5	Na+/K+ -ATPase alpha 1 subunit isoform a proprotein [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.1708	0.2909	1106.13	1106.267	7553.7	9	1098.3	77.8	1	K.TSATWLALSR.I
	HsFLAG-ARP6_Ti_1	4.1322	0.2809	1585.15	1585.844	5336.2	1	1170.4	76.9	3	R.AVFQANQENLPILK.R
	HsFLAG-ARP6_Ti_1	3.672	0.3231	1610.01	1608.853	5790.1	1	882.3	69.2	2	K.NPNTSEPQHLLVMK.G
	HsFLAG-ARP6_Ti_1	3.8026	0.338	1753.08	1753.909	9046	1	1867.4	70	2	K.DAFQNAYLELGGLGER.V
	HsFLAG-ARP6_Ti_1	3.8098	0.393	1382.25	1382.661	6390.6	1	1135.2	75	2	K.VIMVTGDHPITAK.A
	HsFLAG-ARP6_Ti_1	3.3556	0.3146	1239.06	1237.445	3331.7	1	702.3	85	1	R.LNIPVSQVNPR.D
	HsFLAG-ARP6_Ti_1	3.1901	0.1796	1086.34	1086.199	3516	3	648.9	77.8	1	K.ACVVHGSDLK.D
*	HsFLAG-ARP6_Ti_1	4.0016	0.2496	1408.11	1408.563	7982.1	1	1331.8	77.3	1	K.DMTSEQLDDILK.Y
gi|42544159|r	6	18	9.80%	858	96865	5.4	heat shock 105kD [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	5.3452	0.4229	1716.55	1716.851	8806.7	1	2406.1	82.1	9	K.NQQITHANNTVSNFK.R
*	HsFLAG-ARP6_Ti_1	2.6511	0.2296	1322.17	1322.547	7070.1	1	822.1	66.7	1	K.VLGTAFDPFLGGK.N
	HsFLAG-ARP6_Ti_1	5.0602	0.396	1537.59	1536.744	7693	1	1948.6	80.8	4	R.GCALQCAILSPAFK.V
	HsFlag-FLJ90652_2	2.0861	0.2198	871.37	871.971	2993.4	2	294.8	78.6	1	R.NHAAPFSK.V
*	HsFLAG-ARP6_Ti_1	3.2619	0.2894	2021.28	2022.395	4828.5	1	601.2	52.9	1	K.VVNVELPIEANLVWQLGK.D
*	HsFLAG-ARP6_Ti_1	3.9855	0.3175	1854.09	1855.064	6518.9	1	924.3	63.3	2	K.ELNNTCEPVVTQPKPK.I
gi|17388799|r	2	3	9.80%	326	36087	9.1	DnaJ (Hsp40) homolog, subfamily B, member 6 isoform a [Homo sapiens]				
gi|4885495|re	2	3	13.30%	241	26900	7.6	DnaJ (Hsp40) homolog, subfamily B, member 6 isoform b [Homo sapiens]				
	HsFlag-Ies6_293_Ti_	3.1919	0.3696	1423.4	1423.563	3866.6	1	506.9	70.8	1	K.QVAEAYEVLSDAK.K
	HsFLAG-TCF3_Ti_1	5.2819	0.4197	2376.47	2376.499	6500.8	1	1470.6	63.9	2	R.DPFSFDFFEDPFEDFFGNR.R
gi|68160937|r	4	7	9.70%	630	70974	8.1	tripartite motif-containing 25 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.0825	0.3746	2091.1	2091.338	8765.3	1	753.5	52.9	2	K.NTVLCNVVEQFLQADLAR.E
*	HsSrcap_Ti_203.474	5.3965	0.474	3407.41	3408.805	8387.2	1	1728.7	32.8	3	K.NTVLCNVVEQFLQADLAREPPADVWTPPAR.A
*	HsSrcap_Ti_203.147	3.169	0.3677	1827.46	1826.936	6971.9	1	794.9	59.4	1	R.ASAPSPNAQVACDHCLK.E
*	HsFlag-VPS71_Ti_1	2.7266	0.152	1528.65	1528.789	5532.7	1	892.4	65.4	1	K.LPTFGAPEQLVDLK.Q
gi|64368880|r	2	2	9.70%	544	61475	7.7	zinc finger protein 498 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	4.4344	0.3631	2274.11	2274.628	7121.2	1	815.9	47.6	1	R.AFQEQALPVLQAGPGLPAVNPR.D
*	HsFlag-NUFIP_Ti_1	4.0361	0.2761	3101.96	3103.425	4874	1	604.4	27.5	1	R.VCEQEPGGPAGSAPGLPPPQHGAIPLPDEVK.T
gi|21361282|r	5	11	9.70%	494	56678	11.5	splicing factor, arginine/serine-rich 4 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.5009	0.1095	1434.48	1432.532	6839.9	1	1239.3	77.3	6	K.NGYGFVEFDDLR.D
	HsFLAG-ARP6_Ti_1	3.1669	0.2486	1309.13	1310.36	6762.5	1	593.7	59.1	1	R.DADDAVYELNGK.D
	HsFLAG-ARP6_Ti_1	4.2565	0.1753	1309.27	1310.36	4682.8	1	1253	86.4	2	R.DADDAVYELNGK.D
*	HsFlag-NUFIP_Ti_1	2.6215	0.1725	1618.24	1618.799	6266.2	1	483.9	61.5	1	K.NEGVIEFVSYSDMK.R
*	HsFlag-NUFIP_Ti_1	2.5587	0.1543	1114.89	1115.231	3435.1	3	434.5	72.2	1	K.SKPNLPSESR.S
gi|4502801|re	2	2	9.70%	421	44969	7.5	regulator of chromosome condensation 1 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.9627	0.4409	2864.58	2866.312	6216.9	1	1263.2	35.6	1	R.KKPALVSIPEDVVQAEAGGMHTVCLSK.S
*	HsFLAG-p53-DNA-D	2.6681	0.1266	1528.58	1528.807	8069.3	1	639	50	1	R.DNNGVIGLLEPMKK.S
gi|21361454|r	2	2	9.70%	320	33637	7.8	pyrroline-5-carboxylate reductase family, member 2 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.5805	0.1697	1599.28	1599.808	3906	1	386.4	66.7	1	K.MLLDSEQHPCQLK.D
*	HsFLAG-p53-DNA-D	5.1471	0.4595	1828.64	1829.101	6911.4	1	1354.3	64.7	1	R.VKLESPTVSTLTPSSPGK.L
gi|27482992|r	2	13	9.70%	155	17219	11.1	PREDICTED: similar to 60S ribosomal protein L29 (Cell surface heparin binding protein HIP) [Homo sapiens]				
gi|89042710|r	2	13	9.70%	155	17219	11.1	PREDICTED: similar to 60S ribosomal protein L29 (Cell surface heparin binding protein HIP) [Homo sapiens]				

gi|88999346|r	2	13	9.60%	157	17368	11.2	PREDICTED: similar to 60S ribosomal protein L29 (Cell surface heparin binding protein HIP) [Homo sapiens]				
gi|88997659|r	2	13	9.60%	157	17368	11.2	PREDICTED: similar to 60S ribosomal protein L29 (Cell surface heparin binding protein HIP) isoform 2 [Homo				
gi|88997656|r	2	13	9.60%	157	17368	11.2	PREDICTED: similar to 60S ribosomal protein L29 (Cell surface heparin binding protein HIP) isoform 1 [Homo				
gi|88987619|r	2	13	9.70%	155	17138	10.8	PREDICTED: similar to 60S ribosomal protein L29 (Cell surface heparin binding protein HIP) [Homo sapiens]				
gi|88982429|r	2	13	9.70%	155	17138	10.8	PREDICTED: similar to 60S ribosomal protein L29 (Cell surface heparin binding protein HIP) [Homo sapiens]				
gi|4506629|re	2	13	9.40%	159	17752	11.7	ribosomal protein L29 [Homo sapiens]				
	HsTIP60_Ti_103.129	2.6712	0.3983	1377.55	1378.571	6754.6	2	619.2	53.6	6	K.AQAAAPASVPAQAPK.G
	HsFLAG-ARP6_Ti_1	4.3209	0.3117	1378.57	1378.571	3297.4	1	658.3	71.4	7	K.AQAAAPASVPAQAPK.G
gi|56676371|r	8	12	9.60%	1443	160883	6.4	cleavage and polyadenylation specific factor 1, 160kDa [Homo sapiens]				
*	HsFLAG-FLJ20729_	3.6792	0.3061	1634.96	1634.829	6414.2	1	669.8	62.5	1	K.TLSLHYFEEPELR.D
*	HsARP6-FLAG_Ti_1	3.2621	0.1384	1397.51	1397.614	3631.1	1	827.4	81.8	1	R.SSFLPSYIIDVR.A
*	HsARP6-FLAG_Ti_1	3.005	0.2008	1245.32	1245.508	5976.4	2	1034.2	80	1	R.YIVQVSPLGIR.L
*	HsFLAG-Lin9_Ti_20	4.4388	0.363	1792.8	1792.943	4647.6	1	916	68.8	2	R.VLVDSSFGQPTTQGEAR.R
*	HsFLAG-ARP6_Ti_2	3.5117	0.3533	1948.53	1948.272	6418.2	1	806.6	56.2	4	R.ISVLPAYLSYDAPWPVR.K
*	HsFLAG-Lin9_Ti_20	3.9246	0.1998	2997.45	2996.395	4444.4	2	480.1	30	1	R.YIHPQQEAFSIQLISPVSWEAIPNAR.I
*	HsFLAG-ARP6_Ti_1	2.7756	0.252	2093.49	2092.542	8514.4	2	538.3	41.7	1	R.ILIMDVIEVVPEPGQPLTK.N
*	HsFlag-VPS71_Ti_1	3.6771	0.2226	2585.09	2584.929	7682.4	1	794.6	30.7	1	K.KIGTTPDIILDDLLETDRVTAHF.-
gi|46852388|r	8	53	9.60%	1150	132821	5.8	cell-cycle and apoptosis regulatory protein 1 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.1032	0.3473	1951.71	1952.218	4494.7	1	590.6	62.5	10	R.IQTLPNQNQSQTQPLLK.T
*	HsFLAG-FLJ20729_	3.5187	0.3611	1761.07	1761.935	3878.9	1	615.8	69.2	2	K.FSLDCPSCDMMELR.R
*	HsFlag-DPCD_Ti_20	3.0911	0.1323	1196.95	1197.296	9439.5	4	984.1	75	3	R.YHRPEETHK.G
*	HsFLAG-p53-DNA-D	4.7566	0.4026	2722.53	2722.128	7441.5	1	1612.9	39.8	5	R.TVPAHVETVVLFFPDVWHCLPTR.S
*	HsFLAG-FLJ20729_	3.7656	0.3791	2049.19	2048.392	7012.1	1	949.8	55.9	5	R.YILPDEPAIIVHPNWAAK.S
*	HsFLAG-Lin9_Ti_20	4.877	0.4001	1772.81	1773.039	6594.2	1	1226.9	71.4	20	K.DLEEILYTLGLHLSR.A
*	HsARP6-FLAG_Ti_1	4.037	0.2956	1773.35	1773.039	5097.6	1	964.8	48.2	3	K.DLEEILYTLGLHLSR.A
*	HsFLAG-p53-DNA-D	3.9885	0.3909	1601.22	1600.871	6480	1	1126.5	73.1	5	R.NLSTVMDEIHTVLK.K
gi|4501891|re	7	31	9.60%	892	103058	5.4	actinin, alpha 1 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.2973	0.3143	1392.39	1393.511	7905.9	1	1434.5	85	3	K.TFTAWCNSHLR.K
	HsFLAG-FLJ20729_	3.9341	0.4516	2007.79	2009.287	7496.6	1	1006	55.9	4	K.AIMTYVSSFYHAFSGAQK.A
	HsFLAG-p53-DNA-D	3.8305	0.2522	1216.95	1216.423	7573.3	1	1642.6	94.4	1	K.LASDLLEWIR.R
	HsFLAG-p53-DNA-D	4.1643	0.2635	1422.27	1422.58	8347.1	1	1715	85	2	K.GYEEWLLNEIR.R
*	HsFLAG-p53-DNA-D	3.9626	0.1707	1294.34	1294.537	7619	1	1365.7	81.8	2	R.LAILGIHNEVSK.I
	HsFLAG-Lin9_Ti_20	4.3758	0.2651	1387.59	1387.622	9291.5	1	1782.9	81.8	18	R.VGWEQLLTTIAR.T
	HsFLAG-p53-DNA-D	3.8681	0.3006	1430.49	1430.601	7341.8	1	1291	81.8	1	R.TINEVENQILTR.D
gi|66529294|r	2	3	9.60%	354	39381	5.6	paraoxonase 2 isoform 1 [Homo sapiens]				
gi|66529396|r	2	3	9.90%	342	37980	5.7	paraoxonase 2 isoform 2 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.3791	0.2082	1679.53	1679.1	7917.3	1	998.9	56.2	2	R.LVAVGLLGIALALLGER.L
	HsFLAG-ARP6_Ti_1	3.1477	0.3032	2028.65	2027.371	10147.2	1	611.6	46.9	1	K.YIYVADILAHEIHVLEK.H
gi|7705855|re	2	4	9.60%	312	34324	9.3	steroid dehydrogenase homolog [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.6609	0.3912	1978.44	1979.122	9440.2	1	1821.7	71.4	2	K.TFVDFFSQCLHEEYR.S
*	HsFLAG-ARP6_Ti_1	3.1589	0.2186	1657.35	1655.977	5037.4	4	364.7	50	2	K.GVFVQSVLPYFVATK.L
gi|4502899|re	1	2	9.60%	218	23662	4.5	clathrin, light polypeptide A isoform a [Homo sapiens]				
	HsFlag-VPS71_Ti_1	2.8336	0.288	2352.84	2353.417	8337.6	1	1199.8	55	2	R.AAEEAFVNDIDESSPGTEWER.V

gi|52486999|r	9	22	9.50%	1478	169581	8.7	THO complex 2 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.5939	0.1983	1415.78	1415.589	7328.9	8	935.8	68.2	2	K.NETYNSHPLLVK.V
*	HsFlag-VPS71_Ti_1	2.5686	0.3874	2218.68	2218.558	7421.6	2	359.1	38.9	1	K.LSHSNPTILFDYILSQIQK.Y
*	HsARP6-FLAG_Ti_1	3.0774	0.1425	1479.15	1477.698	5222.9	2	689.6	66.7	2	K.YDNLITPVVDSLK.Y
*	HsFLAG-Lin9_Ti_20	3.8189	0.3289	2676.55	2675.017	7929.3	1	492.7	34.1	1	K.YLTSLNYDVLAYCIIEALANPEK.E
*	HsARP6-FLAG_Ti_1	4.0183	0.115	1920.19	1920.259	6282	2	1253.2	43.8	1	K.YPIDLAGLLQYVANQLK.A
*	HsFlag-VPS71_Ti_1	5.0282	0.4424	1920.69	1920.259	5892.8	1	1878.1	75	6	K.YPIDLAGLLQYVANQLK.A
*	HsFlag-VPS71_Ti_1	4.0969	0.1564	2308.57	2307.68	6952.3	1	1175.6	39.5	2	K.DALLDHDLALPLCLLMAQQR.N
*	HsARP6-FLAG_Ti_1	2.8365	0.3401	1540.42	1540.725	4177.9	1	362.3	58.3	2	K.ECGNYPGFLTILR.A
*	HsFLAG-Lin9_Ti_20	5.797	0.5295	2116.72	2117.237	8777.3	1	1486.1	54.3	5	R.NAVASVQNGPGGGPSSSSIGSASK.S
gi|4505117|re	1	4	9.50%	411	43255	10	methyl-CpG binding domain protein 2 isoform 1 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	5.1282	0.2605	3723.77	3722.101	4456.2	1	454.1	21.7	4	N
gi|41327764|r	2	4	9.50%	359	39589	7.2	aldo-keto reductase family 7, member A2 [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	4.2871	0.4645	1584.92	1585.843	6244.7	1	1133.8	71.4	2	R.FYAYNPLAGGLLTGK.Y
*	HsFLAG-ARP6_Ti_2	3.7573	0.3816	1805.68	1806.029	5877.3	1	1144.4	63.9	2	K.ALQAAYGASAPSVTSAALR.W
gi|11034845|r	2	3	9.50%	326	36900	6	hypothetical protein LOC58490 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.7147	0.4418	1706.66	1706.896	7148.8	1	846.2	60.7	1	R.EFESVLVDAFSHVAR.E
*	HsARP6-FLAG_Ti_1	2.6028	0.2704	1769.88	1770.033	4557.6	3	255.9	43.3	2	K.IASLPQEVQDVSLLEK.I
gi|21237802|r	8	42	9.40%	1105	122721	5.8	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c1 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	6.2645	0.45	2078.89	2078.416	11722.4	1	2719.6	66.7	25	K.TLAGLVVQLLQFQEDAFGK.H
*	HsFLAG-Lin9_Ti_20	4.4275	0.3229	1401.68	1402.602	10566.5	1	1623.2	69.2	1	K.AGGALCHILGAAYK.Y
*	HsSrcap_Ti_204.322	3.9364	0.287	2613.96	2615.011	4563.5	3	368.9	40.5	2	K.TLVQNNCLTRPNIYLIPDIDLK.L
*	HsSrcap_Ti_204.321	4.4564	0.1512	2615.29	2615.011	9122.4	1	1750.3	38.1	2	K.TLVQNNCLTRPNIYLIPDIDLK.L
	HsFlag-VPS71_Ti_1	3.4336	0.1859	2240.34	2240.573	8004.4	1	732.2	50	1	R.EWTEQETLLLLEALEMYK.D
	HsFlag-VPS71_Ti_1	4.0724	0.2671	1432.39	1432.585	6575.7	1	1169.4	80	6	R.TQDECILHFLR.L
	HsFLAG-p53-DNA-D	2.1902	0.198	924.5	925.032	4939.2	1	519.1	78.6	1	K.HLAAVEER.K
	HsARP6-FLAG_Ti_1	4.2653	0.3252	1332.08	1332.642	7108.5	1	1762	86.4	4	K.SLVALLVETQMK.K
gi|5803092|re	3	3	9.40%	478	52892	5.8	methionyl aminopeptidase 2 [Homo sapiens]				
*	HsFLAG-FLJ20729_	3.4627	0.2809	1694.96	1694.798	7220	1	783.1	57.7	1	K.ALDQASEEIWNDFR.E
*	HsFLAG-FLJ20729_	2.8753	0.229	1520.62	1520.778	4606.8	4	258.1	54.2	1	K.NFDVGHVPIRLPR.T
*	HsFLAG-FLJ20729_	3.2438	0.3398	2102.48	2103.352	7834.8	5	533.4	44.1	1	K.NLCDLGIVDPYPPLCDIK.G
gi|29731731|r	2	21	9.40%	361	37974	5.6	PREDICTED: similar to eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa isoform 1 [Homo sap				
gi|88954796|r	2	21	10.10%	336	35417	5.4	PREDICTED: similar to eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa isoform 6 [Homo sap				
gi|88954792|r	2	21	9.40%	361	37974	5.6	PREDICTED: similar to eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa isoform 5 [Homo sap				
gi|88954789|r	2	21	9.40%	361	37974	5.6	PREDICTED: similar to eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa isoform 4 [Homo sap				
gi|88953071|r	2	21	10.10%	336	35417	5.4	PREDICTED: similar to eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa isoform 3 [Homo sap				
gi|88953069|r	2	21	9.40%	361	37974	5.6	PREDICTED: similar to eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa isoform 2 [Homo sap				
gi|4503519|re	2	21	9.50%	357	37564	5.4	eukaryotic translation initiation factor 3, subunit 5 epsilon, 47kDa [Homo sapiens]				
	HsARP6-FLAG_Ti_1	2.5973	0.2924	1712.15	1712.987	5713.7	1	478	53.6	1	R.LHPVILASIVDSYER.R
	HsFlag-FLJ90652_2	6.5528	0.548	2050.63	2051.301	6746.8	1	1863.9	72.2	20	R.IQDALSTVLQYAEDVLSGK.V
gi|22538431|r	2	6	9.40%	339	37822	6.3	cathepsin B preproprotein [Homo sapiens]				
gi|4503139|re	2	6	9.40%	339	37822	6.3	cathepsin B preproprotein [Homo sapiens]				
gi|22538437|r	2	6	9.40%	339	37822	6.3	cathepsin B preproprotein [Homo sapiens]				

gi|22538435|r	2	6	9.40%	339	37822	6.3	cathepsin B preproprotein [Homo sapiens]				
gi|22538433|r	2	6	9.40%	339	37822	6.3	cathepsin B preproprotein [Homo sapiens]				
	HsFLAG-FLJ20729_	3.9594	0.4684	1635.19	1635.687	6351	1	1278.6	76.9	1	K.HYGYNSYSVSNSEK.D
	HsFLAG-ARP6_Ti_1	3.9686	0.4258	2006.6	2007.25	8678.8	1	652.4	47.1	5	K.NGPVEGAFSVYSDFLLYK.S
gi|40254924|r	2	3	9.40%	307	34930	9.6	hypothetical protein LOC55379 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.1973	0.3741	1802.59	1803.075	3599.3	1	399.5	60	1	K.LTTLPSDFCGLTHLVK.L
*	HsFLAG-ARP6_Ti_1	4.6517	0.2921	1535.06	1534.799	7496.2	1	1469.3	79.2	2	R.LVNLQHLDLLNNK.L
gi|21071006|r	2	4	9.40%	329	34326	5.2	tumor suppressing subtransferable candidate 4 [Homo sapiens]				
*	HsFlag-ZnF-HIT2_Ti_	5.134	0.4471	1850.76	1850.016	8950.9	1	1572.6	64.7	2	R.RAPSSVAHTSMSDNGGFK.R
*	HsFlag-ZnF-HIT2_Ti_	3.0573	0.444	1476.34	1476.675	5447	1	926.3	75	2	R.VPPVPDYVAHPER.W
gi|21071056|r	10	20	9.30%	1647	184644	7.9	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a4 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.7451	0.3554	1726.24	1725.94	4662.7	1	560.4	66.7	2	R.IQELENLPGSLAGDLR.T
*	HsFLAG-p53-DNA-D	2.5679	0.3115	1232.14	1233.326	6173.3	6	499.3	70	1	K.AVATYHANTER.E
*	HsFlag-VPS71_Ti_1(	3.1129	0.256	2353.32	2353.678	10246.1	1	861.1	44.7	1	R.LAYLLQQTDEYVANLTELVR.Q
*	HsFLAG-p53-DNA-D	2.3471	0.2332	868.48	869.009	6177.2	3	652.7	71.4	1	K.VIHVESGK.I
*	HsFLAG-p53-DNA-D	4.0778	0.4407	1665.59	1665.846	7635.9	1	1948.7	75	1	R.GLQSYYAVAHAVTER.V
*	HsFlag-VPS71_Ti_1(	3.9075	0.3789	2639.02	2639.066	3455	1	278.2	38.6	2	R.INGPFLIIVPLSTLSNWAYEFDK.W
	HsARP6-FLAG_Ti_1	4.3946	0.2088	1618.2	1617.926	5797.2	1	1207.8	79.2	3	K.FNVLLTTYEYIIK.D
	HsARP6-FLAG_Ti_1	3.4162	0.2719	1512.2	1512.752	7683.9	1	1469.3	70.8	6	K.LTQVLNTHYVAPR.R
	HsFLAG-Lin9_Ti_20(	3.0111	0.1977	2028.36	2029.516	8605	1	667.2	46.9	1	K.LPELWALLNFLLPTIFK.S
*	HsARP6-FLAG_Ti_1	2.6924	0.3089	2020.7	2022.265	5407.2	1	850.7	62.5	2	K.TFNEPGSEYFIFLLSTR.A
gi|24432016|r	2	16	9.30%	471	52050	8	pre-mRNA cleavage factor I, 59 kDa subunit [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.1893	0.3215	2036.3	2037.203	7355.8	1	629.5	50	1	R.DSGPPPSTVSEAEFEDIMK.R
*	HsFlag-VPS71_Ti_1(	6.1295	0.4065	2437.03	2437.75	8341.3	1	2345.2	58.3	15	K.AVSGASAGDYSDAIETLLTAIAVIK.Q
gi|37588859|r	1	2	9.30%	246	27965	6.6	ring finger protein 41 isoform 2 [Homo sapiens]				
gi|5032071|re	1	2	7.30%	317	35905	6.1	ring finger protein 41 isoform 1 [Homo sapiens]				
gi|37588861|r	1	2	7.30%	317	35905	6.1	ring finger protein 41 isoform 1 [Homo sapiens]				
	HsFlag-NUFIP_Ti_1(	4.4989	0.324	2581.82	2581.811	12323.2	4	816.2	26.1	2	K.RSLVESGCPASIVNELIENAHER.S
gi|6005757|re	5	8	9.20%	1047	119914	5.7	chromatin-specific transcription elongation factor large subunit [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20:	3.006	0.1605	1624.97	1624.837	7659	2	695.8	53.3	1	K.GNENANGAPAITLLIR.E
*	HsFLAG-FLJ20729_	5.4652	0.2806	3122.71	3123.545	10192	1	2552.1	38	1	R.TLMVDPSQEVQENYNFLLQLQEELLK.E
*	HsFLAG-p53-DNA-D	4.3661	0.4032	2476.74	2478.011	5628.8	1	685.5	47.6	1	K.KYETVIMPVFGIATPFHIATIK.N
*	HsH2AZ-FLAG_293_	3.8226	0.1939	1677.33	1677.854	4125.1	2	869.1	75	1	R.NEGNIFPNPEATFVK.E
*	HsFLAG-p53-DNA-D	4.0876	0.4469	1826.87	1827.05	3432.1	1	539.2	65.6	4	K.APGEQTVPALNLQNAFR.I
gi|56788366|r	3	4	9.20%	652	70755	7.9	phosphatidylinositol-binding clathrin assembly protein isoform 1 [Homo sapiens]				
gi|56788368|r	3	4	9.80%	610	66393	8.8	phosphatidylinositol-binding clathrin assembly protein isoform 2 [Homo sapiens]				
	HsFlag-VPS71_Ti_1(	3.7644	0.4575	1456.62	1457.627	5394.8	1	689.3	64.3	2	R.ITAAQHSVTGSAVSK.T
	HsFLAG-p53-DNA-D	2.8167	0.3322	1923.26	1923.171	9742.2	1	522.7	39.5	1	R.ATTLSNAVSSLASTGLSLTK.V
	HsYL1_Ti_102.3404.	4.9209	0.4354	2474.62	2474.728	5651.5	1	801	47.9	1	K.LVSDDLDSSLANLVGNLGIGNGTTK.N
gi|25777617|r	3	5	9.20%	598	66482	9.5	chromodomain protein, Y chromosome-like isoform a [Homo sapiens]				
gi|25777619|r	3	5	10.10%	544	60609	9.2	chromodomain protein, Y chromosome-like isoform b [Homo sapiens]				
	HsH2AZ-FLAG_293_	2.744	0.2484	1197.93	1197.377	8264.2	9	689.7	65	1	K.ALVIGKDHESK.N
	HsH2AZ-FLAG_293_	3.6737	0.1345	3117.44	3116.681	5871.4	1	695.7	25.9	1	K.KPIIVAVNGPAIGLGASILPLCDVVWANEK.A

	HsH2AZ-FLAG_293_	4.5113	0.4108	1575.21	1575.722	7224.6	1	1512.3	76.9	3	K.ELASCNPVVLEESK.A
gi|20149629|r	3	8	9.20%	455	50647	9.1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47 isoform 1 [Homo sapiens]				
gi|41327776|r	3	8	10.30%	406	45169	9.2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47 isoform 2 [Homo sapiens]				
	HsARP6-FLAG_Ti_1	3.8813	0.284	1423.25	1422.711	4408.8	1	1047.9	83.3	2	K.IQIEAIPLALQGR.D
	HsFLAG-p53-DNA-D	3.735	0.3775	1926.14	1926.266	6176.7	1	935.9	58.8	4	K.TGAFALPILNALLETPQR.L
	HsFLAG-Lin9_Ti_20	2.9088	0.2468	1203.48	1203.473	7177	1	941.3	75	2	K.KPHIIIATPGR.L
gi|38016127|r	2	6	9.20%	425	48063	10.1	RNA binding motif protein 34 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.5517	0.4101	2312.6	2313.742	4771.9	1	559.2	47.5	5	R.LASLFSSLEPQIQPVYVPVPK.Q
*	HsFLAG-TCF3_Ti_1	3.6386	0.1445	2011.18	2010.295	5490	1	405.2	47.1	1	R.SVFVGNLPYKVEESAIEK.H
gi|5032173|re	1	2	9.20%	423	46156	8.3	nuclear receptor subfamily 2, group F, member 1 [Homo sapiens]				
*	HsSrcap_Ti_204.150	4.9655	0.4305	3481.4	3482.621	8665	1	1044.4	24.3	2	DK.G
gi|5453706|re	2	3	9.20%	346	38926	7.9	SPFH domain family, member 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.6309	0.1325	1490.04	1491.687	5759.7	2	404.5	58.3	1	K.RISEIEDAAFLAR.E
*	HsFLAG-ARP6_Ti_1	3.3604	0.2934	2163.87	2164.447	3449	1	351.1	47.2	2	K.IYFGSNIPNMFVDSSCALK.Y
gi|22538467|r	1	2	9.10%	264	29204	6	proteasome beta 4 subunit [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.1615	0.362	2632.76	2633.889	7723.3	1	614.5	39.1	2	K.GVEIEGPLSTETNWDIAHMISGFE.-
gi|21359860|r	1	2	9.10%	110	12016	3.8	prothymosin, alpha (gene sequence 28) [Homo sapiens]				
gi|89036005|r	1	2	8.50%	118	12983	3.9	PREDICTED: similar to prothymosin, alpha (gene sequence 28) isoform 2 [Homo sapiens]				
gi|89036003|r	1	2	8.50%	118	12983	3.9	PREDICTED: similar to prothymosin, alpha (gene sequence 28) isoform 1 [Homo sapiens]				
gi|89035371|r	1	2	8.50%	118	12983	3.9	PREDICTED: similar to prothymosin, alpha (gene sequence 28) isoform 2 [Homo sapiens]				
gi|89035369|r	1	2	8.50%	118	12983	3.9	PREDICTED: similar to prothymosin, alpha (gene sequence 28) isoform 1 [Homo sapiens]				
	HsH2AZ-FLAG_293_	2.9302	0.1716	1132.46	1132.172	8126.7	3	999.3	77.8	2	K.EVVEEAENGR.D
gi|41872631|r	14	28	9.00%	2511	273424	6.4	fatty acid synthase [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.4681	0.3131	1253.21	1252.415	7053.2	1	1338.5	85	2	R.FDASFFGVHPK.Q
*	HsFLAG-TCF3_Ti_1	3.3093	0.2698	2542.59	2543.749	5481	1	348.7	34.8	1	R.SLYQSAGVAPESFEYIEAHGTGTK.V
*	HsFLAG-ARP6_Ti_1	3.5849	0.2785	1651.32	1651.878	3618.4	1	610.7	62.5	2	K.SNMGHPEPASGLAALAK.V
*	HsFLAG-TCF3_Ti_1	3.2581	0.3054	1970.5	1970.195	3362.3	3	217.4	46.9	2	R.WLSTSIPEAQWHSSLAR.T
*	HsFlag-FLJ90652_2	4.4308	0.1392	2786.43	2787.315	5736.7	1	942.4	32	3	R.ALGLGVEQLPVVFEDVVLHQATILPK.T
*	HsFLAG-ARP6_Ti_1	5.6817	0.4503	2841.36	2842.177	5648.5	1	1124.5	36.5	2	R.LFDHPESPTPNPTEPLFLAQAEVYK.E
*	HsFLAG-ARP6_Ti_1	2.6811	0.2088	957.46	957.12	5833.6	1	990.9	85.7	1	K.HGLYLPTR.V
*	HsFlag-FLJ90652_2	2.9416	0.1345	1495.91	1496.707	5287.3	1	779.8	72.7	1	R.RQQEQQVPILEK.F
*	HsFLAG-ARP6_Ti_1	3.9563	0.4875	1870.26	1870.945	5812.8	1	828.7	71.4	2	K.FCFTPHTEEGCLSER.A
*	HsFLAG-FLJ20729_	4.8714	0.4227	1778.64	1779.084	5991.7	1	1583	75	5	K.LPEDPLLSGLLDSPALK.A
*	HsFLAG-ARP6_Ti_1	3.3129	0.2234	1470.33	1470.582	8664.1	1	1404.3	75	1	R.FPQLDSTSFANSR.D
*	HsFLAG-ARP6_Ti_1	4.266	0.3293	2150.49	2150.405	8886.9	1	2046.3	43.1	1	R.AAPLDSIHSLAAYYIDCIR.Q
*	HsFLAG-TCF3_Ti_1	3.8475	0.3967	2423.05	2423.769	10841.7	1	1029	45.5	3	R.TLLEGSGLESIISIIHSSLAEPR.V
*	HsFLAG-TCF3_Ti_1	3.8126	0.3199	2423.86	2423.769	4986.3	1	655.9	34.1	2	R.TLLEGSGLESIISIIHSSLAEPR.V
gi|4503509|re	10	19	8.80%	1382	166569	6.8	eukaryotic translation initiation factor 3, subunit 10 theta, 150/170kDa [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	3.0425	0.3229	1523.44	1523.856	4698.8	2	597.5	65.4	2	R.VLLATLSIPITPER.T
*	HsScrap_Ti_104.235	2.4232	0.214	1350.53	1351.632	4394.5	6	218	58.3	1	R.LATLLGLQAPPTR.I
*	HsFlag-VPS71_Ti_1	3.4955	0.267	1351.77	1351.632	4927.6	1	763	70.8	3	R.LATLLGLQAPPTR.I
*	HsARP6-FLAG_Ti_1	3.8531	0.2891	1435.95	1435.706	6321.1	1	1640.1	86.4	2	R.FNVLQYVVPEVK.D
*	HsSrcap_Ti_202.484	4.2721	0.2761	1781.55	1781.018	9229.7	2	1483.7	65.4	3	K.DLYNWLEVEFNPLK.L

*	HsSrcap_Ti_205.351	3.2651	0.1619	1941.64	1940.206	6101.9	1	671.5	56.7	1	R.LLQQVSQIYQSIEFSR.L
*	HsFLAG-p53-DNA-D	2.6556	0.1136	1735.04	1736.021	3193.6	1	246.5	53.6	1	R.LTSLVPFVDAFQLER.A
*	HsScrap_Ti_102.223	2.1515	0.3081	1262.36	1263.495	6514.2	1	377.7	59.1	1	R.NQLTAMSSVLAK.A
*	HsFlag-FLJ90652_2	2.7478	0.1543	936.09	936.099	7082.6	1	928.9	92.9	1	K.PAHILQEK.E
*	HsFLAG-FLJ20729_	4.5952	0.4358	2121.53	2122.349	5264.7	1	1149.1	67.6	4	K.DIDIEDLEELDPDFIMAK.Q
gi|22094121|r	7	11	8.80%	1297	146610	8.1	SCC-112 protein [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	3.7915	0.3843	1574.28	1573.833	10024.3	1	1289.3	65.4	2	R.DLALVNDQLLGFVR.E
*	HsFLAG-p53-DNA-D	2.944	0.2251	1663.32	1663.955	6116.7	1	893.1	60	2	R.IAPVHIDSEAISALVK.L
*	HsFLAG-FLJ20729_	3.3353	0.1738	1699.59	1699.898	9817.1	1	805.7	53.6	1	K.LWSPDEEVSPEVLAK.V
*	HsFlag-VPS71_Ti_1	4.7749	0.4426	1608.81	1608.881	7231.1	1	1502.5	68.8	2	K.PAGVLGAVNKPLSATGR.K
*	HsSrcap_Ti_201.072	4.8462	0.3396	2164.57	2163.173	6432.5	1	936.6	55.3	1	R.EQSSEAAETGVSENEENPVR.I
*	HsFlag-VPS71_Ti_1	3.9542	0.2582	1488.84	1487.656	8292.5	1	1542.3	76.9	1	K.RTVTAAGAENIQQK.T
*	HsFlag-VPS71_Ti_1	5.0513	0.4523	1712.61	1712.86	8649.9	1	1563.8	64.7	2	K.RAAVGQESPGGLEAGNAK.A
gi|4503403|re	5	7	8.80%	1117	122385	5.3	desmoglein 2 preproprotein [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.3073	0.223	1850.56	1851.196	3949.4	1	633.2	60	2	R.IVSLEPAYPPVFYLNK.D
*	HsFLAG-ARP6_Ti_1	4.5867	0.3615	1582.37	1582.794	5452.3	1	1491.2	84.6	1	R.ILDVNDNIPVVENK.V
*	HsFLAG-ARP6_Ti_1	2.7825	0.2005	1727.84	1728.001	3619.3	1	809.3	68.8	1	K.VVPSFLPVDQGGSLVGR.N
*	HsFLAG-ARP6_Ti_1	4.8031	0.3661	2579.67	2580.854	5791.9	1	1460.7	58.7	1	R.VYAPASTLVDQPYANEGTVVVTER.V
*	HsFLAG-ARP6_Ti_1	5.0432	0.4644	2930.09	2930.311	7680.9	1	1123.2	32.7	2	R.VIQPHGGGSNPLEGTQHLQDVPYVMVR.E
gi|5454172|re	5	8	8.80%	633	69526	6.4	X-ray repair cross complementing protein 1 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.201	0.2374	1662.57	1662.97	4399	1	550.7	63.3	1	K.KTPSKPPAQLSPSVPK.R
*	HsFLAG-FLJ20729_	3.1742	0.2697	1534.39	1534.796	3863.6	2	380.4	57.1	1	K.TPSKPPAQLSPSVPK.R
*	HsFLAG-p53-DNA-D	2.1459	0.2116	980.57	981.14	2311.4	2	127.2	66.7	2	R.TPATAPVPAR.A
*	HsARP6-FLAG_Ti_1	3.3741	0.2791	1875.39	1874.236	7387.3	1	1390.8	62.5	2	K.ILQGVVVVLSGFQNPFR.S
*	HsFLAG-p53-DNA-D	4.4866	0.2919	1614.63	1614.757	7308.6	1	1703.5	79.2	2	K.HFFLYGEFPGDER.R
gi|89062143|r	2	5	8.80%	430	47445	6.1	PREDICTED: similar to Ig gamma-4 chain C region [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.8632	0.1415	1808.66	1809.118	7769	1	1530.5	70	3	R.VVSVLTVLHQDWLNGK.E
	HsFLAG-p53-DNA-D	4.9004	0.3252	2544.62	2545.681	8013.6	1	1240.8	50	2	K.GFYPSDIAVEWESNGQPENNYK.T
gi|14269586|r	1	2	8.80%	205	24212	10.4	mitochondrial ribosomal protein S26 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	3.8711	0.3967	2064.07	2063.437	4360.9	1	622.6	61.8	2	R.VNMPPAVDPAEFFVLMER.Y
gi|89052386|r	4	10	8.70%	835	89356	9.5	PREDICTED: widely-interspaced zinc finger motifs isoform 1 [Homo sapiens]				
gi|89057269|r	4	10	8.70%	835	89356	9.5	PREDICTED: similar to widely-interspaced zinc finger motifs isoform 1 isoform 10 [Homo sapiens]				
	HsSrcap_Ti_202.448	5.6218	0.4861	2318.91	2319.614	5862.4	1	1015.3	57.1	4	R.QLGVAESESSGAPIDLLYELVK.Q
	HsSrcap_Ti_205.239	4.5287	0.4722	1456.72	1456.728	6473.2	1	1445.8	75	2	K.GLPDAHLGLPPGLAK.K
	HsMRGBP-FLAG_Ti_	3.3799	0.279	1151.61	1153.364	7785.7	1	1617.5	81.8	1	K.TPLALAGSPTPK.N
	HsSrcap_Ti_203.236	3.2728	0.3117	2332.71	2333.687	6242.7	1	373.4	37	3	R.ELSLTPITGAKPSATGYLGSVAAK.R
gi|76150623|r	4	7	8.70%	808	88973	9.2	nucleolar protein 1, 120kDa [Homo sapiens]				
gi|76150625|r	4	7	8.70%	808	88973	9.2	nucleolar protein 1, 120kDa [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.6018	0.1883	1183.57	1183.44	5109.7	6	1009.8	88.9	2	K.RIQDIVGILR.D
	HsFLAG-ARP6_Ti_1	4.119	0.3245	1546.42	1546.723	6860.4	1	1033.1	65.4	2	R.LGVTNTIISHYDGR.Q
	HsFLAG-ARP6_Ti_1	5.5514	0.4183	3199.01	3200.53	6333.3	1	989.1	30.2	2	K.KFSNSIPQSQTGNSETATPTNVDLPQVIPK.S
	HsH2AZ-FLAG_293_	3.7209	0.3352	1626.45	1626.677	8549.2	1	1230.5	63.3	1	K.TQASSSFQDSSQPAGK.A
gi|45593130|r	2	6	8.70%	549	61993	9.2	guanine nucleotide binding protein-like 3 isoform 1 [Homo sapiens]				

gi|45643129|r	2	6	8.90%	537	60540	8.8	guanine nucleotide binding protein-like 3 isoform 2 [Homo sapiens]				
gi|45643127|r	2	6	8.90%	537	60540	8.8	guanine nucleotide binding protein-like 3 isoform 2 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	5.3037	0.416	2530.34	2530.924	5765.1	1	1474.3	56.5	5	K.QITIIDSPSFIVSPLNSSSALALR.S
	HsFLAG-TIP49b_Ti_	4.7979	0.492	2442.49	2442.79	3930.3	1	757	54.3	1	R.SPASIEVVKPMEAASAILSQADAR.Q
gi|4557237|re	2	3	8.70%	427	45200	8.8	acetyl-Coenzyme A acetyltransferase 1 precursor [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.2709	0.3215	1702.4	1703.032	7185.7	1	805.1	56.2	2	R.TPIGSFLGSLSLLPATK.L
*	HsFlag-NUFIP_Ti_11	3.8107	0.4401	1907.43	1908.186	7826.9	1	1019.1	52.6	1	K.VNINGGAVSLGHPIGMSGAR.I
gi|5454004|re	2	3	8.70%	391	44156	6.3	D4, zinc and double PHD fingers family 2 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1(	2.5964	0.3436	1509.41	1509.559	4873.9	1	426.7	68.2	1	K.DAMEQCHNYNAR.L
*	HsFLAG-p53-DNA-D	4.3918	0.2332	2642.06	2642.697	7649.7	1	876	45.2	2	R.ILEPDDFLDDLDDEDYEEDTPK.R
gi|21361659|r	7	23	8.60%	1041	115963	4.8	importin 9 [Homo sapiens]				
*	HsH2AZ-FLAG_293_	3.7578	0.3293	1940.25	1941.232	5315.4	1	1026.8	64.7	4	K.EALVDTLTGILSPVQEVR.A
*	HsH2AZ-FLAG_293_	2.7213	0.1962	1133.53	1133.249	3944.4	1	714.5	81.2	1	K.FRPPETTER.A
*	HsH2AZ-FLAG_293_	3.7384	0.3453	1768.5	1767.976	5563.1	1	1379.5	73.3	2	K.YSNDPVVASLAQDIFK.E
*	HsH2AZ-FLAG_293_	5.8874	0.4734	1884.52	1885.221	8706.5	1	2129.4	67.6	13	K.IPAGLCATAIDILTTVVR.N
*	HsH2AZ-FLAG_293_	4.0004	0.234	1886.03	1885.221	8342.5	1	1338.3	42.6	1	K.IPAGLCATAIDILTTVVR.N
*	HsH2AZ-FLAG_293_	3.5313	0.2941	1224.05	1224.359	7033.2	2	1499.7	85	1	K.LLQHGINADDK.R
*	HsH2AZ-FLAG_293_	3.9278	0.4438	2253.29	2254.189	7478.7	1	1655.8	64.7	1	K.YEEDYYEDDEEDDPDALK.D
gi|4557761|re	6	32	8.60%	934	104743	5.8	mutS homolog 2 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.0937	0.4429	1638.93	1639.91	3587.9	1	394.6	61.5	3	R.FFQGMPEKPTTTVR.L
*	HsFlag-VPS71_Ti_1(	5.2991	0.373	2478.8	2478.762	7912.9	1	1359.9	52.2	5	R.ALNLFQGSVEDTTGSQSLAALLNK.C
*	HsFLAG-ARP6_Ti_1	5.5593	0.3939	1942.15	1942.266	4177.8	1	1234.6	78.1	10	R.LYQGINQLPNVIQALEK.H
*	HsARP6-FLAG_Ti_1	3.869	0.3427	1570.72	1571.944	6485.2	1	1276.6	76.9	12	K.LLLAVFVTPLTDLR.S
*	HsYL1_Ti_105.1427.	2.5585	0.1685	1205.61	1206.446	2958.7	2	249	70	1	K.KMQSTLISAAR.D
*	HsYL1_Ti_105.1424.	3.2396	0.1729	1207.61	1206.446	4890.7	8	975.9	85	1	K.KMQSTLISAAR.D
gi|25777671|r	4	10	8.60%	940	99058	9.2	protein phosphatase 1, regulatory subunit 10 [Homo sapiens]				
*	HsFlag-DPCD_Ti_20	3.1409	0.2855	1709.72	1709.856	7648.6	4	642.7	50	2	K.RQSNVAAPGDATPPAEK.K
*	HsFLAG-FLJ20309_	2.8022	0.2107	1893.45	1892.162	7429	1	674.4	50	1	R.PLVLPSPLVTPGSNSQER.Y
*	HsFLAG-p53-DNA-D	6.0894	0.4917	3303.79	3302.684	10621.8	1	1459.3	28.1	3	K.GPQGPGGGGINVQEILTSIMGSPNSHPSEELLK.Q
*	HsFLAG-Lin9_Ti_20(	3.8634	0.3643	1197.99	1198.203	9301.2	1	2193.5	83.3	4	R.GHDGPGHGGGGHR.G
gi|58761546|r	5	14	8.60%	852	92903	6.5	amine oxidase (flavin containing) domain 2 isoform b [Homo sapiens]				
*	HsFlag-VPS71_Ti_1(	3.2256	0.3262	2322.4	2320.607	7454.1	1	753.1	47.4	1	R.LLEATSYLSHQLDFNVLNNK.P
*	HsFLAG-ARP6_Ti_1	3.0835	0.3099	1808.09	1807.02	3278.8	1	378.1	56.2	2	R.NGYSCVPVALAEGLDIK.L
*	HsARP6-FLAG_Ti_1	2.5271	0.2391	1431.44	1430.689	6515.5	5	530	60	1	R.GELFLFWNLYK.A
*	HsFLAG-FLJ20729_	3.1685	0.0826	1191.18	1191.375	7506	1	1047.1	83.3	2	R.LFFAGEHTIR.N
*	HsFlag-VPS71_Ti_1(	3.6715	0.3605	1569.54	1569.804	4688	1	650.8	64.3	8	R.NYPATVHGALLSGLR.E
gi|4507457|re	5	6	8.60%	760	84901	6.6	transferrin receptor [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.8803	0.2233	1748.7	1746.917	8316.6	1	749.9	53.3	1	R.SAFSNLFGGEPLSYTR.F
*	HsFlag-VPS71_Ti_1(	3.4942	0.3859	1562.19	1562.587	9354.6	1	1214.7	65.4	2	K.LAVDEEENADNNTK.A
*	HsFLAG-ARP6_Ti_1	2.4215	0.3074	986.24	987.147	5706.2	1	490.4	68.8	1	K.LVHANFGTK.K
*	HsFlag-VPS71_Ti_1(	3.0222	0.3009	1435.18	1434.716	4389.3	2	464.8	62.5	1	K.VSASPLLYTLIEK.T
*	HsFlag-VPS71_Ti_1(	4.0624	0.3105	1566.6	1566.797	6360.3	1	1114.7	75	1	R.VEYHFLSPYVSPK.E
gi|56243583|r	3	10	8.60%	432	47405	6.7	WD repeat domain 18 [Homo sapiens]				

*	HsH2AZ-FLAG_293_	4.5152	0.4649	1745.33	1745.072	8187.1	1	1754.4	68.8	7	R.GLALLNGEYLLAAQLGK.N
*	HsH2AZ-FLAG_293_	4.1864	0.2799	1331.49	1331.431	5772.6	1	1209.9	81.8	2	K.HLLGAEHGDEPR.H
*	HsH2AZ-FLAG_293_	2.8601	0.2258	1001.22	1001.084	3387.1	1	607.7	85.7	1	R.DLFDFSTR.F
gi|4503097|re	2	5	8.60%	350	41213	8.6	casein kinase 2, alpha prime polypeptide [Homo sapiens]				
*	HsFlag-FLJ90652_2	2.7839	0.2806	1349.44	1347.535	4519.4	1	585.8	75	1	K.PHNVMIDHQQK.K
*	HsFlag-FLJ90652_2	4.2892	0.4363	2321.98	2322.585	8346.8	1	1162.7	58.3	4	R.LIDWGLAEFYHPAQEYNVR.V
gi|13435356|r	1	2	8.60%	279	31621	4.9	HCLS1 associated protein X-1 isoform a [Homo sapiens]				
gi|66363694|r	1	2	10.40%	231	26100	5.2	HCLS1 associated protein X-1 isoform b [Homo sapiens]				
	HsFLAG-TCF3_Ti_1	4.7822	0.2159	2599.44	2599.903	8085.9	1	1330.6	33.7	2	R.GDPESPRPPALDDAFSILDLFLGR.W
gi|4507659|re	14	41	8.50%	2349	265598	5.1	translocated promoter region (to activated MET oncogene) [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	3.1344	0.0863	1568.41	1567.733	7322.6	1	1078.4	66.7	3	R.LSQELEYLTEDVK.R
*	HsFlag-VPS71_Ti_1	4.2174	0.4379	2835.96	2836.255	3423.1	1	323.3	37	2	R.ILLSQTTGVAIPLHASSLDDVSLASTPK.R
*	HsFLAG-p53-DNA-D	4.7857	0.4493	2836.08	2836.255	7057.2	1	1583.9	36.1	4	R.ILLSQTTGVAIPLHASSLDDVSLASTPK.R
*	HsFLAG-p53-DNA-D	6.1986	0.4876	2696.1	2697.015	8167.5	1	1453.2	36	4	K.RPSTSQTVSTPAPVPVIESTEAIEAK.A
*	HsFLAG-p53-DNA-D	6.6144	0.5285	2024.8	2025.356	11049.1	1	3418.4	76.5	12	R.GQNLLLTNLQTIQGILER.S
*	HsARP6-FLAG_Ti_1	4.9281	0.3905	2025.25	2025.356	9448.6	1	1531.1	41.2	1	R.GQNLLLTNLQTIQGILER.S
*	HsFlag-VPS71_Ti_1	4.6183	0.3598	2461.05	2460.672	8179.6	1	1516.6	54.8	1	K.TSTSNVEQYQAMVTSLEESLNK.E
*	HsFlag-VPS71_Ti_1	3.2803	0.2567	1803.9	1803.921	8463.4	1	940.4	60.7	1	R.ELQELEDSLNAEREK.V
*	HsFLAG-ARP6_Ti_1	4.6919	0.3476	2154.32	2154.466	3697.3	1	779.2	66.7	3	R.KLELDILPLQEANAELSEK.S
*	HsARP6-FLAG_Ti_1	3.6896	0.2558	2156.13	2154.466	6534.4	2	664.9	34.7	1	R.KLELDILPLQEANAELSEK.S
*	HsFlag-VPS71_Ti_1	3.5027	0.176	1343.52	1343.526	6519.8	1	931	75	2	K.RIQQLTEEIGR.L
*	HsFLAG-p53-DNA-D	2.0164	0.1388	808.67	808.999	3891.4	2	474.8	78.6	2	K.IAHLAGVK.D
*	HsFlag-VPS71_Ti_1	3.9117	0.103	2366.07	2366.674	4080.1	1	453.5	47.8	3	R.GIASTSDPPTANIKPTPVVSTPSK.V
*	HsFLAG-p53-DNA-D	2.9852	0.2762	1753.94	1754.042	3579.6	1	530.7	63.3	2	R.LTIHAPPQELGPPVQR.I
gi|19924129|r	8	21	8.50%	1312	153892	6.9	RAD50 homolog isoform 1 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.0932	0.4407	2074.93	2074.471	5867.5	1	811.3	52.6	6	K.QIITFFSPLTILVGPNGAGK.T
	HsFlag-VPS71_Ti_1	3.8304	0.3613	2036.84	2036.246	8886.2	1	1415.1	55.9	2	R.DSLIQSLATQLELDGFER.G
	HsFlag-VPS71_Ti_1	4.0794	0.3146	1512.67	1512.616	8129.3	1	1565.8	86.4	1	K.RKEEQLSSYEDK.L
	HsFlag-VPS71_Ti_1	4.4925	0.3993	2064.96	2065.285	7139.6	1	1508.5	61.8	4	R.VFQTEAELQEVISDLQSK.L
	HsFlag-DPCD_Ti_20	5.3788	0.2867	2066.28	2065.285	7959.3	2	1627.4	45.6	1	R.VFQTEAELQEVISDLQSK.L
	HsFlag-DPCD_Ti_20	3.9081	0.4002	2377.89	2377.579	8671.5	1	746	45	1	K.NDIEEQETLLGTIMPEEESAK.V
	HsFLAG-FLJ20729_	4.1175	0.2165	1621.22	1621.834	11041.2	1	1765.9	75	4	K.LIQDQQEQIQHLK.S
	HsFLAG-FLJ20729_	3.2146	0.2958	1051.27	1051.197	5841.8	1	822.7	87.5	2	K.RNHNLALGR.Q
gi|4758304|re	3	3	8.50%	645	72933	5.1	protein disulfide isomerase-associated 4 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	2.9752	0.2611	2136.86	2137.437	3884.1	3	261.1	41.7	1	R.EVSQPDWTPPPEVTLVLTK.E
*	HsFLAG-FLJ20729_	3.3432	0.2671	1737.28	1735.925	10803.9	1	936.5	53.3	1	R.SHMMDVQGSTQDSAIK.D
*	HsFLAG-ARP6_Ti_1	2.8022	0.3141	2310.04	2310.432	9042.4	1	602.8	42.1	1	K.DFPEYTFAIADEEDYAGEVK.D
gi|16117787|r	1	2	8.50%	117	13293	11.5	ribosomal protein L34 [Homo sapiens]				
gi|89036972|r	1	2	8.00%	125	14515	11.4	PREDICTED: similar to ribosomal protein L34 [Homo sapiens]				
gi|89036654|r	1	2	18.50%	54	6255	10.9	PREDICTED: similar to ribosomal protein L34 [Homo sapiens]				
gi|16117789|r	1	2	8.50%	117	13293	11.5	ribosomal protein L34 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	2.827	0.0908	1155.59	1154.268	7431.8	3	1035.4	77.8	2	R.RLSYNTASNK.T
gi|13435359|r	5	11	8.40%	1140	126988	5.3	damage-specific DNA binding protein 1 [Homo sapiens]				

gi|89034790|r	5	11	8.40%	1140	126968	5.3	PREDICTED: similar to DNA damage binding protein 1 (Damage-specific DNA binding protein 1) (DDB p127 s				
gi|89034782|r	5	11	8.40%	1140	126968	5.3	PREDICTED: similar to DNA damage binding protein 1 (Damage-specific DNA binding protein 1) (DDB p127 s				
	HsFLAG-ARP6_Ti_1	2.8356	0.2085	1195.13	1195.401	4085.1	1	777.7	83.3	1	R.LEELHVIDVK.F
	HsFLAG-ARP6_Ti_1	3.5925	0.364	2420.86	2421.647	8036	1	1167.1	52.6	1	K.FLYGCQAPTICFVYQDPQGR.H
	HsFLAG-ARP6_Ti_1	4.3968	0.3842	2585.47	2585.799	5749.6	1	923.4	34.1	1	R.SLSTTNVFACSDRPTVIYSSNHK.L
	HsFlag-VPS71_Ti_1	3.5482	0.2356	2182.8	2181.555	3391.7	1	326.8	50	3	R.SVLLLAYKPMEGNFEEIAR.D
	HsFlag-VPS71_Ti_1	6.0234	0.3726	2651.33	2650.988	6654.5	1	1319.5	38	5	R.KTEPATGFIDGDLIESFLDISRPK.M
gi|38202257|r	6	19	8.40%	944	106874	6.1	alpha glucosidase II alpha subunit isoform 2 [Homo sapiens]				
gi|38230585|r	6	19	8.20%	963	109042	6.2	alpha glucosidase II alpha subunit isoform 3 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.0581	0.1542	1105.24	1105.366	5537.2	2	1272.8	77.8	3	K.LVAIVDPHIK.V
	HsFLAG-ARP6_Ti_1	2.8057	0.2627	1320.39	1320.552	6949.9	1	913.9	72.7	1	R.SGGMERPFVLAR.A
	HsFlag-VPS71_Ti_1	2.6033	0.3021	977.59	978.055	5850.7	1	538.1	75	1	R.AHAHLDTGR.R
	HsFLAG-ARP6_Ti_1	3.0657	0.2941	2072.82	2072.417	5019.1	1	391.5	50	1	R.YSLLPFWYTLLYQAHR.E
	HsFlag-VPS71_Ti_1	4.5714	0.4201	1666.56	1665.073	4977.3	1	1030.2	68.8	10	R.VVIIGAGKPAAVVLQTK.G
	HsFLAG-p53-DNA-D	3.5123	0.2661	1742.71	1741.985	5222.1	3	669.7	60.7	3	R.LSFQHDPETSVLVLR.K
gi|63252886|r	4	6	8.40%	534	60967	6	prolyl 4-hydroxylase, alpha I subunit isoform 1 precursor [Homo sapiens]				
gi|63252888|r	4	6	8.40%	534	61049	6	prolyl 4-hydroxylase, alpha I subunit isoform 2 precursor [Homo sapiens]				
	HsFLAG-TIP49b_Ti_	2.5955	0.176	1845.04	1845.106	8220.2	2	521.6	50	1	K.RLNTEWSELENLVLK.D
	HsFLAG-TCF3_Ti_1	3.393	0.3059	2179.22	2177.416	7189.7	1	638.6	47.2	1	K.VSVLDYLSYAVYQQGDLDK.A
	HsFLAG-TIP49b_Ti_	2.6091	0.2969	1165.54	1166.332	6268.6	1	572.5	60	2	R.HAACPVLVGNK.W
	HsFLAG-TIP49b_Ti_	3.9774	0.4209	1166.14	1166.332	7022.2	1	1769.5	90	2	R.HAACPVLVGNK.W
gi|6857818|re	1	3	8.40%	178	19344	4.6	nucleophosmin/nucleoplasmin 3 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.5363	0.3628	1684.86	1685.88	6069	1	1266.9	75	3	R.NHDHQEIAVPVANLK.L
gi|18104971|r	1	4	8.40%	167	19127	8.4	protein tyrosine phosphatase type IVA, member 2 isoform 1 [Homo sapiens]				
gi|88947673|r	1	4	8.40%	167	19127	8.4	PREDICTED: similar to Protein tyrosine phosphatase type IVA protein 2 (Protein-tyrosine phosphatase 4a2) (				
gi|88947671|r	1	4	8.40%	167	19127	8.4	PREDICTED: similar to Protein tyrosine phosphatase type IVA protein 2 (Protein-tyrosine phosphatase 4a2) (				
gi|88947669|r	1	4	8.40%	167	19127	8.4	PREDICTED: similar to Protein tyrosine phosphatase type IVA protein 2 (Protein-tyrosine phosphatase 4a2) (				
gi|88947667|r	1	4	8.40%	167	19127	8.4	PREDICTED: similar to Protein tyrosine phosphatase type IVA protein 2 (Protein-tyrosine phosphatase 4a2) (				
gi|88947665|r	1	4	8.40%	167	19127	8.4	PREDICTED: similar to Protein tyrosine phosphatase type IVA protein 2 (Protein-tyrosine phosphatase 4a2) (				
gi|88947663|r	1	4	8.40%	167	19127	8.4	PREDICTED: similar to Protein tyrosine phosphatase type IVA protein 2 (Protein-tyrosine phosphatase 4a2) (				
gi|88947661|r	1	4	8.40%	167	19127	8.4	PREDICTED: similar to Protein tyrosine phosphatase type IVA protein 2 (Protein-tyrosine phosphatase 4a2) (				
gi|88947659|r	1	4	8.40%	167	19127	8.4	PREDICTED: similar to Protein tyrosine phosphatase type IVA protein 2 (Protein-tyrosine phosphatase 4a2) (				
gi|88947657|r	1	4	10.30%	136	15669	8.5	PREDICTED: similar to Protein tyrosine phosphatase type IVA protein 2 (Protein-tyrosine phosphatase 4a2) (				
gi|88947653|r	1	4	13.10%	107	12071	5.8	PREDICTED: similar to Protein tyrosine phosphatase type IVA protein 2 (Protein-tyrosine phosphatase 4a2) (				
gi|88947651|r	1	4	19.20%	73	8167	6.5	PREDICTED: similar to Protein tyrosine phosphatase type IVA protein 2 (Protein-tyrosine phosphatase 4a2) (				
gi|88947649|r	1	4	9.90%	142	16367	8.6	PREDICTED: similar to Protein tyrosine phosphatase type IVA protein 2 (Protein-tyrosine phosphatase 4a2) (				
gi|88947647|r	1	4	13.10%	107	12071	5.8	PREDICTED: similar to Protein tyrosine phosphatase type IVA protein 2 (Protein-tyrosine phosphatase 4a2) (				
gi|88947645|r	1	4	21.20%	66	7494	7.4	PREDICTED: similar to Protein tyrosine phosphatase type IVA protein 2 (Protein-tyrosine phosphatase 4a2) (				
gi|4506285|re	1	4	8.40%	167	19127	8.4	protein tyrosine phosphatase type IVA, member 2 isoform 1 [Homo sapiens]				
gi|4506283|re	1	4	8.10%	173	19815	9	protein tyrosine phosphatase type IVA, member 1 [Homo sapiens]				
gi|18104973|r	1	4	17.10%	82	9241	8.7	protein tyrosine phosphatase type IVA, member 2 isoform 2 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	3.405	0.1138	1584.44	1584.815	6967.8	1	1729.2	80.8	4	R.FLITHNPTNATLNK.F
gi|7662238|re	7	28	8.30%	1341	151887	6.4	apoptotic chromatin condensation inducer 1 [Homo sapiens]				

*	HsSrcap_Ti_201.061	5.2211	0.4327	2119.54	2119.117	4450.6	1	1021.3	66.7	2	K.LSEGSQPAEEEEDQETPSR.N
*	HsFLAG-Lin9_Ti_20	3.2513	0.3371	1722.79	1722.078	5729.3	1	910.5	63.3	7	R.SAQPLPLKIEELALAK.G
*	HsFlag-NUFIP_Ti_1	3.7227	0.3504	2364.03	2364.581	3577.4	3	298.8	40.5	1	K.DPSSGQEVATPPVPQLQVCEPK.E
*	HsFlag-NUFIP_Ti_2	3.3112	0.254	1304.33	1304.527	6593.2	1	833.5	72.7	5	K.KPSISITTESLK.S
*	HsFLAG-FLJ20309_	3.6151	0.2805	1509.46	1509.699	7129.9	1	1094.9	66.7	1	R.TGTLVEEAFWIDK.I
*	HsFlag-NUFIP_Ti_2	3.0485	0.2698	1215.41	1215.392	7278	2	915.2	70	2	R.GLLVDRPSETK.T
*	HsFLAG-p53-DNA-D	4.6448	0.4005	2105.42	2104.42	4181.2	1	965.5	70.6	10	K.AAPCIYWLPLTDSQIVQK.E
gi|13376202|r	4	23	8.30%	612	69449	7.8	hypothetical protein LOC79871 [Homo sapiens]				
*	HsFlag-FLJ20643_Ti	3.7019	0.3208	1520.67	1520.596	7740	1	1169.1	69.2	2	K.VNTQSSSNSTLPER.L
*	HsFLAG-UTX1_Ti_2	2.5378	0.0806	1676.56	1675.922	4509.1	4	451.5	56.7	1	R.GSGTAIKPLPSYENLK.K
*	HsFLAG-BC014022_	4.8512	0.432	2295.68	2295.811	8335.9	1	1236.4	37.5	3	K.VLPGLLVPLQITLGDIYTQLK.N
*	HsFlag-NUFIP_Ti_1	4.9609	0.4539	2296.01	2295.811	4098.9	1	1021.7	65	17	K.VLPGLLVPLQITLGDIYTQLK.N
gi|31542539|r	2	2	8.30%	480	52538	9.3	DnaJ (Hsp40) homolog, subfamily A, member 3 [Homo sapiens]				
*	HsSrcap_Ti_205.214	3.3523	0.3037	1824.65	1825.136	6730.8	2	484.3	50	1	K.RVMIPVPAGVEDGQTVR.M
*	HsFLAG-TCF3_Ti_1	2.5869	0.2193	2342.3	2342.614	12796.1	8	521.5	34.1	1	R.DGADIHSDLFISIAQALLGGTAR.A
gi|11496885|r	1	2	8.30%	457	49845	8.4	enigma protein isoform 1 [Homo sapiens]				
gi|42741675|r	1	2	9.00%	423	46510	8.3	enigma protein isoform 2 [Homo sapiens]				
	HsSrcap_Ti_203.280	4.1276	0.2647	3956.41	3956.32	8779.2	2	414	18.2	2	Y
gi|4507499|re	2	2	8.30%	375	41591	7.8	TIA-1 related protein isoform 1 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	3.863	0.2107	2063.62	2061.392	9570.8	1	1471.5	55.9	1	R.DVTEVLILQLFSQIGPCK.S
	HsFlag-VPS71_Ti_1	2.8324	0.3193	1553.32	1554.804	6457.2	1	538.2	62.5	1	R.QTFSPFGQIMEIR.V
gi|6005747|re	2	4	8.30%	336	37655	6.8	ring finger protein 2 [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.5612	0.1582	1573.08	1573.789	5002.7	4	434.1	53.8	3	R.SLRPDPNFDALISK.I
*	HsFLAG-Lin9_Ti_20	2.6233	0.2042	1794.17	1793.89	9231.7	4	476.2	46.2	1	K.IYPSRDEYEAHQER.V
gi|7705608|re	2	3	8.30%	314	34582	8.2	fumarylacetoacetate hydrolase domain containing 2A [Homo sapiens]				
	HsFLAG-ARP8_Ti_2	2.7245	0.2273	1305.87	1305.61	8753.5	1	980.7	72.7	2	R.RALAAQLPVLPR.S
*	HsFlag-NUFIP_Ti_2	2.9226	0.2235	1560.39	1560.791	6677.1	3	412	50	1	R.SEVTFLAPVTRPDK.V
gi|4503659|re	2	5	8.30%	133	14390	10.2	ubiquitin-like protein fubi and ribosomal protein S30 precursor [Homo sapiens]				
*	HsFlag-NUFIP_Ti_11	3.2691	0.1723	1265.28	1264.513	4535.3	1	811.9	85	4	R.RFVNVVPTFGK.K
*	HsFLAG-TCF3_Ti_1	2.3441	0.2169	1107.46	1108.326	4356.5	1	564.7	77.8	1	R.FVNVVPTFGK.K
gi|70166852|r	6	11	8.20%	1226	135967	8.6	adenosine deaminase, RNA-specific isoform a [Homo sapiens]				
gi|70167113|r	6	11	10.80%	931	103642	8.7	adenosine deaminase, RNA-specific isoform d [Homo sapiens]				
gi|70167032|r	6	11	8.60%	1181	131070	8.6	adenosine deaminase, RNA-specific isoform c [Homo sapiens]				
gi|70166944|r	6	11	8.40%	1200	133175	8.5	adenosine deaminase, RNA-specific isoform b [Homo sapiens]				
	HsFlag-VPS71_Ti_1	4.1147	0.3686	2030.13	2031.236	7586.5	1	1155.2	64.7	1	K.ICDYLFNVSDSSALNLAK.N
	HsFLAG-ARP6_Ti_1	3.6525	0.455	1736.29	1737.044	3522.7	1	637.7	67.9	1	R.AIMEMPSFYSHGLPR.C
	HsFLAG-ARP6_Ti_1	3.6024	0.3849	1843.95	1844.973	5325.6	1	475.3	50	2	K.TAESQTPTPSATSFFSGK.S
	HsFLAG-p53-DNA-D	3.5229	0.3592	2144.46	2145.386	8174	1	806.4	50	1	K.FQYCVAVGAQTFPSVSAPSK.K
	HsFLAG-ARP6_Ti_1	4.4553	0.362	1680.59	1680.901	4242.4	1	1080.6	82.1	2	R.YLNTNPVGGLLEYAR.S
	HsFLAG-ARP6_Ti_1	3.2001	0.4027	1678.97	1679.916	8229.2	1	587.3	50	4	K.SVTLGYLFSQGHLTR.A
gi|42734339|r	4	9	8.20%	906	102387	6.8	hypothetical protein LOC55215 [Homo sapiens]				
*	HsYL1_Ti_103.3375.	4.1551	0.379	1876.58	1876.178	8195.1	1	992.7	56.2	3	R.NSQLANSVMQTLLSQLK.Q
*	HsFLAG-Lin9_Ti_20	5.5926	0.4641	3897.89	3899.078	7936.3	1	1448	30.5	3	K.NTVIPLQQGEEEEEEEEAFYEDLDDILESITNR.M

*	HsARP6-FLAG_Ti_1	3.1896	0.323	1487.33	1487.82	8968.6	1	1194.5	65.4	1	K.EALLLVTVLTSLSK.L
*	HsFLAG-ARP6_Ti_1	3.2476	0.3378	1185.43	1185.371	5895.2	1	1462.5	94.4	2	K.TNHFAIVNLR.T
gi|56118310|r	2	3	8.20%	243	27296	5.1	nuclear ubiquitous casein kinase and cyclin-dependent kinase substrate [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.03	0.3807	2365.94	2367.401	7903.4	1	754	50	1	R.KVVDYSQFQESDDADEDYGR.D
*	HsFLAG-ARP6_Ti_1	5.313	0.4866	2239.13	2239.227	7447.9	1	1337.8	61.1	2	K.VVDYSQFQESDDADEDYGR.D
gi|42544179|r	4	6	8.10%	898	100045	6.1	Cip1-interacting zinc finger protein [Homo sapiens]				
*	HsSrcap_Ti_203.156	4.2277	0.2975	1980.57	1980.148	6577.4	1	898.6	58.8	3	K.RTPAPEPEPCEASELPAK.R
*	HsScrap_Ti_104.163	3.2296	0.351	1836.98	1837.043	6009.9	1	592.6	56.7	1	K.QAQTQTSPEHLVLQQK.Q
*	HsSrcap_Ti_204.203	3.415	0.37	2885.9	2887.216	7662.4	1	672.7	35.7	1	R.AFSTVPLTPVPRPSDSVSSTPAATSTPSK.Q
*	HsSrcap_Ti_204.169	2.61	0.1263	1172.43	1173.314	6927.4	3	609.7	66.7	1	K.SLGHFENLQK.Y
gi|33239445|r	4	16	8.10%	814	92482	5	eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa isoform a [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.5115	0.2286	3233.19	3232.719	5278.5	8	348.2	23.1	1	R.YLVTFSPLMDTQDDPQAIIIWDILTGHK.K
*	HsSrcap_Ti_202.463	4.7414	0.4246	2166.31	2166.397	6602.8	1	835.2	50	9	K.DFSWSPGGNIIAFWVPEDK.D
*	HsFLAG-ARP6_Ti_1	3.1951	0.3167	1097.4	1097.262	6523.3	1	1139.5	77.8	5	K.FAVLHGEAPR.I
*	HsFlag-FLJ90652_2	2.8308	0.2057	1080.3	1080.272	5733	2	722.3	81.2	1	R.ISVSFYHVK.N
gi|8922358|re	2	2	8.10%	546	64441	10.5	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.4158	0.3698	2199.28	2198.644	5653	1	1328.8	66.7	1	K.TMNLNPMILTNILSSPYFK.V
*	HsFLAG-Lin9_Ti_20	3.8742	0.3758	3107.35	3105.294	4952.3	1	298.8	37.5	1	R.YTQPPTDLWDWFESFLDDEEDLDVK.A
gi|31563334|r	2	2	8.10%	614	64256	9.6	forkhead box K2 isoform 2 [Homo sapiens]				
gi|89043065|r	2	2	10.60%	471	49706	9.4	PREDICTED: similar to forkhead box K2 isoform 1 isoform 7 [Homo sapiens]				
gi|89043061|r	2	2	10.10%	494	52411	9.2	PREDICTED: similar to forkhead box K2 isoform 2 isoform 5 [Homo sapiens]				
gi|89043059|r	2	2	9.30%	540	57217	9.1	PREDICTED: similar to forkhead box K2 isoform 1 isoform 4 [Homo sapiens]				
gi|31563338|r	2	2	7.60%	660	69062	9.5	forkhead box K2 isoform 1 [Homo sapiens]				
	HsFLAG-FLJ20436_	3.6795	0.3564	2185.32	2184.5	4407.8	1	553.5	50	1	R.FAQSAPGSPLSSQPVLITVQR.Q
	HsFLAG-Lin9_Ti_20	4.5169	0.3038	3153.11	3153.693	6138.3	1	520	24.1	1	R.IIQTAQTTPVQTVTIVQQAPLGQHQLPIK.T
gi|5453629|re	2	12	8.10%	406	44820	5.2	dynactin 2 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_20	4.8187	0.4127	1865.67	1866.122	8189	1	1295.9	58.3	9	K.LLGPDAAINLTDPDGALAK.R
*	HsFLAG-p53-DNA-D	3.9745	0.3015	1597.26	1597.855	5931.3	1	1312.8	76.9	3	R.WSPIASTLPELVQR.L
gi|11321581|r	2	10	8.10%	333	35059	8.9	succinate-CoA ligase, GDP-forming, alpha subunit [Homo sapiens]				
*	HsFLAG-TIP49b_Ti_	4.1108	0.3213	1568.62	1568.816	6386.6	1	1321	71.4	6	K.GGQTHLGLPVFNTVK.E
*	HsFLAG-TIP49b_Ti_	3.608	0.3045	1082.41	1083.294	6093.7	1	1044.6	72.7	4	R.MGHAGAIIAGGK.G
gi|57164942|r	11	27	8.00%	2032	225493	7.8	colonic and hepatic tumor over-expressed protein isoform a [Homo sapiens]				
gi|57222563|r	11	27	8.30%	1972	218524	8.1	colonic and hepatic tumor over-expressed protein isoform b [Homo sapiens]				
	HsFlag-VPS71_Ti_1	3.692	0.1783	1806.8	1807.103	7377.9	4	666.9	53.3	8	R.DALRPPLQNINSVQLK.E
	HsFLAG-FLJ20729_	4.375	0.3544	1660.52	1659.926	6559	1	1551.7	75	3	K.FGQYAGHVVPTILEK.F
	HsFlag-VPS71_Ti_1	3.2304	0.23	1412.85	1412.589	4712	1	598.4	60	1	K.KGKPAAPGGAGNTGTK.N
	HsFlag-DPCD_Ti_20	2.7074	0.1818	1803.1	1803.967	8875.6	4	535.8	46.4	1	K.EIVEPELSIEVCEEK.A
	HsFlag-NUFIP_Ti_20	3.4111	0.219	1541.41	1541.831	4099.6	7	467.8	61.5	3	K.FIQPNIGELPTALK.G
	HsFLAG-ARP6_Ti_2	3.2115	0.2182	1440.97	1440.723	2704.7	4	462.4	69.2	3	K.NLGIPIITVLGDSK.N
	HsFlag-DPCD_Ti_20	2.8165	0.334	1734.62	1733.98	8421.7	1	483.8	46.9	1	R.AAALATVNAWAEQTGMK.E
	HsFLAG-FLJ20729_	3.191	0.2324	1401.34	1401.598	3818.4	1	396.4	62.5	2	R.SMSGHPEAAQMVR.R
	HsFLAG-ARP6_Ti_2	3.8378	0.3604	1625.43	1625.902	5859.9	1	1189.3	73.1	2	K.LDDIFEPVLIPEPK.I
	HsARP6-FLAG_Ti_1	2.5007	0.1207	1484.4	1484.693	5665	1	624.3	66.7	1	R.LLPDTINSINLDR.I

	HsFlag-DPCD_Ti_20	3.4939	0.3164	1641.48	1641.88	7104.1	1	903.3	60	2	K.PAVPTVASSTDMLHSK.L
gi|40786394|r	1	2	8.00%	314	34613	7.8	hypothetical protein DKFZp434N062 [Homo sapiens]				
gi|88956612|r	1	2	8.10%	307	33797	7.2	PREDICTED: similar to fumarylacetoacetate hydrolase domain containing 2A [Homo sapiens]				
	HsFLAG-ARP8_Ti_2	3.149	0.3619	2752.59	2751.241	7711.1	1	754.5	39.6	2	R.ALAAQLPVLPWSEVTFLAPVTWPDK.V
gi|33239451|r	1	2	8.00%	261	28769	4.7	proliferating cell nuclear antigen [Homo sapiens]				
gi|4505641|re	1	2	8.00%	261	28769	4.7	proliferating cell nuclear antigen [Homo sapiens]				
	HsFlag-VPS71_Ti_1	3.2679	0.221	2465.76	2466.772	7420.2	1	535.8	40	2	K.LMDLDVEQLGIPEQEYSCVVK.M
gi|5032013|re	3	4	7.90%	890	100278	6.9	kinesin family member 20A [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.3583	0.1984	2465.49	2465.811	9723.9	1	597.2	38.1	1	R.FTFSQIFGPEVGQASFFNLTVK.E
*	HsFLAG-ARP6_Ti_1	4.5307	0.3545	3686.7	3689.29	8219.1	1	636.6	22.7	1	R.SLALIFNSLQGQLHPTPDLKPLLSNEVIWLDSK.Q
*	HsFLAG-ARP6_Ti_1	4.2899	0.3533	1691.33	1691.757	7673.5	1	1249.3	67.9	2	K.NQSFASTHLNQNSSR.S
gi|7657671|re	5	8	7.90%	764	89406	5.8	upstream binding transcription factor, RNA polymerase I [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.6291	0.3756	1583.46	1583.744	7031.8	1	1494.6	79.2	2	R.FREDHPDLIQNAK.K
*	HsFlag-VPS71_Ti_1	3.2213	0.2794	1432.03	1431.591	6363.5	1	915.7	75	1	K.TPQQLWYTHEK.K
*	HsFLAG-p53-DNA-D	2.9623	0.2535	2035.92	2035.267	6510.9	1	474.5	50	1	K.RAEEIWQQSVIGDYLAR.F
*	HsFLAG-p53-DNA-D	4.4565	0.2715	1939.27	1940.207	6472	1	1222.4	62.5	3	K.FSQELLSNGELNHLPLK.E
*	HsFLAG-p53-DNA-D	3.0079	0.2643	2224.5	2225.509	7402.7	1	445.8	38.9	1	K.FSQELLSNGELNHLPLKER.M
gi|19913424|r	3	6	7.90%	617	68304	5.5	ATPase, H+ transporting, lysosomal 70kD, V1 subunit A, isoform 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.8241	0.4804	1672.46	1672.943	5966.7	1	917.1	63.3	2	K.RTALVANTSNMPVAAR.E
*	HsFLAG-ARP6_Ti_1	3.8701	0.3668	2055.11	2056.318	8261.9	1	863.1	50	2	K.EILQEEEDLAEIVQLVGK.A
*	HsFLAG-ARP6_Ti_1	5.0863	0.4348	1802.15	1801.968	7812.1	1	1631.2	71.4	2	K.SDYAQLLEDMQNAFR.S
gi|4758958|re	2	4	7.90%	404	45518	5.1	cAMP-dependent protein kinase, regulatory subunit alpha 2 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	5.2557	0.499	2037.87	2037.252	9515.9	1	2070.6	68.8	2	K.NLDQEQLSQVLDAMFER.I
	HsFLAG-ARP6_Ti_1	3.3438	0.3219	1694.28	1693.943	6147	1	599.6	57.1	2	K.GQYFGELALVTNKPR.A
gi|25470886|r	2	10	7.90%	407	43383	8.6	DAZ associated protein 1 isoform b [Homo sapiens]				
gi|25470890|r	2	10	8.50%	378	40530	8.3	DAZ associated protein 1 isoform a [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	3.9307	0.3098	1825.17	1824.043	8167.1	1	1936.2	76.7	2	K.LFVGGLDWSTTQETLR.S
	HsFLAG-p53-DNA-D	3.8601	0.317	1799.99	1799.99	4066.6	1	552.3	66.7	8	K.IFVGGIPHNCGETELR.E
gi|25777600|r	3	5	7.80%	953	105836	5.4	proteasome 26S non-ATPase subunit 1 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.5254	0.2417	3871.52	3873.271	8318.6	4	425.8	18.8	1	K.DTSPGSAYQEGGGLYALGLIHANHGGDIIDYLLNQLK.N
*	HsFlag-VPS71_Ti_1	5.8636	0.4002	2400.48	2400.617	9215.9	1	2534.3	46.2	3	R.TPEQCPSVVSLLSESYNPHVR.Y
*	HsFLAG-ARP6_Ti_1	2.9039	0.2617	1789.43	1788.227	3812.5	1	461.4	60	1	R.YQPFKPLSIGGIIILK.D
gi|4758032|re	3	7	7.80%	906	102487	5.3	coatomer protein complex, subunit beta 2 (beta prime) [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.6073	0.318	3825.77	3826.144	6119.7	1	782	26.5	1	K.TCVQTLEGHAQNVSCASFHPELPIIITGSEDGTVR.I
*	HsFLAG-Lin9_Ti_20	3.4442	0.1925	1738.34	1736.919	6018.5	1	903	59.4	1	R.GSNNVALGYDEGSIIVK.L
*	HsFlag-VPS71_Ti_1	5.2319	0.412	2066.7	2066.272	4880.2	1	1148.1	63.9	5	K.AAESLADPTEYENLFPGLK.E
gi|7705437|re	1	2	7.80%	180	20463	8.5	60S ribosome subunit biogenesis protein NIP7 homolog [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.8018	0.3394	1575.59	1575.848	7235.9	1	1729.6	76.9	2	R.LHVTALDYLAPYAK.Y
gi|62865879|r	1	2	7.80%	180	19325	8.7	Bcl-2 inhibitor of transcription isoform a [Homo sapiens]				
gi|7706351|re	1	2	7.80%	179	19194	8.7	Bcl-2 inhibitor of transcription isoform b [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.8402	0.3346	1463.65	1463.599	8555	1	1226.4	69.2	2	K.VAAQCSHAAVSAYK.Q
gi|4505185|re	1	2	7.80%	115	12476	7.9	macrophage migration inhibitory factor (glycosylation-inhibiting factor) [Homo sapiens]				
*	HsH2AZ-FLAG_293_	3.7463	0.2139	1046.24	1045.233	4522.5	1	963.7	93.8	2	K.LLCGLLAER.L

gi|70980549|r	10	17	7.70%	1871	208699	8.9	programmed cell death 11 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.5433	0.3712	1526.46	1526.73	5430.9	1	844.5	67.9	1	R.KPALVSTVEGGQDPK.N
*	HsFLAG-FLJ20729_	3.8503	0.3078	1802.68	1803.172	5129.3	1	733.8	63.3	1	K.NFSEIHPGMLLIGFVK.S
*	HsFLAG-FLJ20729_	4.1781	0.3793	1896.43	1897.181	6211	1	1287.4	64.7	1	K.DYGVFIQFPSGLSGLAPK.A
*	HsFLAG-FLJ20729_	4.4826	0.3798	1476.17	1476.632	9361.6	1	1871.1	79.2	2	K.GSEHQAIVQHLEK.S
*	HsFLAG-Lin9_Ti_20	4.7765	0.3415	1824.48	1825.112	8809.4	1	2112.5	66.7	2	K.TTEPGVTGLLLAVEGPAAK.R
*	HsFLAG-p53-DNA-D	3.2174	0.0989	1233.19	1232.549	6327.7	3	1338.7	85	1	R.IPLLLTSLSFK.V
*	HsFLAG-Lin9_Ti_20	3.3603	0.3352	1564.16	1564.787	5429.7	1	647	65.4	1	R.GYVGSIQPHGVFFR.L
*	HsFLAG-Lin9_Ti_20	2.7123	0.2384	2929.3	2930.325	8284.4	4	214.7	24.1	1	K.NLVELSFLPGDTGKPDVLSASLEGQLTK.Q
*	HsFLAG-Lin9_Ti_20	5.3769	0.3097	2930.27	2930.325	6111.6	1	736.6	29.6	3	K.NLVELSFLPGDTGKPDVLSASLEGQLTK.Q
*	HsFLAG-p53-DNA-D	3.6039	0.3391	1290.43	1290.548	7496.7	1	2187.1	90	4	K.VFLHLADIYAK.S
gi|4826806|re	4	7	7.70%	801	88061	9.1	bromodomain containing protein 2 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_2	4.5353	0.4318	1888.64	1890.147	10041.3	1	928.9	50	2	K.LPGEGNAGLLGLGPEAAAPGK.R
	HsFLAG-Lin9_Ti_20	3.2822	0.1463	1254.16	1254.433	6148.2	1	1259	88.9	1	K.HAAYAWPFYK.P
*	HsFLAG-FLJ20729_	5.4778	0.5032	1874.45	1875.178	9842.5	1	2230.4	70.6	2	R.AVHEQLAALSQGPISKPK.R
*	HsFLAG-FLJ20729_	3.648	0.3053	1447.14	1446.604	7584.8	1	841.9	62.5	2	K.RLQDVSGQLNSTK.K
gi|20149709|r	3	4	7.70%	542	60083	7.7	heterogeneous nuclear ribonucleoprotein L-like [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	3.2991	0.3107	1079.16	1079.288	5067.7	1	845	88.9	1	K.VSVSPVVHVR.G
*	HsFLAG-p53-DNA-D	4.4453	0.3883	1703.69	1703.898	8003	1	1713.5	73.3	2	R.HDGYGSHGPLLPLPSR.Y
*	HsFLAG-Lin9_Ti_20	4.3785	0.3437	1815.7	1816.024	8323.3	1	1727.1	70	1	K.TDAVEALTALNHYQIR.V
gi|88953744|r	2	5	7.70%	429	50740	8.7	PREDICTED: formin binding protein 3 isoform 1 [Homo sapiens]				
gi|88957856|r	2	5	8.30%	398	47130	9.2	PREDICTED: similar to Formin-binding protein 3 (Huntingtin yeast partner A) (Huntingtin-interacting protein H				
gi|88957853|r	2	5	7.70%	429	50740	8.7	PREDICTED: similar to Formin-binding protein 3 (Huntingtin yeast partner A) (Huntingtin-interacting protein H				
gi|88953746|r	2	5	8.30%	398	47130	9.2	PREDICTED: formin binding protein 3 isoform 2 [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.0407	0.3935	1840.63	1841.132	4263.6	1	677.6	65.6	3	R.FTNMLGQPGSTALDLFK.F
	HsFLAG-p53-DNA-D	2.7692	0.1889	1823.91	1824.043	6168.9	1	353.8	50	2	K.QAAPPIELDAVWEDIR.E
gi|56699409|r	3	5	7.70%	391	42332	10.1	RNA binding motif protein, X-linked [Homo sapiens]				
	HsARP6-FLAG_Ti_1	2.9816	0.0993	1488.09	1487.652	8463.9	2	822.3	57.7	1	R.GFAFVTFESPADAK.D
	HsFLAG-p53-DNA-D	4.5817	0.3147	1748.62	1748.977	6133.7	1	1134	66.7	2	K.AIKVEQATKPSFESGR.R
	HsFlag-DPCD_Ti_20	3.4139	0.2866	1435.23	1436.564	4755.1	1	530.5	62.5	2	K.VEQATKPSFESGR.R
gi|4885079|re	2	3	7.70%	297	32881	9.3	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma subunit isoform H (heart) precursor [Homo				
gi|50345988|r	2	3	7.70%	298	32996	9.2	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma subunit isoform L (liver) precursor [Homo s				
	HsFLAG-ARP6_Ti_1	3.2372	0.263	1214.08	1214.373	6501.4	1	1437.9	81.8	2	R.GLCGAIHSSIAK.Q
	HsFLAG-ARP6_Ti_1	2.7915	0.2886	1294.48	1293.465	5235	1	515.5	70	1	R.THSDQFLVAFK.E
gi|27597059|r	1	2	7.70%	260	29910	5.7	DnaJ homolog, subfamily C, member 9 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.502	0.3499	2177.7	2178.45	5840.3	1	720.2	50	2	R.NIIQQAIDAGEVPSYNAFVK.E
gi|19920317|r	3	5	7.60%	602	66023	5.9	cytoskeleton-associated protein 4 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.4425	0.442	1797.48	1798.049	7388.5	1	820	56.7	2	K.VQSLQATFGTFESILR.S
*	HsFLAG-ARP6_Ti_1	2.8736	0.347	1773.64	1773.953	8877.3	1	1183.7	64.3	1	R.STLQTMESDIYTEVR.E
*	HsFLAG-ARP6_Ti_1	4.3037	0.3128	1630.76	1630.839	8260.5	1	1469	67.9	2	K.RSVGELPSTVESLQK.V
gi|51092299|r	1	2	7.60%	223	25268	8.4	adenylate kinase 3-like 2 [Homo sapiens]				
gi|89035941|r	1	2	7.60%	223	25240	8.4	PREDICTED: similar to Adenylate kinase isoenzyme 4, mitochondrial (ATP-AMP transphosphorylase) [Homo				
gi|89035461|r	1	2	7.60%	223	25208	8.4	PREDICTED: similar to Adenylate kinase isoenzyme 4, mitochondrial (ATP-AMP transphosphorylase) [Homo				

gi|8051579|re	1	2	7.60%	223	25268	8.4	adenylate kinase 3-like 1 [Homo sapiens]				
gi|53832003|r	1	2	7.60%	223	25268	8.4	adenylate kinase 3-like 1 [Homo sapiens]				
gi|53832001|r	1	2	7.60%	223	25268	8.4	adenylate kinase 3-like 1 [Homo sapiens]				
	HsFLAG-FLJ20729_	2.8991	0.0939	1928.78	1926.188	8260.4	1	669	50	2	R.IAQNFGLQHLSSGHFLR.E
gi|4507669|re	1	3	7.60%	172	19595	4.9	tumor protein, translationally-controlled 1 [Homo sapiens]				
gi|89030551|r	1	3	9.40%	138	15483	5.1	PREDICTED: similar to Translationally-controlled tumor protein (TCTP) (p23) (Histamine-releasing factor) (HR				
gi|89029983|r	1	3	9.40%	138	15492	5.2	PREDICTED: similar to Translationally-controlled tumor protein (TCTP) (p23) (Histamine-releasing factor) (HR				
gi|46409468|r	1	3	9.30%	140	15757	6.2	hypothetical protein LOC392490 [Homo sapiens]				
	HsFLAG-p53-DNA-D	2.9403	0.1099	1420.61	1420.71	3955.3	4	530.5	70.8	3	R.VKPFMTGAAEQIK.H
gi|50582540|r	6	11	7.50%	1285	148698	8.5	myosin VI [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.8678	0.2539	1922.33	1923.173	7226.5	2	685.8	46.9	1	K.TFLALINQVFPAEEDSK.K
*	HsFLAG-ARP6_Ti_1	3.4197	0.285	1608.98	1609.869	7448.3	1	786.4	57.1	2	K.SLGTRPPHVFAIADK.A
*	HsFLAG-ARP6_Ti_1	3.7595	0.3401	1622.52	1622.861	8082.6	1	1190.1	60.7	3	K.SSVVGGFVSHYLLEK.S
*	HsFLAG-ARP6_Ti_1	4.1266	0.3449	2645.07	2645.895	11865.9	1	1079.8	27	2	R.VVAGVLHLGNIDFEEAGSTSGGCNLK.N
*	HsFLAG-ARP6_Ti_1	2.9472	0.2436	1339.32	1339.538	6021.7	1	918.2	77.3	2	K.VPLKVEQANNAR.D
*	HsFLAG-ARP6_Ti_1	2.6221	0.2689	1402.68	1403.595	8996.7	1	1203.9	70	1	R.ASFHELYNMYK.K
gi|21361794|r	6	11	7.50%	1230	136375	5.8	TIP120 protein [Homo sapiens]				
*	HsFLAG-FLJ20729_	3.7294	0.2162	1484.76	1484.779	8891	1	1077.1	65.4	3	K.ISGSILNELIGLVR.S
*	HsFLAG-Lin9_Ti_20	2.7657	0.1991	1487.58	1487.696	6648.6	1	632.3	57.7	1	K.EGPAVVGQFIQDVK.N
*	HsFLAG-Lin9_Ti_20	5.0594	0.3537	3281.01	3281.73	8924.9	1	1096	29.2	2	K.SAASYALGSISVGNLPEYLPFVLQEITSQPK.R
*	HsFLAG-p53-DNA-D	3.6234	0.1857	1938.9	1939.268	4321.3	1	691.9	39.7	1	R.VALVTFNSAAHNKPSLIR.D
*	HsFLAG-p53-DNA-D	4.8451	0.3916	1938.92	1939.268	10146.2	2	956.6	47.1	2	R.VALVTFNSAAHNKPSLIR.D
*	HsFLAG-FLJ20729_	3.907	0.3946	1772.29	1772.008	4592	1	690.1	60.7	2	R.DLLDTVLPHLYNETK.V
gi|24307879|r	2	5	7.50%	638	71457	5.2	dynein, cytoplasmic, intermediate polypeptide 2 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.2965	0.4845	1951.5	1951.955	7129.7	1	890.1	52.5	4	K.SVSTPSEAGSQDSGDGAVGSR.T
*	HsFLAG-FLJ20729_	4.1953	0.3108	2953.26	2954.223	8328.4	4	608.2	25	1	R.LDLWNLNNDTEVPTASISVEGNPALNR.V
gi|4508017|re	2	4	7.50%	478	50751	9.1	zinc finger protein 207 isoform a [Homo sapiens]				
gi|73808090|r	2	4	7.80%	463	49692	9.1	zinc finger protein 207 isoform b [Homo sapiens]				
	HsFLAG-FLJ20729_	3.0502	0.315	1825.49	1826.133	11206.2	1	950.6	50	1	K.LYTGPGLAIHCMQVHK.E
	HsFlag-VPS71_Ti_1	4.8467	0.4017	1935.68	1935.182	3467.2	1	942.9	68.4	3	K.PAASITSKPATLTTTSATSK.L
gi|19923748|r	2	6	7.50%	453	48755	9	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) [Homo sapiens]				
*	HsFLAG-p53-DNA-D	2.777	0.1899	1192.71	1193.389	4280	4	605.1	66.7	2	K.AKPAEAPAAAAPK.A
*	HsFLAG-p53-DNA-D	5.5798	0.4439	2217.2	2218.469	6115.3	1	1036.6	55	4	K.ASAFALQEQPVVNAVIDDTTK.E
gi|45505149|r	1	2	7.50%	428	47629	8.2	nuclear factor I/C isoform 1 [Homo sapiens]				
gi|45505151|r	1	2	6.40%	499	54682	8.5	nuclear factor I/C isoform 2 [Homo sapiens]				
	HsFlag-VPS71_Ti_1	4.0132	0.3735	3284.14	3284.653	5353.9	1	471.8	23.4	2	R.TPVVTGTGPNFSLGELQGHLAYDLNPASTGLR.R
gi|4505775|re	2	13	7.50%	361	39959	9.4	solute carrier family 25 member 3 isoform b precursor [Homo sapiens]				
gi|47132595|r	2	13	7.50%	361	39959	9.4	solute carrier family 25 member 3 isoform b precursor [Homo sapiens]				
	HsSrcap_Ti_205.423	3.353	0.4894	2910.89	2912.331	10420.5	1	865.4	36.5	1	K.YYALCGFGGVLSCGLTHTAVVPLDLVK.C
	HsSrcap_Ti_205.422	6.3471	0.5698	2911.66	2912.331	7982.4	1	1477.9	33.7	12	K.YYALCGFGGVLSCGLTHTAVVPLDLVK.C
gi|6006001|re	1	2	7.50%	226	25402	8.1	plasma glutathione peroxidase 3 precursor [Homo sapiens]				
*	HsSrcap_Ti_206.277	4.1573	0.288	1956.72	1956.254	7633.6	1	786.8	56.2	2	K.YVRPGGGFVPNFQLFEK.G
gi|8923579|re	1	3	7.50%	161	17745	5.1	hypothetical protein LOC55004 [Homo sapiens]				

*	HsFLAG-ARP6_Ti_1	3.5945	0.3206	1342.45	1342.581	5979.3	1	1382.6	81.8	3	R.LAVLSSSLTHWK.K
gi|23510338|r	4	8	7.40%	1058	117849	5.8	ubiquitin-activating enzyme E1 [Homo sapiens]				
gi|23510340|r	4	8	7.40%	1058	117849	5.8	ubiquitin-activating enzyme E1 [Homo sapiens]				
	HsFlag-VPS71_Ti_1	5.4438	0.3325	2602.57	2601.745	8473.5	1	1917.1	56.8	3	R.IYDDDFFQNLDGVANALDNVDAR.M
	HsFLAG-ARP6_Ti_1	3.1642	0.2518	1243.91	1244.474	5445.1	1	700.6	72.7	2	R.KPLLESGTLGTK.G
	HsFLAG-ARP6_Ti_1	2.5565	0.1102	2317.22	2317.781	9129.5	3	403.6	33.3	1	K.IIPAIATTTAAVVGLVCLELYK.V
	HsFLAG-p53-DNA-D	2.756	0.1668	2278.72	2279.646	5250.4	2	273.4	35	2	K.NGFLNLALPFFGFSEPLAAPR.H
gi|18860916|r	5	8	7.40%	950	108583	7.5	5'-3' exoribonuclease 2 [Homo sapiens]				
*	HsFLAG-FLJ20729_	5.2167	0.2983	2122.03	2122.392	6745.8	1	1079.5	40.8	1	K.RDQPAFTPSGILTPHALGSR.N
*	HsFlag-NUFIP_Ti_1	4.6737	0.4589	1965.66	1966.204	4820.7	1	669.4	58.3	4	R.DQPAFTPSGILTPHALGSR.N
*	HsFLAG-ARP6_Ti_1	2.732	0.1212	1763.88	1765.021	6416.2	1	770.4	57.1	1	K.YAWQGVALLPFVDER.R
*	HsFlag-VPS71_Ti_1	3.3393	0.2068	2530.45	2530.905	4017.8	1	484	47.6	1	K.FSLDEEAILPDQIVCSPVPMLR.D
*	HsFLAG-Lin9_Ti_20	3.0392	0.2897	1470.04	1469.724	6351.1	1	752.9	70.8	1	R.KPAAVLKPSDWEK.S
gi|45333883|r	4	4	7.40%	674	76138	6.1	kelch repeat and BTB (POZ) domain-containing 6 [Homo sapiens]				
	HsFlag-FLJ90652_2	3.7114	0.1904	1339.65	1339.534	6758.8	1	1439.5	79.2	1	K.DTAHSAALLAQLK.S
*	HsFlag-FLJ90652_2	2.6272	0.1955	921.09	921.003	5987.7	1	992.2	85.7	1	K.FADAFGHR.K
	HsFlag-FLJ90652_2	3.0677	0.2614	1869.66	1870.197	7970.7	1	820	56.2	1	R.EETLADLTLAQLLAVLR.L
*	HsFlag-FLJ90652_2	2.9014	0.2614	1353.27	1352.543	7470.6	1	888.2	72.7	1	K.VPSPLTCLAHTR.T
gi|35493916|r	3	7	7.40%	631	69284	5.7	ribophorin II precursor [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.3961	0.2174	1373.33	1373.546	8923.6	1	2087	86.4	2	R.SIVEEIEDLVAR.L
*	HsFLAG-ARP6_Ti_1	4.3202	0.4194	1840.52	1841.158	5329	1	1096.3	65.6	2	R.LQVTNVLSQPLTQATVK.L
*	HsFLAG-ARP6_Ti_1	4.3688	0.4851	2045.92	2046.345	6110.5	1	1282.8	61.8	3	K.TSFTPVGDVFELNFMNVK.F
gi|5031815|re	2	2	7.40%	597	68048	6.4	lysyl-tRNA synthetase [Homo sapiens]				
*	HsFlag-FLJ90652_2	3.0093	0.2195	1838.43	1839.058	5694.4	2	599.9	56.7	1	K.YSHLQPGDHLTDITLK.V
*	HsFlag-VPS71_Ti_1	3.7789	0.2024	3232.83	3231.707	5958.1	1	856.8	27.8	1	K.LVGEFLEVTCINPTFICDHPQIMSPLAK.W
gi|38569466|r	2	2	7.40%	552	59690	9	ROD1 regulator of differentiation 1 [Homo sapiens]				
*	HsFLAG-FLJ20729_	3.9819	0.3224	2517.29	2518.014	5576.9	1	628.1	36.2	1	R.IIIENLFYPVTLEVLHQIFSK.F
*	HsFLAG-Lin9_Ti_20	3.6136	0.2989	2306.68	2306.542	7768	1	471.3	42.1	1	K.NNQFQALLQYADPVNAHYAK.M
gi|4503521|re	2	6	7.40%	445	52221	6	murine mammary tumor integration site 6 (oncogene homolog) [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.4535	0.1741	1542.71	1542.905	4893.4	1	644.4	66.7	4	R.HLVFPLLEFLSVK.E
*	HsSrcap_Ti_205.209	5.4321	0.472	2183.85	2184.518	8999	1	2005.6	65.8	2	K.LGHVVMGNNAVSPYQQVIEK.T
gi|14719402|r	2	2	7.40%	365	41193	10.7	homolog of yeast ribosome biogenesis regulatory protein RRS1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	5.3066	0.452	2171.8	2172.399	3677.5	1	610.3	61.1	1	K.EWLIEVPGNADPLEDQFAK.R
*	HsFLAG-TCF3_Ti_1	2.0823	0.0995	956.3	957.118	3216.7	3	284.3	78.6	1	K.KPQLDVTR.A
gi|21536449|r	2	3	7.40%	122	14210	6.8	prefoldin 1 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	2.6424	0.0939	1035.51	1036.216	5812.8	5	692.4	75	2	K.KAFTELQAK.V
*	HsFLAG-p53-DNA-D	3.6705	0.1388	1036.39	1036.216	4591	1	1084.9	93.8	1	K.KAFTELQAK.V
gi|50428935|r	4	5	7.30%	1059	112211	7.3	BPY2 interacting protein 1 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	2.881	0.1648	2507.89	2507.887	9167.4	1	741.3	39.1	1	R.GEDEAELALSLLAQLGITPLPLSR.G
*	HsFLAG-Lin9_Ti_20	2.5014	0.2758	1986.71	1986.294	6036.3	8	259.5	41.2	1	R.VLFPGCTPPACLLDGLVR.L
*	HsFLAG-p53-DNA-D	3.9266	0.2772	1910.82	1911.168	9559.3	1	1043.8	59.4	1	R.FLREPVVTPQDLEGPGR.A
*	HsFLAG-FLJ20729_	2.8745	0.2258	1639.76	1640.794	5747.7	1	607.2	52.9	2	R.GPSGSASSRPGVSATPPK.S
gi|6912752|re	4	8	7.30%	895	96915	8.5	zinc finger protein 281 [Homo sapiens]				

*	HsYL1_Ti_104.1359.	3.1506	0.3146	1432.71	1431.591	7145.3	1	1040.4	69.2	1	K.KEPAASAAAFPSQR.T
*	HsYL1_Ti_102.2774.	2.5816	0.1577	1805.46	1805.084	3915.9	3	333.9	46.7	1	K.NYLNFVSPLPDIVGQK.S
*	HsYL1_Ti_102.3314.	4.1008	0.2755	2008.36	2007.205	6843.1	2	1018.1	58.8	4	K.SGIPDEVLQSILDQYSNK.S
*	HsH2AZ-FLAG_293_	2.9671	0.3432	1981	1981.172	10535.9	1	814.1	50	2	R.TTYQIENFAQAFGSQFK.S
gi|56711248|r	3	4	7.30%	785	88802	6.5	hypothetical protein LOC23167 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.3919	0.3547	2687.89	2687.889	4163.2	1	859	35.4	2	R.IGPPSSPSATDKEENPAVLAENCFR.E
*	HsFLAG-ARP6_Ti_1	4.8762	0.3571	1580.64	1580.952	10043.3	1	2256.4	70	1	R.AGIIQVLLEAVAIAAK.G
*	HsFLAG-ARP6_Ti_1	2.7761	0.227	1688.98	1689.005	4710.3	1	446.6	53.3	1	K.GSIGPTVLEVFNTLLK.H
gi|4826882|re	4	7	7.30%	657	75627	5	nuclear matrix protein p84 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.6923	0.3119	2089.57	2089.353	6329.9	1	1138.6	61.1	2	K.NIKPLLSTFSQVPGSENEK.K
*	HsFLAG-Lin9_Ti_20	3.3637	0.4045	1733.41	1733.916	4116.5	1	662.9	63.3	1	K.PLLSTFSQVPGSENEK.K
*	HsFLAG-Lin9_Ti_20	3.7433	0.2814	1705.66	1704.834	5392	1	712.8	60.7	3	K.SVYQLLSENPPDGER.F
*	HsFLAG-FLJ20729_	3.5827	0.3166	1762.55	1762.968	6578.5	1	782.6	65.4	1	R.RSPHFFQPTNQQFK.S
gi|10716563|r	3	5	7.30%	592	67568	4.6	calnexin precursor [Homo sapiens]				
gi|66933005|r	3	5	7.30%	592	67568	4.6	calnexin precursor [Homo sapiens]				
	HsFlag-VPS71_Ti_1	2.9837	0.2912	1773.09	1771.924	5010.8	1	756.7	60	2	K.APVPTGEVYFADSFDR.G
	HsFLAG-ARP6_Ti_1	4.1696	0.3261	1457.07	1457.583	7587	1	1149.8	72.7	2	K.TPELNLDQFHDK.T
	HsFLAG-ARP6_Ti_1	2.8174	0.3169	1864.66	1865.095	5938.2	1	634.2	57.1	1	R.KIPNPDFFEDLEPFR.M
gi|15147335|r	2	4	7.30%	579	65536	9.6	nuclear receptor coactivator 5 [Homo sapiens]				
*	HsScrap_Ti_105.199	3.2314	0.3845	1777.48	1777.959	5164.2	1	838.8	64.3	3	R.SCTVNIMFGTPQEHR.N
*	HsSrcap_Ti_204.195	3.1042	0.3836	2846.97	2848.16	10507	1	515	30.8	1	R.LAPASNMTSQRPVSSTGINFDNPSVQK.A
gi|21040255|r	2	5	7.30%	508	59380	10.4	splicing factor, arginine/serine-rich 12 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.6534	0.3963	2490.56	2490.772	9352.1	1	674.8	40.5	3	R.TVYVGNLNSQTTTADQLLEFFK.Q
*	HsFLAG-p53-DNA-D	4.3172	0.3093	1637.43	1636.952	8778.3	1	1205.6	64.3	2	R.ALAFNGVMFGDRPLK.I
gi|4507903|re	2	3	7.30%	396	45476	8.9	vaccinia related kinase 1 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	2.6627	0.0962	1547.8	1546.717	3420	5	340.1	61.5	1	K.VEPSDNGPLFTELK.F
*	HsFLAG-FLJ20729_	4.2218	0.4204	1787.24	1786.982	7714.5	1	976.1	60.7	2	K.NPDQVYLVDYGLAYR.Y
gi|22547114|r	1	4	7.30%	261	29283	9.6	mitochondrial ribosomal protein L10 isoform a [Homo sapiens]				
gi|22547125|r	1	4	7.00%	271	30307	9.2	mitochondrial ribosomal protein L10 isoform b [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.1963	0.3369	2089.22	2088.418	5159	1	483.8	50	4	R.TVPFLPLLGGCIDDTILSR.Q
gi|34101286|r	4	8	7.20%	1074	117012	9	zinc finger RNA binding protein [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	5.6554	0.4395	3156.38	3156.438	10380.9	1	1441	29	1	R.PAPVAVAAAATAAAYGGYPTAHTATDYGYTQR.Q
*	HsFLAG-p53-DNA-D	4.0165	0.3025	1601.48	1601.85	7887.5	1	1554.6	73.1	2	R.NVNLVLLCSEKPSK.T
*	HsFLAG-p53-DNA-D	3.9452	0.3451	2135.76	2136.47	6160.7	1	712.9	52.9	4	R.VPTWSDFPSWAMELLVEK.A
*	HsYL1_Ti_101.1715.	2.986	0.1795	1327.58	1326.316	4090.3	1	719.9	70.8	1	R.DSDGVDGFEAEGK.K
gi|5031569|re	2	7	7.20%	376	42614	6.6	ARP1 actin-related protein 1 homolog A, centractin alpha [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	3.0768	0.236	1401.09	1401.574	5265	1	506.3	65	1	K.YCFPNYVGRPK.H
*	HsFLAG-p53-DNA-D	5.5537	0.4665	1684.66	1684.973	6760.4	1	1830.7	80	6	R.TLFSNIVLSGGSTLFK.G
gi|4506203|re	1	2	7.20%	277	29965	7.7	proteasome beta 7 subunit proprotein [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.4504	0.392	2090.32	2088.441	7017.2	1	576.6	44.7	2	K.LPYVTMGSGSLAAMAVFEDK.F
gi|4502171|re	1	2	7.20%	180	19608	6	adenine phosphoribosyltransferase isoform a [Homo sapiens]				
*	HsH2AZ-FLAG_293_	2.8913	0.1389	1524.41	1524.8	3911.3	1	489.5	62.5	2	K.LAPVPFFSLLQYE.-
gi|89030031|r	15	98	7.10%	2229	242964	8.3	PREDICTED: hypothetical protein LOC84726 isoform 1 [Homo sapiens]				

gi|89030655|r	15	98	7.10%	2229	242964	8.3	PREDICTED: similar to HLA-B associated transcript-2 isoform a isoform 15 [Homo sapiens]				
gi|89030647|r	15	98	7.10%	2229	242964	8.3	PREDICTED: similar to HLA-B associated transcript-2 isoform a isoform 10 [Homo sapiens]				
gi|89030045|r	15	98	7.10%	2229	242964	8.3	PREDICTED: hypothetical protein LOC84726 isoform 9 [Homo sapiens]				
gi|89030039|r	15	98	7.10%	2229	242964	8.3	PREDICTED: hypothetical protein LOC84726 isoform 6 [Homo sapiens]				
	HsFLAG-KIAA0515_	2.391	0.2466	1073.61	1074.219	6657.1	1	636.5	75	7	K.YSTLSLFDK.Y
	HsFLAG-KIAA0515_	3.0827	0.1453	840.29	839.97	3998.2	1	991.8	100	1	R.HGLQSLGK.V
	HsFLAG-KIAA0515_	2.466	0.0825	1164.3	1165.436	5127.9	9	530.4	65	2	R.MPPPANLPSLK.S
	HsFLAG-KIAA0515_	3.6077	0.1581	1168.37	1166.363	6498.3	2	1325.2	85	1	K.GNDPNIVIVPK.D
	HsFLAG-KIAA0515_	3.3926	0.3814	2010.42	2011.196	3303.4	1	372.1	50	4	K.SSSATASQPPESLPQPGLQK.S
	HsFLAG-KIAA0515_	4.3695	0.245	2598.44	2598.83	4752.8	1	785	47.9	7	K.SVSNLQKPTQSISQENTNSVPGGPK.S
	HsFLAG-KIAA0515_	5.3966	0.2823	2598.52	2598.83	6457.6	1	1407.9	38.5	2	K.SVSNLQKPTQSISQENTNSVPGGPK.S
	HsFLAG-KIAA0515_	4.8296	0.3679	1841.54	1841.973	5817.7	1	1305.1	67.6	4	K.PTQSISQENTNSVPGGPK.S
	HsFLAG-KIAA0515_	4.3862	0.2627	1843.34	1841.973	7585.6	2	1078	41.2	1	K.PTQSISQENTNSVPGGPK.S
	HsFLAG-KIAA0515_	2.4348	0.0813	903.46	904.013	4020.5	8	315.1	71.4	1	K.SWAQLNGK.P
	HsFLAG-KIAA0515_	3.2516	0.2889	1896.38	1896.15	4673.3	1	582.9	56.2	1	R.GSSRLLSFSPEEFPTLK.A
	HsFLAG-KIAA0515_	3.7032	0.0989	1509.55	1508.755	4468.6	1	796.7	70.8	9	R.LLSFSPEEFPTLK.A
	HsFLAG-KIAA0515_	2.9535	0.2142	1431.48	1431.632	4961	1	663.7	61.5	1	K.GVLDLSYGPGPSLR.P
	HsFLAG-KIAA0515_	5.6894	0.4755	1857.7	1858.059	7413.6	1	2156.5	76.5	56	R.HIISATSLSTSPTELGSR.N
	HsFLAG-KIAA0515_	2.7436	0.2778	1729.02	1729.675	3017.7	1	377.2	55.9	1	R.NSSTGDGAPSSACTSDSK.D
gi|14211540|r	4	6	7.10%	1003	113671	8.8	Mov10, Moloney leukemia virus 10, homolog [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.5105	0.1581	1901.57	1902.127	9034	2	599.1	40.6	1	R.NGGTQSVTLTHLFPLCR.T
*	HsFlag-NUFIP_Ti_11	4.5612	0.3232	1537.63	1537.845	6362.5	1	1966.4	85.7	2	R.FLAAVAHSPLAAQLK.P
*	HsFlag-NUFIP_Ti_1	3.0118	0.1567	1966.46	1967.316	7917.4	1	481.5	44.1	1	R.LLTLEVPGVTESRPSVLR.G
*	HsFLAG-ARP6_Ti_1	3.6191	0.228	2289.61	2289.46	5879.5	1	532.5	45	2	R.EGNSPSFFNPEEAATVTSYLK.L
gi|7705433|re	3	3	7.10%	564	66727	6.3	eukaryotic translation initiation factor 3 subunit 6 interacting protein [Homo sapiens]				
*	HsFlag-FLJ90652_2	2.6951	0.1441	990.39	991.086	7004.8	2	1053.6	81.2	1	R.VSSDVIDQK.V
*	HsScrap_Ti_102.272	2.5728	0.1717	1789.42	1788.951	5115.1	1	561.5	53.8	1	K.VYEIQDIYENSWTK.L
*	HsFLAG-FLJ20729_	5.393	0.3282	1973.99	1974.313	5810.9	1	1650.3	50	1	K.IWNVHSVLNVLHSLVDK.S
gi|25188179|r	2	3	7.10%	283	30659	8.6	voltage-dependent anion channel 3 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.9631	0.1959	2101.89	2102.442	6071.2	1	821.7	35.5	1	K.VNNASLIGLGYTQTLRPGVK.L
*	HsFLAG-ARP6_Ti_1	3.7192	0.2164	2103.3	2102.442	5286.9	1	682.9	52.6	2	K.VNNASLIGLGYTQTLRPGVK.L
gi|5454158|re	4	12	7.00%	1264	140476	7.6	valyl-tRNA synthetase [Homo sapiens]				
	HsFLAG-FLJ20729_	3.5004	0.3427	1597.96	1598.674	6123.2	1	910.7	66.7	1	R.YGEAGEGPGWGGAHPR.I
*	HsFLAG-ARP6_Ti_1	2.6719	0.2751	2188.25	2188.5	11876.4	1	586.4	36.8	1	R.SLPIVFDEFVDMDFGTGAVK.I
*	HsFlag-VPS71_Ti_1	6.1766	0.4768	3907.32	3906.382	5247.5	1	766	27.9	8	K.SLGNVIDPLDVIYGISLQGLHNQLLNSNLDPSEVEK.A
*	HsFLAG-ARP6_Ti_1	2.8099	0.3126	1953.67	1955.322	4360.8	1	380.5	50	2	R.LLSPFMPFVTEELFQR.L
gi|7661952|re	3	4	7.00%	963	109935	5.6	squamous cell carcinoma antigen recognized by T cells 3 [Homo sapiens]				
*	HsH2AZ-FLAG_293_	3.4633	0.2621	1779.82	1779.002	6151.7	1	545	53.6	1	K.YKPYEEALLQAEAPR.L
*	HsFlag-VPS71_Ti_1	4.2041	0.3655	2402.91	2401.691	3974.9	1	454.5	50	1	K.LFISGLPFSCTKEELEEICK.A
*	HsH2AZ-FLAG_293_	5.7648	0.3707	2968.21	2967.311	4181.9	1	712.4	30.6	2	R.ALQRPSAAAPQAENGPAAAPAVAAPAATEAPK.M
gi|7705373|re	5	9	7.00%	759	85226	6.8	epithelial protein lost in neoplasm beta [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	3.9068	0.3262	1174.33	1174.299	10397.5	1	2228.4	90	2	K.ISANENSLAVR.S
*	HsFLAG-ARP6_Ti_1	4.0557	0.4193	1733.72	1733.977	6998.8	1	1176	69.2	2	R.LLANQQVFHISCFR.C

*	HsFLAG-ARP6_Ti_1	2.5716	0.3032	1274.85	1275.45	8313.1	3	612.3	59.1	1	K.LSLGTYASLHGR.I
*	HsFLAG-Lin9_Ti_205	4.7323	0.3499	1713.41	1713.931	9429.8	1	1792.5	70	2	R.SRPFTVAASFQSTSVK.S
*	HsFLAG-ARP6_Ti_1	4.405	0.4113	1713.99	1713.931	11405.3	1	2379.6	48.3	2	R.SRPFTVAASFQSTSVK.S
gi|20070197|r	2	2	7.00%	456	50702	6.4	dolichyl-diphosphooligosaccharide-protein glycosyltransferase [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.6196	0.228	1211.58	1211.406	5283.5	1	578.6	70	1	K.PITQYPHAVGK.N
*	HsFLAG-ARP6_Ti_1	3.2805	0.3473	2346.02	2343.598	6554.2	1	547.9	47.5	1	R.VIFSGSLDFFSDSFFNSAVQK.A
gi|20127499|r	3	5	7.00%	344	39587	11.4	arginine/serine-rich splicing factor 6 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.3368	0.2897	1421.21	1420.478	6440.6	1	1207.5	77.3	2	K.NGYGFVEFEDSR.D
	HsFLAG-ARP6_Ti_1	3.1669	0.2486	1309.13	1310.36	6762.5	1	593.7	59.1	1	R.DADDAVYELNGK.E
	HsFLAG-ARP6_Ti_1	4.2565	0.1753	1309.27	1310.36	4682.8	1	1253	86.4	2	R.DADDAVYELNGK.E
gi|75709192|r	1	2	7.00%	329	36560	4.6	hypothetical protein LOC29086 [Homo sapiens]				
gi|75709194|r	1	2	7.00%	329	36560	4.6	hypothetical protein LOC29086 [Homo sapiens]				
	HsSrcap_Ti_201.067	4.7952	0.4202	2107.6	2108.094	6235.3	1	1459.3	59.1	2	R.SEGEGEAASADDGSLNTSGAGPK.S
gi|5453567|re	1	2	7.00%	299	33593	4.8	craniofacial development protein 1 [Homo sapiens]				
*	HsH2AZ-FLAG_293_	4.0732	0.4306	2062.46	2062.374	4078	1	462.7	52.5	2	K.EKPQANVPSALPSLPAGSGLK.R
gi|71143137|r	1	2	7.00%	200	22980	8.4	high-mobility group box 3 [Homo sapiens]				
gi|89030313|r	1	2	6.20%	224	25484	8.8	PREDICTED: similar to high-mobility group box 3 [Homo sapiens]				
gi|89029245|r	1	2	6.20%	224	25484	8.8	PREDICTED: similar to high-mobility group box 3 [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.2159	0.1984	1606.53	1606.819	4034.3	3	523.5	65.4	2	K.KNPEVPVNFAEFSK.K
gi|50363217|r	2	3	6.90%	418	46737	5.6	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [Homo sapien				
gi|50363221|r	2	3	6.90%	418	46737	5.6	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [Homo sapien				
gi|50363219|r	2	3	6.90%	418	46737	5.6	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [Homo sapien				
	HsFLAG-p53-DNA-D	3.4401	0.3178	1780.45	1780.808	7687.4	1	721.1	53.6	2	K.TDTSHHDQDHPTFNK.I
	HsFLAG-p53-DNA-D	2.7344	0.136	1642.21	1642.895	4497.1	1	382.3	57.7	1	K.ITPNLAEFAFSLYR.Q
gi|13899265|r	2	4	6.90%	390	43880	9	Ras association (RalGDS/AF-6) domain family 5 isoform D [Homo sapiens]				
gi|32996735|r	2	4	10.20%	265	30359	8.1	Ras association (RalGDS/AF-6) domain family 5 isoform C [Homo sapiens]				
gi|32996731|r	2	4	6.50%	418	47090	9.1	Ras association (RalGDS/AF-6) domain family 5 isoform A [Homo sapiens]				
	HsFLAG-FLJ20729_	2.8225	0.134	1425.01	1424.683	6687	1	705.9	59.1	1	K.RTSFYLPLDAIK.Q
	HsFLAG-FLJ20729_	3.6059	0.2429	1603.6	1602.912	9561.7	1	956	60.7	3	R.LLAGPDTEVLSFVLK.E
gi|4502101|re	2	2	6.90%	346	38714	7	annexin I [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.4273	0.3246	2357.13	2357.585	4963.4	2	311.5	34.8	1	K.GGPGSAVSPYPTFNPSSDVAALHK.A
*	HsFlag-VPS71_Ti_1	3.9151	0.2913	2358.8	2357.585	5543.3	1	538.9	28.3	1	K.GGPGSAVSPYPTFNPSSDVAALHK.A
gi|31795538|r	1	2	6.90%	202	22710	9	replication factor C 3 isoform 2 [Homo sapiens]				
gi|4506489|re	1	2	3.90%	356	40556	8.3	replication factor C 3 isoform 1 [Homo sapiens]				
	HsFlag-VPS71_Ti_1	4.4431	0.4183	1590.48	1590.69	8330	1	2056.5	84.6	2	K.TVAQSQQLETNSQR.D
gi|5032169|re	2	2	6.80%	500	55551	9.2	telomeric repeat binding factor 2 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_205	4.5523	0.414	2164.06	2165.413	5214.5	1	828.3	61.8	1	K.NLAHPVIQNFSYETFQQK.M
*	HsFlag-NUFIP_Ti_20	3.2438	0.33	1634.35	1634.957	6527.8	1	844.9	63.3	1	K.DLVLPTQALPASPALK.N
gi|19923106|r	1	2	6.80%	355	39731	5.2	paraoxonase 1 [Homo sapiens]				
*	HsSrcap_Ti_202.433	4.6065	0.2315	2459.75	2461.772	4768.5	3	421.7	39.1	2	K.GIETGSEDLEILPNGLAFISSGLK.Y
gi|4557495|re	3	10	6.70%	717	82922	8.1	cleavage stimulation factor subunit 3 isoform 1 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.6849	0.244	1731.65	1730.989	5765.9	1	860.7	65.4	1	R.GCVNPMINIEQLWR.D
*	HsFLAG-FLJ20729_	3.5894	0.2226	2138.46	2139.555	7812.1	1	485.1	44.1	3	R.LLAIEDIDPTLVYIQYMK.F

*	HsFLAG-p53-DNA-D	4.9358	0.3663	1739.31	1739.021	7831.9	1	1524.8	70	6	R.FLAFESNIGDLASILK.V
gi|11024686|r	3	4	6.70%	706	80103	6.8	hypothetical protein LOC55726 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	2.6133	0.3421	2302.63	2303.54	10624.2	1	504.4	39.5	1	K.CELVLIHTYPVGEDSLVSDR.S
*	HsFlag-FLJ90652_2	4.0623	0.3291	1712.2	1712.825	7772.9	1	1212.2	69.2	1	R.TNNIELHYCTGAYR.I
*	HsFlag-FLJ90652_2	3.4726	0.2387	1398.33	1398.602	4595.6	1	806.3	75	2	R.KNDPLPISTVGTR.G
gi|21359951|r	2	2	6.70%	480	50414	9.6	hypothetical protein LOC79171 [Homo sapiens]				
*	HsFlag-DPCD_Ti_20	2.9846	0.135	1922.57	1922.068	11294.7	1	890.7	50	1	R.IFCGDLGNEVNDDILAR.A
*	HsFLAG-p53-DNA-D	3.6691	0.2631	1739.58	1737.909	6124.5	2	527.3	53.6	1	K.GYGFVSFKDPSDYVR.A
gi|4826762|re	2	2	6.70%	406	45205	6.6	haptoglobin [Homo sapiens]				
*	HsFLAG-p53-DNA-D	2.7682	0.2566	1835.57	1836.122	5002.7	1	694.8	60	1	R.VMPICLPSKDYAEVGR.V
*	HsFLAG-p53-DNA-D	3.0994	0.1811	1275.4	1275.404	7500.2	2	971.9	75	1	R.HYEGSTVPEKK.T
gi|4503609|re	1	2	6.70%	255	27844	8.1	electron-transfer-flavoprotein, beta polypeptide isoform 1 [Homo sapiens]				
gi|62420877|r	1	2	4.90%	346	37434	7.2	electron-transfer-flavoprotein, beta polypeptide isoform 2 [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.8814	0.3907	1812.85	1813.145	5678.4	1	1152.8	68.8	2	K.KIEVIKPGDLGVDLTSK.L
gi|4502013|re	1	2	6.70%	239	26478	7.8	adenylate kinase 2 isoform a [Homo sapiens]				
gi|7524346|re	1	2	6.90%	232	25615	7.9	adenylate kinase 2 isoform b [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.8827	0.4047	1996.84	1998.246	9463.2	1	1745.9	70	2	R.LQAYHTQTTPLIEYYR.K
gi|6453818|re	3	5	6.60%	665	73262	9.5	kinesin family member 22 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.3943	0.5014	1720.26	1720.984	7402.3	1	2049.2	76.7	2	K.THTMLGSPEQPGVIPR.A
*	HsFLAG-ARP6_Ti_1	5.4944	0.5034	1669.57	1668.931	6968.1	1	1749.9	75	2	R.LLASQGSQGAPLLSTPK.R
*	HsFLAG-ARP6_Ti_1	3.1746	0.2387	1084.17	1084.264	7669.9	2	1192.7	80	1	K.ANILGLAAGQR.C
gi|21361399|r	2	2	6.60%	589	65309	5.1	alpha isoform of regulatory subunit A, protein phosphatase 2 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	3.3167	0.3485	2213.34	2214.486	10591.3	1	722.8	44.7	1	R.AISHEHSPSDLEAHFVPLVK.R
*	HsFlag-VPS71_Ti_1	2.6175	0.1426	2138.56	2139.342	6272.5	1	355	41.7	1	K.SEIIPMFSNLASDEQDSVR.L
gi|29789415|r	1	5	6.60%	243	27021	8.5	juxtaposed with another zinc finger gene 1 [Homo sapiens]				
*	HsTIP60_Ti_105.252	4.5155	0.4206	1923.19	1924.164	4622.4	1	709.6	63.3	5	K.QELQQPTYVALSYINR.F
gi|31543653|r	1	2	6.60%	136	14514	10	signal recognition particle 14kDa (homologous Alu RNA binding protein) [Homo sapiens]				
*	HsFLAG-p53-DNA-D	2.3228	0.1552	948.52	949.136	5436.8	1	562.9	75	2	K.KISTVVSSK.E
gi|62241042|r	6	10	6.50%	1512	170590	7.3	glutamyl-prolyl tRNA synthetase [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.6526	0.1421	1614.87	1614.885	7462.5	1	861	61.5	2	K.NPEVGLKPVWYSPK.V
*	HsFLAG-ARP6_Ti_1	4.2969	0.2592	3104.23	3105.342	8182.8	1	1038.5	29.3	1	K.TGQEYKPGNPPAEIGQNISSNSSASILESK.S
*	HsFlag-FLJ90652_2	2.603	0.2274	1864.53	1865.091	8007.9	2	383	41.2	1	K.SLIGVEYKPVSATGAEDK.D
*	HsFLAG-ARP6_Ti_1	3.3539	0.2257	1588.26	1588.631	6633.8	1	999.6	58.8	3	K.NQGGGLSSSGAGEGQGPK.K
*	HsFlag-VPS71_Ti_1	2.8288	0.1962	1717.82	1716.805	7651.7	2	499.7	38.9	1	K.NQGGGLSSSGAGEGQGPKK.Q
*	HsFlag-VPS71_Ti_1	3.0345	0.1887	1960.99	1959.268	4102.8	9	264	40.6	2	K.SLCIPFKPLCELQPGAK.C
gi|42476022|r	3	9	6.50%	843	96632	5.6	hypothetical protein LOC55622 [Homo sapiens]				
*	HsFlag-ZnF-HIT2_Ti_	3.1923	0.3087	2445.58	2443.602	8229.8	1	644.6	42.5	2	K.ETPSLYCLLGDVLGDHSCYDK.A
*	HsFlag-ZnF-HIT2_Ti_	3.2074	0.2503	993.49	993.238	6389	1	1235.1	88.9	4	R.ALGLAHVAIK.C
*	HsFlag-ZnF-HIT2_Ti_	5.6222	0.3932	2739.82	2740.011	7042.1	1	1303.8	52.2	3	R.ELADDITAMDTLVTELQDLSNQFR.N
gi|24475847|r	2	3	6.50%	642	71729	5.5	influenza virus NS1A binding protein isoform a [Homo sapiens]				
gi|54144642|r	2	3	19.00%	221	25381	5.1	influenza virus NS1A binding protein isoform b [Homo sapiens]				
	HsFLAG-TCF3_Ti_1	4.2027	0.3339	2528.86	2527.833	10043.8	1	1010.6	45.2	2	K.FDDLNPEAVEVLLNYAYTAQLK.A
	HsFlag-FLJ90652_2	3.6306	0.2842	2435.84	2434.705	9766.6	1	951.9	47.4	1	K.VDAYIQEHLLQISEEEEFLK.L

gi|42519916|r	2	2	6.50%	673	71277	5.2	forkhead box O3A [Homo sapiens]				
gi|4503739|re	2	2	6.50%	673	71277	5.2	forkhead box O3A [Homo sapiens]				
	HsMRGBP-FLAG_Ti_	2.9775	0.4183	1916.67	1917.037	3948	1	411.6	50	1	K.AALQTAPESADDSPSQLSK.W
	HsYL1_Ti_103.2423.	3.4343	0.3838	2456.6	2457.659	5424.1	1	514.8	39.6	1	K.GSGLGSPTSSFNSTVFGPSSLNSLR.Q
gi|40556376|r	2	17	6.50%	553	60547	9.2	cytokine-like nuclear factor n-pac [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	4.3263	0.3848	1889.63	1890.335	7055	1	1418.5	63.9	2	K.IGFLGLGLMGSGIVSNLLK.M
*	HsFLAG-TCF3_Ti_1	4.7965	0.3943	1706.76	1707.026	8421	1	2284.7	75	15	K.DLVLGPSGVLQGIRPGK.C
gi|25777615|r	2	3	6.50%	324	37025	6.8	proteasome 26S non-ATPase subunit 7 [Homo sapiens]				
*	HsFlag-FLJ90652_2	2.9983	0.2567	1011.17	1010.181	5799.2	1	939.5	87.5	1	R.ITNQVHGLK.G
*	HsFLAG-ARP6_Ti_1	4.1248	0.2445	1322.3	1322.55	6703.2	1	1592.4	86.4	2	R.SVVALHNLINNK.I
gi|4504195|re	1	2	6.50%	291	33044	9.7	general transcription factor IIE, polypeptide 2, beta 34kDa [Homo sapiens]				
*	HsSrcap_Ti_202.451	5.001	0.2084	1997.83	1997.253	7456.8	1	1148.7	55.6	2	R.GLGGILLEDIEEALPNSQK.A
gi|45643123|r	3	12	6.40%	856	95051	6.5	nuclear VCP-like isoform 1 [Homo sapiens]				
gi|45643125|r	3	12	7.30%	750	82746	6.4	nuclear VCP-like isoform 2 [Homo sapiens]				
	HsFLAG-TCF3_Ti_1	5.3939	0.5088	1788.52	1789.169	8398.4	1	2138.1	71.9	3	K.TLLAHAIAGELDLPILK.V
	HsFLAG-ARP6_Ti_1	4.889	0.4578	1848.61	1849.19	5827.5	1	922.3	55.3	7	K.ALGLVTPAGVLLAGPPGCGK.T
	HsFLAG-ARP6_Ti_1	4.5849	0.4856	2110.65	2111.291	8147.6	1	1260.4	61.8	2	K.NSAPCVIFFDEVDALCPR.R
gi|40018640|r	2	5	6.40%	531	60577	9.6	parafibromin [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.0258	0.3385	2083.79	2083.578	4073.5	1	655.2	55.3	3	R.TPIIIIPAATTSLITMLNAK.D
*	HsARP6-FLAG_Ti_1	3.7292	0.3833	1576.28	1576.882	8135.2	1	1088.3	61.5	2	R.VVAVFVQGPAWQFK.G
gi|10801345|r	1	2	6.40%	218	25060	4.9	eukaryotic translation initiation factor 3, subunit 12 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.3372	0.4548	1631.97	1631.835	3285	2	312.1	57.7	2	K.ALTNLPHTDFTLCK.C
gi|13376623|r	1	2	6.40%	204	23671	5.8	Ngg1 interacting factor 3 like 1 binding protein 1 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.2665	0.2917	1610.71	1610.816	7060.7	1	854.4	66.7	2	K.VIQHHPDRHETLK.E
gi|17105400|r	7	13	6.30%	2044	231290	6.9	phosphatidylinositol 4-kinase, catalytic, alpha polypeptide isoform 2 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.5341	0.2737	1983.4	1983.315	6760.6	1	1067.9	55.9	1	R.DAVIALGIFLIESDLQHK.D
*	HsFLAG-ARP6_Ti_1	3.4597	0.3492	1874.75	1874.151	5666.9	1	923.9	62.5	3	R.SILPSNLLTVCQEGTLK.R
*	HsFLAG-ARP6_Ti_1	3.0675	0.2146	1938.22	1939.306	7928.3	1	885.4	50	1	K.ASSSAGNLGVLIPVIAVLTR.R
	HsFLAG-ARP6_Ti_1	3.322	0.3376	2118.86	2117.54	6795.3	1	583	44.7	1	K.LLTLGLSLLHADVVPNATIR.N
	HsFLAG-ARP6_Ti_1	2.877	0.2292	2188.44	2189.605	5847.4	1	452	47.2	2	R.SFPPDAILFYIPQIVQALR.Y
	HsFLAG-ARP6_Ti_1	4.2832	0.2978	1445.46	1444.757	6877	1	1183.2	75	4	K.ITNVSAIIKPYPK.G
	HsFLAG-ARP6_Ti_1	3.1988	0.3359	2391.64	2392.677	3842.4	1	492.1	52.5	1	K.VQPGCYLPSNPEAIVLDIDYK.S
gi|7657269|re	4	8	6.30%	1447	164666	8.5	androgen-induced prostate proliferative shutoff associated protein [Homo sapiens]				
gi|7705288|re	4	8	6.50%	1391	158035	8.6	androgen-induced prostate proliferative shutoff associated protein isoform 2 [Homo sapiens]				
	HsFLAG-FLJ20729_	3.0878	0.2252	2007.52	2008.368	10006.6	1	928	53.1	1	K.ELYLNLALHLASDFFLK.H
	HsFLAG-FLJ20729_	4.538	0.3571	2735.53	2736.106	9261.8	1	1085.5	31.5	1	K.VLSFTHPISFHSAETFESLLACLK.M
	HsFLAG-Lin9_Ti_20	5.293	0.4492	3505.74	3507.111	9598.1	1	916.4	25	3	K.SLDPSNLEHLITPLVTIGHIALLAPDQFAAPLK.S
	HsFLAG-p53-DNA-D	4.3483	0.3753	1657.5	1657.908	6074.9	1	981.3	62.5	3	K.TTNVLGAVNKPLSSAGK.Q
gi|32307148|r	4	7	6.30%	1046	116924	6.7	O-linked GlcNAc transferase isoform 1 [Homo sapiens]				
gi|32307150|r	4	7	6.40%	1036	115706	6.7	O-linked GlcNAc transferase isoform 2 [Homo sapiens]				
	HsFlag-FLJ90652_2	1.9168	0.1465	1074.29	1075.253	4102.2	4	350.8	61.1	1	R.SAHFSTLAIK.Q
	HsH2AZ-FLAG_293_	4.2258	0.3637	2191.58	2191.532	6652.9	1	762.4	50	4	K.AVTLDPNFLDAYINLGNVLK.E
	HsFlag-VPS71_Ti_1	3.0852	0.3199	1781.64	1781.973	6146.9	1	869.4	63.3	1	R.LCPTHADSLNNLANIK.R

	HsFLAG-Lin9_Ti_20	3.0803	0.3059	2423.56	2423.65	7279.6	4	261.2	31.6	1	R.SQYGLPEDAIVYCNFNQLYK.I
gi|21361918|r	2	3	6.30%	804	90544	5.8	leucine proline-enriched proteoglycan (leprecan) 1 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.9696	0.454	4350.18	4351.658	9336.5	1	704.8	21.4	2	R.ALCEGPYDYDGYNYLEYNADLFQAITDHYIQVLNCK.Q
*	HsFlag-VPS71_Ti_1	3.8808	0.3912	1488.63	1487.612	7820.8	1	1050.5	64.3	1	R.AVGFSSGTENPHGVK.A
gi|11863154|r	1	6	6.30%	511	57210	6.2	archain [Homo sapiens]				
*	HsFLAG-FLJ20729_	5.8393	0.3303	3086.13	3086.441	11732.2	1	1426.7	28.2	6	K.APGFGGFGSSAVSGGSTAAMITETIIETDKPK.V
gi|4503735|re	2	2	6.30%	553	56788	8.6	forkhead box C1 [Homo sapiens]				
*	HsFLAG-FLJ20729_	3.5412	0.3937	1347.22	1347.513	4934	1	544.5	68.2	1	R.AYGPYTPQPQPK.D
*	HsFLAG-Lin9_Ti_20	2.5938	0.2781	2090.64	2090.255	7667.7	2	394.2	36.4	1	R.GSPQSAAAELSSGLLASAAASSR.A
gi|22027516|r	2	9	6.30%	476	54192	5.6	serine carboxypeptidase vitellogenic-like [Homo sapiens]				
gi|22027518|r	2	9	6.30%	476	54192	5.6	serine carboxypeptidase vitellogenic-like [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.8072	0.3574	2124.41	2123.456	5762.5	1	910.9	59.4	8	R.DLYSALIQFFQIFPEYK.N
	HsFLAG-ARP6_Ti_1	3.0068	0.1226	1423.23	1423.615	4095.3	1	675.6	66.7	1	R.GGGHILPYDQPLR.A
gi|88998579|r	1	5	6.30%	271	29390	8.2	PREDICTED: similar to lactate dehydrogenase A-like 6B [Homo sapiens]				
gi|88999411|r	1	5	6.30%	271	29390	8.2	PREDICTED: similar to lactate dehydrogenase A-like 6B [Homo sapiens]				
gi|88998821|r	1	5	6.30%	271	29390	8.2	PREDICTED: similar to lactate dehydrogenase A-like 6B [Homo sapiens]				
	HsFlag-VPS71_Ti_1	5.8428	0.1271	1944.84	1946.297	4268.8	1	1346.3	81.2	5	K.LIIVSNPVDNLTYVAWK.L
gi|27477134|r	7	9	6.20%	1887	205109	6.8	nucleoporin 210 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.8836	0.4048	2772.54	2773.038	8886.5	1	1366.6	35.9	2	R.WLSTRPEVASIEPLGLDEQQCSQK.A
*	HsFLAG-ARP6_Ti_1	3.3259	0.3126	1877.34	1878.176	8277.8	1	558.3	46.9	1	R.LTSIIFAEDITTGQVLR.C
*	HsFLAG-ARP6_Ti_1	3.6785	0.24	1449.34	1449.641	5473.3	1	1174.2	81.8	1	R.ELYLEDSPLELK.I
*	HsFLAG-ARP6_Ti_1	3.7468	0.3138	2152.49	2153.4	7908.6	1	654.6	44.4	2	R.VSPEEVTIYNHPGIQAELR.I
*	HsFLAG-ARP6_Ti_1	3.0674	0.0984	2546.75	2544.966	9801.4	1	1188	45.2	1	K.LQLLNPEIEAEQILMSPNSYIK.L
*	HsFLAG-ARP6_Ti_1	2.9911	0.3629	1021.71	1022.189	4419.9	1	868	87.5	1	K.VPVVHVDEK.G
*	HsFLAG-ARP6_Ti_1	4.1598	0.2214	1544.3	1544.788	3344.5	1	1204.4	84.6	1	R.VFGAPEVLENLEVK.S
gi|19923399|r	2	2	6.20%	482	54121	5.6	Ras-GTPase activating protein SH3 domain-binding protein 2 isoform a [Homo sapiens]				
gi|45359849|r	2	2	6.20%	482	54121	5.6	Ras-GTPase activating protein SH3 domain-binding protein 2 isoform a [Homo sapiens]				
gi|45359846|r	2	2	6.70%	449	50817	5.4	Ras-GTPase activating protein SH3 domain-binding protein 2 isoform b [Homo sapiens]				
	HsFlag-VPS71_Ti_1	2.8053	0.3374	1465.34	1465.649	3423.6	1	486.2	70.8	1	R.VEAKPEVQSQPPR.V
	HsFlag-VPS71_Ti_1	4.8442	0.472	1968.25	1967.188	6393.2	1	1282.9	65.6	1	K.LPNFGFVVFDDSEPVQR.I
gi|4502317|re	1	2	6.20%	226	26145	8	ATPase, H+ transporting, lysosomal 31kD, V1 subunit E isoform 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.6929	0.2731	1587.61	1587.77	6522.9	1	2050.5	80.8	2	R.ARDDLITDLLNEAK.Q
gi|4506331|re	1	5	6.20%	145	16386	6.7	6-pyruvoyltetrahydropterin synthase [Homo sapiens]				
*	HsFLAG-FLJ20436_	2.0017	0.1779	987.89	988.258	3539.8	1	610.3	81.2	5	K.VLPVGVLYK.V
gi|52630322|r	7	25	6.10%	1966	222859	7.5	chromodomain helicase DNA binding protein 3 isoform 2 [Homo sapiens]				
gi|52630326|r	7	25	6.00%	2000	226590	7.3	chromodomain helicase DNA binding protein 3 isoform 1 [Homo sapiens]				
gi|52630324|r	7	25	5.90%	2045	231360	6.4	chromodomain helicase DNA binding protein 3 isoform 3 [Homo sapiens]				
	HsFlag-VPS71_Ti_1	2.7171	0.3393	2040.89	2041.283	6293.3	1	574.1	44.4	1	R.FSWAQGTDTILADEMGLGK.T
	HsSrcap_Ti_203.417	4.7188	0.4454	1902.17	1901.216	4477.5	1	929.1	68.8	14	K.GPFLVSAPLSTIINWER.E
	HsFLAG-Lin9_Ti_20	4.5874	0.4438	3037.87	3037.529	4231.5	1	517.6	30	2	K.LLLTGTPLQNNLEELFHLLNFLTPER.F
	HsFLAG-Lin9_Ti_20	2.9889	0.1994	2022.9	2022.258	7243.5	1	803.3	56.2	3	K.CCNHPYLFPVAAMESPK.L
	HsSrcap_Ti_204.333	5.2483	0.5175	1857.91	1858.073	4627.8	1	861.4	73.3	3	R.FNAPGAQQFCFLLSTR.A
	HsFLAG-ARP5_Ti_1	2.8267	0.2021	1554.29	1554.619	6562.7	3	601.9	68.2	1	R.HHYEQQQEDLAR.N

	HsSrcap_Ti_203.304	3.709	0.2644	1554.79	1554.827	7815.9	1	1364.1	75	1	K.LLEQALVIEEQLR.R
gi|39995084|r	4	6	6.10%	1042	118013	5.8	hypothetical protein LOC65123 [Homo sapiens]				
*	HsFLAG-FLJ20729_	3.9719	0.1821	1953.09	1954.026	7430.5	1	2510.8	40.7	1	K.GAAAAAAASGAAGGGGGGAGAGAPGGGR.L
*	HsFLAG-FLJ20729_	4.5343	0.3789	1953.14	1954.026	5845.5	1	2009.1	61.1	1	K.GAAAAAAASGAAGGGGGGAGAGAPGGGR.L
*	HsSrcap_Ti_204.285	3.7378	0.3162	2305.72	2306.587	5797.3	1	704.5	52.8	2	R.LLCHLTPSIYTEFPDETLR.S
*	HsFlag-VPS71_Ti_1	4.9794	0.3499	2020.71	2020.337	8298.6	1	1389.4	59.4	2	K.LAQLTLEQILEHLDNLR.L
gi|7705369|re	4	7	6.10%	953	107142	6	coatomer protein complex, subunit beta [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	5.1285	0.4119	2491.35	2491.806	8316.1	1	1880.7	41.2	2	R.NFEHLIPDAPELIHDFLVNEK.D
*	HsFLAG-Lin9_Ti_20	4.1968	0.3469	1953.56	1954.185	4126.1	1	805.2	61.8	2	K.EAGELKPEEEITVGPVQK.L
*	HsFLAG-Lin9_Ti_20	4.0682	0.2115	2091.59	2091.458	6197.4	5	764.4	36.1	1	K.LVEKPSPLTLAPHDFANIK.A
*	HsFLAG-Lin9_Ti_20	4.0232	0.4227	2091.91	2091.458	5901.4	1	751.5	52.8	2	K.LVEKPSPLTLAPHDFANIK.A
gi|7706427|re	2	4	6.10%	684	77486	5.6	cleavage and polyadenylation specific factor 3, 73kDa [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	2.766	0.3732	1375.35	1375.493	5704.3	2	617.7	70	1	R.FCNTVHDIVNR.G
*	HsFlag-VPS71_Ti_1	5.5019	0.3361	3684.64	3685.171	6531	1	895.7	28.3	3	R.AQELLLILDEYWQNHPELHDIPIYYASSLAK.K
gi|5032093|re	2	4	6.10%	541	56598	5.5	solute carrier family 1 (neutral amino acid transporter), member 5 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.3911	0.3665	1436.38	1436.654	4427.8	1	617.3	70.8	2	R.NIFPSNLVSAAFR.S
*	HsFLAG-ARP6_Ti_1	3.5872	0.3832	2158.29	2159.485	4872.3	1	735.6	57.9	2	K.SELPLDPLPVPTEEGNPLLK.H
gi|50811883|r	2	2	6.10%	524	51391	12.4	decreased expression in renal and prostate [Homo sapiens]				
gi|50811885|r	2	2	6.10%	524	51391	12.4	decreased expression in renal and prostate [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	2.6458	0.2743	1654.9	1654.91	5933.1	1	465.7	47.1	1	R.PGGLLGPGPGPGPTLNPR.T
	HsFLAG-ARP6_Ti_1	3.2386	0.1778	1334.07	1334.518	3899.2	2	651.1	69.2	1	R.TGALPGPGPLSNPR.L
gi|42560246|r	1	4	6.10%	346	39250	5.5	RNA polymerase I subunit isoform 1 [Homo sapiens]				
gi|4759046|re	1	4	6.10%	342	38647	6	RNA polymerase I subunit isoform 2 [Homo sapiens]				
	HsFlag-NUFIP_Ti_1	5.5614	0.3961	2294.64	2295.592	5071.6	1	911.2	57.5	4	R.LLPDITLLEPVEGEAAEELSR.C
gi|16905517|r	1	7	6.10%	262	31301	11.3	FUS interacting protein (serine-arginine rich) 1 isoform 2 [Homo sapiens]				
gi|88952702|r	1	7	15.10%	106	12581	9.4	PREDICTED: similar to FUS interacting protein (serine-arginine rich) 1 [Homo sapiens]				
gi|88944399|r	1	7	23.20%	69	8329	9.4	PREDICTED: similar to FUS interacting protein (serine-arginine rich) 1 isoform 10 [Homo sapiens]				
gi|88944397|r	1	7	6.10%	262	31301	11.3	PREDICTED: similar to FUS-interacting serine-arginine-rich protein 1 (TLS-associated protein with Ser-Arg re				
gi|88944395|r	1	7	23.20%	69	8329	9.4	PREDICTED: similar to FUS interacting protein (serine-arginine rich) 1 isoform 9 [Homo sapiens]				
gi|88944389|r	1	7	8.70%	183	22222	10.3	PREDICTED: similar to FUS interacting protein (serine-arginine rich) 1 isoform 6 [Homo sapiens]				
gi|88944257|r	1	7	9.20%	173	21000	10.5	PREDICTED: similar to FUS interacting protein (serine-arginine rich) 1 isoform 4 [Homo sapiens]				
gi|88944255|r	1	7	23.20%	69	8329	9.4	PREDICTED: similar to FUS interacting protein (serine-arginine rich) 1 isoform 3 [Homo sapiens]				
gi|88944253|r	1	7	23.20%	69	8329	9.4	PREDICTED: similar to FUS interacting protein (serine-arginine rich) 1 isoform 2 [Homo sapiens]				
gi|5730079|re	1	7	8.70%	183	22222	10.3	FUS interacting protein (serine-arginine rich) 1 isoform 1 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	3.9271	0.2452	1919.5	1918.199	7294.2	1	828.5	53.3	7	R.YGPIVDVYVPLDFYTR.R
gi|7427519|re	3	4	6.00%	821	92889	5.4	minichromosome maintenance protein 6 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.2841	0.3474	2473.11	2473.714	10771.7	1	597.9	37.5	1	K.NLYHNLCTSLFPTIHGNDEVK.R
*	HsFLAG-ARP6_Ti_1	2.6864	0.3828	1686.11	1686.865	5590	1	451.6	50	1	R.TSILAAANPISGHYDR.S
*	HsFlag-VPS71_Ti_1	4.0241	0.2195	1406.42	1406.486	7460.9	1	1105.5	77.3	2	R.KVEEEEDESALK.R
gi|41148718|r	2	3	6.00%	752	85887	7.1	PREDICTED: v-myb myeloblastosis viral oncogene homolog (avian)-like 1 isoform 1 [Homo sapiens]				
gi|89028677|r	2	3	6.00%	752	85887	7.1	PREDICTED: similar to Myb-related protein A (A-Myb) isoform 7 [Homo sapiens]				
gi|89028675|r	2	3	6.50%	692	78951	6.7	PREDICTED: similar to Myb-related protein A (A-Myb) isoform 12 [Homo sapiens]				
gi|89028669|r	2	3	5.90%	765	87369	7	PREDICTED: similar to Myb-related protein A (A-Myb) isoform 9 [Homo sapiens]				

gi|89028072|r	2	3	6.50%	692	78951	6.7	PREDICTED: v-myb myeloblastosis viral oncogene homolog (avian)-like 1 isoform 6 [Homo sapiens]				
gi|89028066|r	2	3	5.90%	765	87369	7	PREDICTED: v-myb myeloblastosis viral oncogene homolog (avian)-like 1 isoform 3 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	3.2949	0.204	1274.15	1274.425	7167.9	1	997.5	77.8	2	R.WHNHLNPEVK.K
	HsFLAG-Lin9_Ti_20	5.097	0.411	3958.44	3960.278	10278	1	891	24.3	1	K.TLPFSPSQFFNTCPGNEQLNIENPSFTSTPICGQK.A
gi|32483367|r	3	4	6.00%	711	82254	7.6	origin recognition complex, subunit 3 isoform 2 [Homo sapiens]				
gi|32483369|r	3	4	6.00%	712	82325	7.6	origin recognition complex, subunit 3 isoform 1 [Homo sapiens]				
	HsFLAG-FLJ20729_	3.5932	0.3021	1496.55	1494.731	8823.1	2	1127	72.7	1	K.NLFDNLIEFLQK.S
	HsFLAG-FLJ20729_	3.0419	0.2227	1937.62	1937.159	8804.2	1	949.1	56.7	1	K.NIWDSEEYASVLQLLR.M
	HsFLAG-Lin9_Ti_20	4.6468	0.3483	1794.31	1795.091	9681.2	1	2183	75	2	R.IALHTALNNPYYYLK.N
gi|7706485|re	2	2	6.00%	704	80011	8	TNF receptor-associated protein 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.3326	0.2411	1493.5	1493.746	5126.1	3	561	62.5	1	R.AQLLQPTLEINPR.H
*	HsFLAG-FLJ20729_	4.0957	0.1609	3070.27	3071.472	8204.2	1	1084.2	28.6	1	R.ASEPGLAQLLVDQIYENAMIAAGLVDDPR.A
gi|4503523|re	2	2	6.00%	548	63973	6	eukaryotic translation initiation factor 3 subunit 7 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.6011	0.2037	1617.15	1615.827	9392.1	1	1226	65.4	1	R.IFHTVTTTDDPVIR.K
*	HsFlag-VPS71_Ti_1	4.6106	0.4027	2310.12	2311.543	6491.9	1	1017	55.6	1	R.NLAMEATYINHNFSQQCLR.M
gi|31543419|r	2	2	6.00%	521	57076	8.5	polynucleotide kinase 3'-phosphatase [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.7446	0.2384	1429.54	1429.746	8258.3	6	785.1	57.7	1	K.LLVFTAAGVKPQGK.V
*	HsFLAG-p53-DNA-D	3.6294	0.3438	1842.44	1842.194	6442.9	1	886.6	62.5	1	K.LGVPFQVLVATHAGLYR.K
gi|7706310|re	2	2	6.00%	402	47620	10	LUC7-like 2 [Homo sapiens]				
*	HsFLAG-FLJ20729_	4.1226	0.4106	1616.59	1617.71	6165.8	1	1225.1	71.4	1	K.VEQLGAEGNVEESQK.V
*	HsFlag-NUFIP_Ti_1	2.7581	0.1777	1098.7	1098.334	5512.8	2	1016.7	87.5	1	K.LHLGFIEIR.E
gi|38049014|r	2	3	6.00%	402	45297	9.3	semenogelin I isoform b preproprotein [Homo sapiens]				
gi|4506883|re	2	5	5.20%	462	52131	9.3	semenogelin I isoform a preproprotein [Homo sapiens]				
	HsFLAG-TCF3_Ti_1	3.4235	0.22	1502.11	1502.67	10298.3	8	625.4	54.2	1	R.LPSEFSQFPHGQK.G
	HsFLAG-TCF3_Ti_1	3.1728	0.2791	1287.48	1287.326	6987.7	1	988.4	80	2	K.ISYQSSSTEER.R
gi|4557321|re	1	2	6.00%	267	30778	5.8	apolipoprotein A-I preproprotein [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.9653	0.43	1934.3	1934.113	6113.2	1	725.3	60	2	R.EQLGPVTQEFWDNLEK.E
SHUFFLED_	1	3	6.00%	251	28638	7.8	FALSE POSITIVE				
SHUFFLED_	1	3	6.00%	251	28638	7.8	FALSE POSITIVE				
	HsScrap_Ti_106.262	3.5195	0.1223	1770.67	1771.968	7974.3	6	630.5	50	3	K.LLEDQILGVDHNNYK.E
SHUFFLED_	1	3	6.00%	151	16311	11.9	FALSE POSITIVE				
SHUFFLED_	1	3	6.00%	151	16311	11.9	FALSE POSITIVE				
SHUFFLED_	1	3	6.00%	151	16311	11.9	FALSE POSITIVE				
	HsScrap_Ti_104.185	3.0961	0.1878	1064.06	1063.222	5825.2	3	1202.7	87.5	3	R.HMQPAVSHR.P
gi|32528306|r	4	4	5.90%	1147	128183	9.4	replication factor C large subunit [Homo sapiens]				
*	HsYL1_Ti_101.1800.	4.0441	0.3877	1934.25	1935.009	6808.9	1	1092.1	61.8	1	K.ELSQNTDESGLNDEAIAK.Q
*	HsFLAG-Lin9_Ti_20	3.5438	0.1155	2863.1	2864.188	4773.9	1	524.8	29	1	K.GAENCLEGLIFVITGVLESIERDEAK.S
*	HsFLAG-Lin9_Ti_20	3.4535	0.2011	1384.15	1384.616	10347.8	4	1288.2	72.7	1	K.IIDEDGLLNLIR.T
*	HsFlag-DPCD_Ti_20	2.0462	0.2963	1067.71	1067.274	7256.3	6	399.2	50	1	K.AALLSGPPGVGK.T
gi|47519639|r	4	5	5.90%	1152	121005	5.4	microtubule-associated protein 4 isoform 1 [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.6318	0.3714	2228.54	2227.43	11156.7	1	1202.4	50	1	R.DFIATLEAEAFDDVVGETVGK.T
	HsFLAG-FLJ20729_	4.6172	0.4658	1565.11	1564.927	6477.3	1	1829	80	2	K.KPMSLASGLVPAAPPK.R
	HsFlag-VPS71_Ti_1	3.2175	0.2257	1383.5	1383.55	7359.1	1	1124.1	73.1	1	K.RASPSKPASAPASR.S

	HsFLAG-p53-DNA-D	3.3931	0.2771	1591.49	1591.808	7520	1	838.5	53.1	1	K.VGSLDNVGHLPAGGAVK.T
gi|32698714|r	4	7	5.90%	1105	120966	8.7	hypothetical protein LOC284058 [Homo sapiens]				
*	HsFLAG-FLJ20436_	2.8837	0.36	1710.37	1709.894	6882.6	1	670.3	53.3	1	K.SPLSSILFSALDSDTR.I
*	HsFLAG-FLJ20436_	3.9256	0.4441	1656.92	1656.787	7290.3	1	1021.1	60	3	K.AASETTTSEGLSNFLK.S
*	HsFLAG-FLJ20436_	4.1325	0.4583	1637.38	1637.753	5374.5	1	1244.8	73.3	1	R.LNLVSSSSDGTCVAAR.T
*	HsFLAG-FLJ20436_	3.1738	0.4116	1773.47	1773.042	7191	1	767	53.1	2	R.SPISPELHSAPLTPVAR.D
gi|21264343|r	3	5	5.90%	915	102642	5.5	scaffold attachment factor B [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	3.5115	0.2398	2976.68	2978.153	10104.6	1	918.5	26.9	1	K.SEPVKEESSELEQPFAQDTSSVGPDRK.L
	HsFlag-NUFIP_Ti_2	3.7156	0.2993	1736	1735.9	7129.6	1	813.8	57.1	2	R.KFDFDACNEVPPAPK.E
*	HsFLAG-p53-DNA-D	3.8017	0.2853	1355.55	1355.493	7409.5	1	1541.5	77.3	2	R.NFWVSGLSSTTR.A
gi|24234690|r	3	4	5.90%	680	77642	5.8	meiotic recombination 11 homolog A isoform 2 [Homo sapiens]				
gi|5031923|re	3	4	5.60%	708	80593	5.9	meiotic recombination 11 homolog A isoform 1 [Homo sapiens]				
	HsARP6-FLAG_Ti_1	4.2987	0.2811	1494.16	1493.657	7544.6	1	1921.3	83.3	1	R.GNDTFVTLDEILR.L
	HsARP6-FLAG_Ti_1	3.6193	0.3605	1404.57	1404.606	7512.4	1	1462.8	70.8	2	K.IALYGLGSIPDER.L
	HsARP6-FLAG_Ti_1	4.0672	0.3421	1573.12	1573.745	5891.3	1	1195.9	73.1	1	R.VDYSGGFEPFSVLR.F
gi|21614525|r	2	5	5.90%	556	62412	6.7	glypican 4 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.6057	0.4227	1933.42	1933.097	11076.3	1	1446.8	56.2	1	K.SVVSEQCNHLQAVFASR.Y
*	HsFLAG-ARP6_Ti_1	3.4842	0.3781	1737.93	1738.991	4184.1	1	683.8	63.3	4	K.VSVVNPTAQCTHALLK.M
gi|24430160|r	2	2	5.90%	389	44173	7.5	proteasome 26S ATPase subunit 6 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	2.5804	0.2099	1799.77	1799.077	4565.6	2	365.1	53.6	1	R.EVIELPLTNPELFQR.V
*	HsFlag-VPS71_Ti_1	2.0579	0.2085	836.56	837.01	5020	3	573.3	78.6	1	K.IHAGPITK.H
gi|6005721|re	2	3	5.90%	339	37840	5.6	SPFH domain family, member 2 isoform 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	5.5529	0.4365	2125.15	2125.535	4892.4	1	1190	65.8	2	K.LALQQDLTSMAPGLVIQAVR.V
*	HsFLAG-ARP6_Ti_1	3.9851	0.2572	2125.66	2125.535	7420.5	3	1080.3	35.5	1	K.LALQQDLTSMAPGLVIQAVR.V
gi|13124875|r	7	24	5.80%	1938	223575	5.5	smooth muscle myosin heavy chain 11 isoform SM2 [Homo sapiens]				
gi|13124879|r	7	24	5.70%	1972	227337	5.5	smooth muscle myosin heavy chain 11 isoform SM1 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	3.8076	0.3868	2125.48	2126.205	8110.7	1	708	44.7	1	R.EDQSILCTGESGAGKTENTK.K
	HsFLAG-ARP6_Ti_1	4.8327	0.3425	2373.85	2373.708	5896	1	1097.7	55	5	R.INFDVTGYIVGANIETYLLEK.S
	HsFLAG-ARP6_Ti_1	2.7773	0.2777	1592.1	1592.678	3561.8	1	582.7	64.3	2	R.NTDQASMPDNTAAQK.V
	HsFLAG-ARP6_Ti_1	3.9279	0.1225	2468.62	2468.789	8469.2	1	1635.8	41.7	1	K.LQQLFNHTMFILEQEEYQR.E
	HsFLAG-ARP6_Ti_1	3.1298	0.1302	1258.36	1258.417	6831.5	4	1016.2	80	1	K.KEEELQAALAR.L
	HsFLAG-Lin9_Ti_20	3.416	0.1163	1220.85	1221.396	6427.8	2	1186.2	83.3	2	R.KFDQLLAEEK.N
	HsFLAG-ARP6_Ti_1	6.8581	0.5173	1962.21	1963.059	10191.7	1	3429.4	81.2	12	K.TQLEELEDELQATEDAK.L
gi|19913418|r	3	8	5.80%	831	95756	6.7	ATPase, H+ transporting, lysosomal V0 subunit a isoform 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.5701	0.3179	1998.09	1998.261	9713.3	1	1082.5	52.9	1	K.ANIPIMDTGENPEVPFPR.D
*	HsFLAG-ARP6_Ti_1	3.3582	0.2747	2051.49	2052.304	10598.2	1	949.4	53.1	2	R.DMIDLEANFEKIENELK.E
*	HsFLAG-ARP6_Ti_1	4.254	0.1953	1543.21	1542.818	5931.4	1	1768.4	83.3	5	K.SVFIIFFQGDQLK.N
gi|31543212|r	3	14	5.80%	711	80320	7.7	macrophage stimulating 1 (hepatocyte growth factor-like) [Homo sapiens]				
*	HsSrcap_Ti_205.385	5.9827	0.473	3183.8	3186.431	4730.2	1	1179	36.6	6	R.GTELQHLLHAVVPGPWQEDVADAEECAGR.C
*	HsSrcap_Ti_204.371	4.9719	0.4357	3183.97	3186.431	4682.6	1	566.3	39.3	6	R.GTELQHLLHAVVPGPWQEDVADAEECAGR.C
*	HsSrcap_Ti_202.204	4.3913	0.344	1516.56	1516.573	7178.4	1	1804.2	86.4	2	K.FLDQGLDDNYCR.N
gi|9910242|re	2	2	5.80%	483	55816	4.9	hypothetical protein LOC57003 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.5603	0.2352	1243.49	1244.398	6658.3	1	752.1	72.2	1	R.LAQAWFNTHR.E

*	HsSrcap_Ti_206.273	3.2253	0.2696	2014.1	2013.304	7851.1	1	613.1	47.1	1	K.RTLLFTFNVPGSGNTYPK.D
gi|45006986|r	1	3	5.80%	312	34353	8.4	small inducible cytokine subfamily E, member 1 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.8684	0.4326	2021.31	2022.33	7107.3	1	602	47.1	3	R.TVVSGLVNHVPLEQMQNR.M
gi|44681484|r	2	3	5.70%	1023	112676	8.4	cell division cycle associated 2 [Homo sapiens]				
*	HsYL1_Ti_101.2084.	4.3674	0.4552	2653.81	2653.748	4293.4	1	454	41.7	1	K.SSSSLGNATSDEDPNTNIMNINENK.N
*	HsYL1_Ti_103.2436.	5.2382	0.4169	3569.08	3569.876	8823.6	1	1445.9	28.1	2	R.VASDSPKPALTLQQGQEFSAGGQNAENLCQFFK.I
gi|4504205|re	2	2	5.70%	911	100680	7.3	general transcription factor IIIC, polypeptide 2, beta 110kDa [Homo sapiens]				
*	HsFlag-DPCD_Ti_20	4.6185	0.3029	3266.25	3267.71	7163.5	1	1092.4	30.8	1	R.AAQVALLYLQELAEELSTALPAPVSCPEGPK.V
*	HsFLAG-Lin9_Ti_20	4.3978	0.3659	2240.6	2240.48	8611.6	1	847.7	45	1	R.FSPNLDSYGWLVSGGQSGLVR.I
gi|4506583|re	2	5	5.70%	616	68138	7.2	replication protein A1, 70kDa [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.6488	0.4349	1486.68	1486.582	7212.2	1	939.2	60	1	K.AAGPSLSHTSGGTQSK.V
*	HsFLAG-p53-DNA-D	5.1414	0.304	2009.42	2009.18	9435.8	1	2075	63.9	4	R.GWFDAEGQALDGVSISDLK.S
gi|30795212|r	2	3	5.70%	579	63705	8.9	insulin-like growth factor 2 mRNA binding protein 3 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	3.081	0.191	2183.25	2182.435	5984.7	1	425.2	39.5	1	K.LYIGNLSENAAPSDLESIFK.D
*	HsFLAG-ARP6_Ti_1	2.7964	0.1003	1487.18	1487.563	4697.2	1	1064.7	75	2	R.DQTPDENDQVVVK.I
gi|41146847|r	2	2	5.70%	581	62543	9.4	PREDICTED: hypothetical protein LOC57606 isoform 1 [Homo sapiens]				
gi|88979579|r	2	2	7.00%	469	51384	8.8	PREDICTED: hypothetical protein LOC57606 isoform 9 [Homo sapiens]				
gi|88979572|r	2	2	5.70%	581	62543	9.4	PREDICTED: hypothetical protein LOC57606 isoform 6 [Homo sapiens]				
gi|88974131|r	2	2	7.00%	469	51384	8.8	PREDICTED: hypothetical protein LOC57606 isoform 3 [Homo sapiens]				
	HsFLAG-FLJ20309_	2.9673	0.2414	2057.61	2057.177	9627.5	1	818.1	50	1	R.LSGWEEEEESWLYSSPK.K
	HsFlag-DPCD_Ti_20	3.5811	0.3664	1738.38	1738.938	5903.9	5	352.4	43.3	1	R.LSLQGHPTDLQTSNVK.N
gi|4507947|re	2	3	5.70%	528	59144	7	tyrosyl-tRNA synthetase [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.7855	0.343	2044.86	2045.343	6192.6	1	661	52.9	2	R.TVVSGLVQFVPKEELQDR.L
*	HsFLAG-ARP6_Ti_1	3.6027	0.3188	1411.5	1411.737	8842.8	1	1615	81.8	1	R.LVVVLCNLKPQK.M
gi|40255127|r	2	3	5.70%	522	58510	4.6	hypothetical protein LOC166968 [Homo sapiens]				
*	HsH2AZ-FLAG_293_	3.4997	0.3724	2336.62	2337.554	4892.9	1	535.2	47.2	1	K.VYENEDQLLWCPDVVLESK.V
*	HsH2AZ-FLAG_293_	4.1209	0.1977	1338.74	1336.485	6458.7	2	1095.4	80	2	R.DNEQALYELLK.C
gi|68303639|r	2	2	5.70%	509	54365	8.7	CUG triplet repeat, RNA binding protein 2 isoform 2 [Homo sapiens]				
gi|68303647|r	2	2	5.70%	508	54285	8.8	CUG triplet repeat, RNA binding protein 2 isoform 3 [Homo sapiens]				
gi|68303645|r	2	2	5.90%	490	52268	8.6	CUG triplet repeat, RNA binding protein 2 isoform 1 [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.9234	0.3119	1913.63	1912.196	6578.1	1	962.7	63.3	1	K.ELFEPYGAVYQINVLR.D
	HsFLAG-Lin9_Ti_20	3.1875	0.1983	1393.06	1393.586	11480.5	1	1312.4	66.7	1	K.AALEAQNALHNIK.T
gi|22095347|r	1	2	5.70%	442	48537	5.1	immunoglobulin superfamily, member 4 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.6532	0.4139	2476.23	2477.471	7658.2	1	1198.6	47.9	2	K.GADDAADADTAIINAEGGQNNSEEK.K
gi|11125772|r	1	4	5.70%	332	31545	4.4	myristoylated alanine-rich protein kinase C substrate [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.6834	0.3466	1786.44	1785.908	7488.6	1	1089.1	55.6	4	K.GEAAAERPGEAAVASSPSK.A
gi|15431303|r	1	2	5.70%	192	21863	10	ribosomal protein L9 [Homo sapiens]				
gi|89039140|r	1	2	5.30%	207	23369	11.1	PREDICTED: similar to ribosomal protein L9 [Homo sapiens]				
gi|89038445|r	1	2	5.30%	207	23369	11.1	PREDICTED: similar to ribosomal protein L9 [Homo sapiens]				
gi|67944630|r	1	2	5.70%	192	21863	10	ribosomal protein L9 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.2022	0.2214	1331.19	1331.539	7406.1	1	828	65	2	R.TICSHVQNMIK.G
gi|5032189|re	5	7	5.60%	1972	213573	4.7	tumor protein p53 binding protein, 1 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.3547	0.2973	1733.54	1734.006	6130.4	1	612.6	56.7	1	K.DIPVTAQPSKDVHVVK.E

*	HsFlag-VPS71_Ti_1	4.4474	0.3338	3762.42	3762.999	6593.8	1	1157.6	27.9	2	K.TVSSDGCSTPSREEGGCSLASTPATTLHLLQLSGQR.S
*	HsFLAG-p53-DNA-D	3.571	0.3801	2039.88	2040.411	4447.1	4	259.7	42.1	1	K.EGDIIPPLTGATPPLIGHLK.L
*	HsFlag-VPS71_Ti_1	3.6517	0.4284	1669.5	1669.761	6216.1	1	967	55.9	1	R.TSSGTSLSAMHSSGSSGK.G
*	HsFLAG-ARP6_Ti_2	4.0568	0.4384	2024.35	2024.106	4327	1	557.6	50	2	R.SNVSSPATPTASSSSSTTPTR.K
gi|42734325|r	4	7	5.60%	1190	132945	5.4	KIAA0261 [Homo sapiens]				
*	HsYL1_Ti_101.1439.	3.5603	0.1933	1438.37	1438.497	5547	1	1039.3	75	2	R.IVEDDASISSCNK.L
*	HsYL1_Ti_103.1786.	3.9093	0.2374	2305.25	2305.593	5021.7	1	682.5	52.6	2	R.VLESVTVHNPENQSYLIAYK.D
*	HsARP6-FLAG_Ti_1	3.5387	0.3322	1730.15	1731.089	7947.2	1	801.7	53.3	1	R.VLGLGLLINLVEYSAR.N
*	HsYL1_Ti_106.3060.	4.5221	0.4122	1979.95	1979.333	7673.5	1	1626.9	61.8	2	R.IGGQVHAVQALVQLFLER.E
gi|40255237|r	4	6	5.60%	1156	132195	6.8	leucine zipper protein 5 [Homo sapiens]				
*	HsYL1_Ti_102.3671.	3.2728	0.3106	1936.8	1936.083	7552.2	1	1078.7	56.2	2	K.EASDPFSLNELLDELSR.K
*	HsYL1_Ti_106.2638.	3.3136	0.222	1601.48	1600.945	4579.1	1	654	65.4	1	K.LSHPLLEQLLPALR.Y
*	HsFlag-VPS71_Ti_1	2.7284	0.2374	1582.88	1582.797	6533.6	2	719.2	57.1	1	K.ADLESLLQTPGGKPR.G
*	HsYL1_Ti_105.3199.	3.7152	0.4142	1990.41	1990.354	3766.3	1	576.1	50	2	R.GVLSTLIAGPVVEISHQLR.K
gi|6912398|re	3	3	5.60%	886	101272	5.1	general transcription factor IIIC, polypeptide 3, 102kDa [Homo sapiens]				
*	HsFLAG-FLJ20309_	2.9693	0.3278	2350.95	2351.529	7267.6	1	269	32.5	1	K.SYYEANDVTSAINIIDEAFSK.H
*	HsFLAG-Lin9_Ti_20	3.8912	0.1866	1671.79	1670.904	7624.7	1	1037.7	64.3	1	R.ISLSTLQQQLGQPEK.A
*	HsFLAG-FLJ20309_	2.9788	0.3022	1572.01	1569.795	9761.5	1	936.1	61.5	1	K.ELEYFGLSAAILDK.N
gi|13375885|r	2	2	5.60%	641	71086	6.5	chromosome 14 open reading frame 169 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_2	3.4589	0.3768	1496.06	1496.666	8495.3	1	892.9	61.5	1	R.LGHFAPVDAVADQR.A
*	HsFLAG-TCF3_Ti_1	3.5491	0.3115	2442.95	2440.63	9191.4	1	642.3	38.1	1	R.VGDLPCDSVEDQLSLATTLYDK.G
gi|24497620|r	2	2	5.60%	627	70730	8.6	signal recognition particle 68kDa [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.5686	0.2269	2570.12	2569.998	6560.3	1	1031.1	52.4	1	R.LYDIILQNLVELLQLPGLEEDK.A
*	HsFLAG-FLJ20729_	4.125	0.2632	1526.27	1526.73	4893	1	774.8	70.8	1	K.DLPDVQELITQVR.S
gi|21361499|r	3	4	5.60%	574	65010	8.6	SUMO1/sentrin/SMT3 specific protease 3 [Homo sapiens]				
*	HsH2AZ-FLAG_293_	4.1173	0.2692	1418.79	1418.679	8556.2	1	1462.4	72.7	2	K.GLVLQLIQSYQR.M
*	HsH2AZ-FLAG_293_	3.0551	0.3286	1451.45	1451.624	3462.7	1	539.3	80	1	K.VHFFNSFFYDK.L
*	HsH2AZ-FLAG_293_	2.618	0.1605	1049.98	1050.243	4706.1	4	929.5	93.8	1	K.YLQAEAVKK.D
gi|34485722|r	1	2	5.60%	521	57811	4.9	karyopherin alpha 3 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	5.2136	0.4039	3023.8	3023.373	10436.9	1	1983.9	33.9	2	K.AQNVTLEAILQNATSDNPVVQLSAVQAAR.K
gi|13399296|r	2	2	5.60%	497	51067	9.3	MYC-associated zinc finger protein [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.4864	0.3053	1552.3	1552.693	4277.8	1	618.9	70.8	1	K.SFSRPDHLNSHVR.Q
*	HsFLAG-FLJ20729_	3.2649	0.3871	1804.07	1802.92	8792.6	1	1253.4	67.9	1	K.VHSQGPHHVCELCNK.G
gi|38044290|r	2	2	5.50%	707	78577	4.9	zinc finger, CCHC domain containing 8 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.1344	0.2856	2262.4	2263.555	8241	1	428.6	39.5	1	K.LGQPLLNENPQLSEGWEIPK.Y
*	HsFLAG-ARP6_Ti_1	3.0552	0.2771	2047.42	2047.313	7057	1	626.5	52.8	1	R.FKPGVISEELQDALGVTDK.S
gi|5454096|re	2	3	5.50%	487	55630	5.1	serine/threonine kinase 4 [Homo sapiens]				
	HsARP6-FLAG_Ti_1	3.132	0.106	1338.68	1338.506	7770.6	1	992.6	66.7	2	K.AGNILLNTEGHAK.L
*	HsFLAG-ARP6_Ti_1	3.0064	0.1605	1727	1726.926	10660.3	1	1092.4	61.5	1	R.KPELWSDNFTDFVK.Q
gi|4506783|re	1	2	5.50%	220	23306	9.2	sin3 associated polypeptide p30 [Homo sapiens]				
*	HsSrcap_Ti_205.233	3.7674	0.3593	1431.22	1429.628	7400.6	1	1302.7	77.3	2	K.AQLVEIVGCHFR.S
gi|6382079|re	12	28	5.40%	3224	358173	6.2	RAN binding protein 2 [Homo sapiens]				
	HsScrap_Ti_102.299	3.205	0.3291	1566.41	1565.764	6188.2	1	497.4	53.8	2	R.ELLQSFDSALQSVK.S

	HsFlag-VPS71_Ti_1(	3.2897	0.217	1788.65	1786.936	8271.5	1	833.8	50	1	K.SGQSALYDALFSSQSPK.D
	HsScrap_Ti_105.186	2.7444	0.1612	1335.54	1336.577	4894.7	1	431.7	70	1	R.LLVQHEINTLR.A
	HsFlag-VPS71_Ti_1(	3.2882	0.2649	1336.77	1336.577	5684.3	1	918.2	80	2	R.LLVQHEINTLR.A
	HsFlag-VPS71_Ti_1(	3.1041	0.1631	2433.63	2433.707	8189.6	1	636.7	42.5	1	K.EMLNSVMQELEDYSEGGPLYK.N
*	HsFLAG-p53-DNA-D	5.5017	0.4409	2599.31	2599.949	8321.2	1	2317.6	45.2	4	R.SFVWHALDYADELPKPEQLAIR.F
*	HsFLAG-FLJ20729_	3.354	0.2935	1487.23	1487.674	6085.9	1	569.3	57.1	1	K.APGTNVAMASNQAVR.I
*	HsScrap_Ti_102.282	2.8716	0.3191	1598.82	1598.88	6280.7	1	727.9	57.1	2	K.ELVGPPLAETVFTPK.T
	HsFlag-VPS71_Ti_1(	3.9782	0.4272	1824.48	1824.896	6290.8	1	725	55.9	10	K.QNQTTSAVSTPASSETSK.A
*	HsFlag-VPS71_Ti_1(	4.7874	0.3993	2097.63	2096.301	3756	1	754.7	67.6	1	K.NLFASFPTEESSINYTFK.T
*	HsScrap_Ti_104.236	2.5791	0.2153	1172.42	1173.363	7167.8	3	607.7	62.5	2	K.LPPTFFCYK.N
*	HsFlag-VPS71_Ti_1(	3.4329	0.2266	1576.52	1576.626	9244.2	1	1084.4	70.8	1	K.CRPLEENTADNEK.E
gi|31621305|r	5	9	5.40%	1394	157904	6.1	leucine-rich PPR motif-containing protein [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.3896	0.3991	1664.38	1663.914	6720	1	1275.8	67.9	1	K.LGAVYDVSHYNALLK.V
*	HsFLAG-ARP6_Ti_1	2.6951	0.2783	1726.68	1725.939	8871.7	1	754.9	50	1	R.SEAANGNLDFVLSFLK.S
*	HsFLAG-ARP6_Ti_1	4.0353	0.3812	2323.4	2324.462	4056.9	1	426.1	50	2	R.EGNQEVPFDVPELWYEDEK.H
*	HsFlag-FLJ90652_2(	2.6785	0.1293	1273.53	1273.389	9439.9	7	795.2	65	1	K.TVLDQQQTPSR.L
*	HsFLAG-p53-DNA-D	3.6668	0.4312	1717.49	1717.02	5680.1	1	923.7	73.1	4	K.VIEPQYFGLAYLFR.K
gi|31563531|r	4	11	5.40%	1231	141326	5.4	stromal antigen 2 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1(	4.6495	0.2924	2126.78	2128.405	8245.6	1	1386.3	58.8	1	R.DIALLDLINFFIQCSGCK.G
	HsFlag-VPS71_Ti_1(	1.8636	0.2099	959.5	960.136	5058.6	1	424.4	68.8	1	R.HTSTLAAMK.L
*	HsFLAG-p53-DNA-D	3.9436	0.37	1628.6	1628.008	7406.5	1	1491	71.4	8	K.ITELFAVALPQLLAK.Y
*	HsARP6-FLAG_Ti_1	3.9846	0.4182	2899.1	2898.103	7970.8	1	685.9	28.1	1	R.LLEDFLQEGEEPDEDDAYQVLSTLK.R
gi|14149627|r	2	3	5.40%	952	109297	5.2	ubiquitin specific protease 15 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1(	4.7632	0.4534	3552.82	3554.863	4299	1	583.1	30.2	1	R.FAPQFSGYQQQDCQELLAFLLDGLHEDLNR.I
*	HsFLAG-FLJ20729_	3.7664	0.3477	2142.55	2143.452	9105.4	1	1123.2	50	2	K.IGNILDLCTALSALSGIPADK.M
gi|6631095|re	3	4	5.40%	808	90981	5.8	minichromosome maintenance protein 3 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.8657	0.2922	2192.81	2194.27	7442.1	1	1119	58.8	1	R.DYLDFLDDEEDQGIYQSK.V
*	HsFLAG-p53-DNA-D	2.5107	0.1223	1062.42	1063.164	6285.8	5	468.4	62.5	2	R.SVHYCPATK.K
*	HsFLAG-ARP6_Ti_1	4.0064	0.4244	1837.8	1837.978	6578.2	1	946.8	62.5	1	R.DSEEPFSSVEIQAALSK.M
gi|38683855|r	3	5	5.40%	689	78550	6.4	hypothetical protein LOC55037 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.973	0.3354	1342.68	1342.582	8067.5	1	1627.1	79.2	2	K.VAVLQALASTVNR.D
*	HsFlag-NUFIP_Ti_11	3.9143	0.4584	1791.55	1792.091	5145.4	1	805.1	63.3	2	K.AIGIEPSLATYHHIIR.L
*	HsFlag-NUFIP_Ti_1(	2.568	0.2269	970.2	970.076	3807.9	3	490.3	85.7	1	K.FIGPDQHR.N
gi|63003897|r	2	3	5.40%	690	77673	8.8	transcription factor NRF [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.6403	0.2866	2892.53	2892.157	9416.1	2	813.5	28	1	K.HWTNFVITENANDAIGILNNSASFNK.M
*	HsFLAG-ARP6_Ti_1	2.8514	0.2082	1256.47	1256.488	5387.1	1	835.1	80	2	K.KTQPTVINNLK.K
gi|27734917|r	2	2	5.40%	589	65472	7	hypothetical protein LOC196463 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.4745	0.2237	1826.27	1826.245	8781.4	6	679.7	56.2	1	R.VLTILEQIPGMVVVADK.T
*	HsFLAG-ARP6_Ti_1	3.7186	0.3257	1601.1	1599.667	4924.1	1	890.6	75	1	K.ACNPQPNGENAISAR.S
gi|22035692|r	2	2	5.40%	460	50838	8	GDNF family receptor alpha 1 isoform b preproprotein [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.1533	0.1979	1364.66	1365.659	3365.8	1	463.2	72.7	1	R.VVPFISVEHIPK.G
	HsFLAG-ARP6_Ti_1	3.2381	0.3419	1637.25	1637.799	7015.4	1	918.5	66.7	1	R.RQTIVPVCSYEER.E
gi|32698750|r	3	12	5.30%	1312	139265	9.2	serine arginine-rich pre-mRNA splicing factor SR-A1 [Homo sapiens]				

*	HsFLAG-ARP6_Ti_1	4.3011	0.4616	1685.51	1684.892	5922.7	1	1509.5	69.4	10	R.SPSPAPAPAPAAAAGPPTR.K
*	HsFlag-NUFIP_Ti_11	3.7929	0.3227	2195.35	2194.495	7102.7	1	1044.7	38.2	1	R.RGAVPPSIQDLTDHDLFAIK.R
*	HsFlag-NUFIP_Ti_1	4.2283	0.4162	2822.86	2822.879	5643	1	696.5	29.3	1	K.ESAPSSGPPPKPPVSSGSGSSSSSSSCSSR.K
gi|4504035|re	2	2	5.30%	693	76715	6.9	guanine monophosphate synthetase [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	2.7395	0.2029	2182.99	2180.549	5035.1	9	296.1	38.9	1	R.ELFVQSEIFPLETPAFAIK.E
*	HsFLAG-p53-DNA-D	3.2816	0.3616	2039.71	2040.515	9496.8	1	839.3	47.1	1	K.LMQITSLHSLNAFLLPIK.T
gi|8922679|re	2	2	5.30%	513	57528	7.2	smu-1 suppressor of mec-8 and unc-52 homolog [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.6784	0.2826	2061.34	2060.439	9586.3	1	1377.1	62.5	1	K.TLIDLYEQVVLELIELR.E
*	HsARP6-FLAG_Ti_1	2.5532	0.1851	1243.45	1242.464	5818.2	4	865.4	83.3	1	R.YIHLENLLAR.S
gi|4505047|re	1	2	5.30%	338	38429	6.6	lumican precursor [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	4.2948	0.3697	1959.71	1958.305	5610	1	404.4	50	2	R.LPSGLPVSLLTLYLDNNK.I
gi|13540523|r	1	2	5.30%	282	31525	4.6	nucleosomal binding protein 1 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.2532	0.0951	1611.13	1610.008	2823.2	1	436.3	64.3	2	R.LSAMLVPVTPEVKPK.R
gi|4557385|re	6	13	5.20%	1663	187163	6.4	complement component 3 precursor [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.4222	0.2361	2445.09	2445.818	5589.5	1	482.8	42.9	1	R.EPGQDLVVLPLSITTDFIPSFR.L
	HsSrcap_Ti_202.327	3.754	0.2305	2158.93	2158.431	6687.1	1	646.5	47.4	4	R.ILLQGTPVAQMTEDAVDAER.L
	HsScrap_Ti_102.331	4.8672	0.3598	2160.98	2158.431	8508.7	1	1138.4	39.5	1	R.ILLQGTPVAQMTEDAVDAER.L
	HsScrap_Ti_103.271	3.6074	0.3745	1339.08	1336.574	4321.9	1	920.9	81.8	4	R.APSTWLTAYVVK.V
	HsSrcap_Ti_205.487	5.5296	0.5112	2217.68	2218.608	8028.6	1	1578.1	60	1	K.VFSLAVNLIAIDSQVLCGAVK.W
	HsScrap_Ti_102.175	2.4215	0.227	1300.28	1301.405	4096.5	1	480.4	65	2	K.ACEPGVDYVYK.T
gi|30794372|r	5	6	5.20%	1602	183689	6.7	polybromo 1 isoform 1 [Homo sapiens]				
gi|41281917|r	5	6	5.20%	1582	182117	6.8	polybromo 1 isoform 4 [Homo sapiens]				
	HsFLAG-FLJ20729_	3.4422	0.2419	2039.65	2040.295	8859.3	1	926.4	56.2	1	R.NQPDYYEVVSQPIDLMK.I
	HsFLAG-Lin9_Ti_20	2.656	0.1819	2053.99	2053.364	11024.5	3	595.2	41.7	2	K.EILEQLLEAIVVATNPSGR.L
	HsFLAG-p53-DNA-D	3.6962	0.2699	1957.27	1957.196	7896.8	7	631.9	50	1	R.NNQGQLIAEPFYHLPSK.K
	HsARP6-FLAG_Ti_1	3.213	0.3778	1444.06	1444.501	8130.2	1	949.3	60.7	1	K.SEDSSGAAGLSGLHR.T
	HsFLAG-p53-DNA-D	2.6361	0.1981	1703.45	1704.063	5494.2	4	381.3	53.6	1	R.KPIVPQKEPSPLLEK.K
gi|47933339|r	3	7	5.20%	977	107188	10.1	RNA binding motif protein 15 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	3.6948	0.3238	2451.29	2451.649	8252.1	1	659.1	40.5	1	K.ISELGSQLSDEAVEDGLFHEFK.R
*	HsFLAG-p53-DNA-D	4.2206	0.3653	1776.45	1777.165	6242	1	1009	68.8	5	R.LWVGGLGPWVPLAALAR.E
*	HsScrap_Ti_106.296	1.8947	0.1431	1516.4	1515.672	2891.1	2	142.8	54.5	1	R.RLRVDFADTEHR.Y
gi|73623028|r	1	3	5.20%	756	86239	8.4	carnitine palmitoyltransferase 1A isoform 2 [Homo sapiens]				
gi|73623030|r	1	3	5.00%	773	88368	8.7	carnitine palmitoyltransferase 1A isoform 1 [Homo sapiens]				
	HsSrcap_Ti_203.567	5.25	0.3945	4426.55	4424.876	3292.7	1	514.4	25	3	R.LQWDIPGECQEVIETSLNTANLLANDVDFHSFPFVAFGK.G
gi|15149476|r	2	3	5.20%	660	75379	6.7	arginyl-tRNA synthetase [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.3739	0.4038	2199.77	2200.539	4289.2	1	706.4	61.1	2	K.FPDYLTVSPPIGDLQVFYK.E
*	HsFLAG-ARP6_Ti_1	3.0944	0.1462	1645.33	1644.017	3502.1	1	577.6	60.7	1	K.IVFVPGCSIPLTIVK.S
gi|45505163|r	2	2	5.20%	630	69558	8.1	LISCH protein isoform 1 [Homo sapiens]				
gi|45593136|r	2	2	5.70%	581	64053	8.8	LISCH protein isoform 3 [Homo sapiens]				
gi|45545424|r	2	2	5.10%	649	71439	8	LISCH protein isoform 2 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	2.8801	0.2108	2189.03	2190.461	4911.6	3	347.9	38.1	1	K.AATSGVPSIYAPSTYAHLSPAK.T
	HsFLAG-ARP6_Ti_1	3.4292	0.3023	1166.41	1166.187	8658.2	1	1405.5	80	1	R.DTDSSVASEVR.S
gi|4758024|re	2	4	5.20%	576	62608	9.1	coilin [Homo sapiens]				

*	HsFLAG-Lin9_Ti_20	3.4906	0.259	1459.42	1459.637	10639.4	7	982.3	58.3	3	K.LPTELSKEEPSTK.N
*	HsFLAG-FLJ20309_	2.5094	0.3363	1785.42	1786.078	8252.4	3	607.3	46.9	1	K.DYSLLPLLAAAPQVGEK.I
gi|14702169|r	2	4	5.20%	516	57371	7.5	plasminogen activator, tissue type isoform 3 precursor [Homo sapiens]				
gi|4505861|re	2	4	4.80%	562	62917	7.8	plasminogen activator, tissue type isoform 1 preproprotein [Homo sapiens]				
	HsFLAG-KIAA0515_	4.8569	0.4492	1618.48	1618.83	4532.3	1	950.5	70	3	K.VYTAQNPSAQALGLGK.H
	HsFlag-FLJ90652_2	3.006	0.1636	1338.67	1336.447	7017.7	7	634.5	65	1	K.HEALSPFYSER.L
gi|4507215|re	2	4	5.20%	504	55705	8.8	signal recognition particle 54kDa [Homo sapiens]				
gi|89061728|r	2	4	15.50%	168	18341	4.7	PREDICTED: similar to signal recognition particle 54kDa [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.1668	0.3098	2164.22	2163.434	10429.4	1	1474.6	55.6	2	K.SPIIFIGTGEHIDDFEPFK.T
	HsFLAG-p53-DNA-D	4.7266	0.3728	2964.5	2965.375	7296.9	1	609	27	2	K.SPIIFIGTGEHIDDFEPFKTQPFISK.L
gi|53759145|r	2	3	5.20%	424	47981	5.6	G-rich RNA sequence binding factor 1 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	5.2454	0.4914	2104.62	2105.444	5553.7	1	1127	63.9	2	R.GLPFQANAQDIINFFAPLK.P
*	HsFlag-NUFIP_Ti_11	3.8071	0.2782	2456.93	2457.881	9484.9	1	1557.9	52.4	1	R.GLPFQANAQDIINFFAPLKPVR.I
gi|57863281|r	1	3	5.20%	421	46175	5.3	Meis1, myeloid ecotropic viral integration site 1 homolog 3 isoform 1 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	3.7873	0.0865	2261.89	2262.537	7525.4	1	778.9	45.2	3	R.RSEAPVLPDVCLGLGSPSPGPR.W
gi|39930353|r	4	4	5.10%	1042	117761	6.7	superkiller viralicidic activity 2-like 2 [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	2.5793	0.2864	1400	1399.589	6496.3	4	557.6	65	1	K.EYPFILDAFQR.E
*	HsARP6-FLAG_Ti_1	3.1378	0.1845	1429.76	1427.686	4220	5	506.8	68.2	1	R.NFQPVIIFSFSK.K
*	HsFLAG-Lin9_Ti_20	2.615	0.3354	1275.32	1276.396	8131.5	1	814.6	75	1	K.SFYQFQHYR.A
*	HsFlag-VPS71_Ti_1	5.11	0.3003	2342.87	2342.698	6823.7	1	1782.3	43.8	1	K.SNVKPNSGELDPLYVVEVLLR.C
gi|13399322|r	2	3	5.10%	1025	115748	8.3	N-acetyltransferase-like protein [Homo sapiens]				
*	HsFLAG-FLJ20729_	6.0984	0.4461	2746.62	2745.194	12112.6	1	2036.7	34.8	1	R.FLALLSYQFSTFSPSLALNIIQNR.N
*	HsFLAG-Lin9_Ti_20	5.051	0.3588	2968.68	2969.497	7135.2	1	1338.7	34.3	2	R.IYFLNQLGDLALSAAQSALLLGIGLQHK.S
gi|4503635|re	2	5	5.00%	622	70037	5.9	coagulation factor II precursor [Homo sapiens]				
*	HsSrcap_Ti_202.254	3.9368	0.2789	1646.62	1646.804	7283.7	1	1095.7	67.9	1	K.SPQELLCGASLISDR.W
*	HsSrcap_Ti_205.349	4.2451	0.2591	1970.57	1971.275	4386	1	1212.7	73.3	4	R.WVLTAAHCLLYPPWDK.N
gi|4885225|re	2	7	5.00%	656	68478	9.3	Ewing sarcoma breakpoint region 1 isoform EWS [Homo sapiens]				
gi|7669490|re	2	7	5.70%	583	61287	9.1	Ewing sarcoma breakpoint region 1 isoform EWS-b [Homo sapiens]				
	HsYL1_Ti_101.1578.	3.4892	0.3967	1451.79	1451.53	4322.6	1	751.6	69.2	2	K.GDATVSYEDPPTAK.A
	HsFLAG-Lin9_Ti_20	4.3423	0.4127	2235.76	2236.3	6214.9	1	1363.8	66.7	5	R.AGDWQCPNPGCGNQNFAWR.T
gi|17975755|r	1	2	5.00%	416	47950	8.4	male-specific lethal 3-like 1 isoform d [Homo sapiens]				
gi|88959236|r	1	2	4.70%	447	51070	8.4	PREDICTED: similar to male-specific lethal 3-like 1 isoform a [Homo sapiens]				
gi|41126910|r	1	2	4.70%	447	51070	8.4	PREDICTED: similar to male-specific lethal 3-like 1 isoform a [Homo sapiens]				
gi|17975761|r	1	2	5.90%	355	40577	8.9	male-specific lethal 3-like 1 isoform c [Homo sapiens]				
gi|17975759|r	1	2	4.50%	462	53043	8	male-specific lethal 3-like 1 isoform b [Homo sapiens]				
gi|17975757|r	1	2	4.00%	521	59808	8.3	male-specific lethal 3-like 1 isoform a [Homo sapiens]				
	HsFLAG-p53-DNA-D	3.376	0.1322	2579.32	2579.995	7461.1	1	527.7	40	2	R.ITFDYTLPLVLLYPYEQAQYK.K
gi|5174429|re	1	2	5.00%	397	42039	8.3	acetyl-coenzyme A acyltransferase 2 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.8918	0.4702	1835.72	1836.018	7802	1	1395.9	60.5	2	K.TNVNGGAIALGHPLGGSGSR.I
gi|7662018|re	4	6	4.90%	2039	229479	7	PHD finger protein 3 [Homo sapiens]				
*	HsMRGBP-FLAG_Ti_	2.6308	0.2778	2607.07	2607.804	3779.7	1	233.9	36.4	1	K.TENSLVGLPSCVDEVTECNLELK.D
*	HsFLAG-UTX1_Ti_2	3.2487	0.3426	2145.82	2146.448	4696.8	1	362.7	44.4	2	K.SFSLDEPPLFIPDNIATIR.R
*	HsMRGBP-FLAG_Ti_	4.0087	0.2242	3742.66	3741.912	12092.2	1	1110.1	25.8	1	K.HSDNEAESIADALSSTSNILASEFFEEEKQESPK.S

*	HsMRGBP-FLAG_Ti_	4.3212	0.2884	2553.07	2551.769	6353.3	1	868.5	47.8	2	K.AYPVSGSPEYLTEDLPDSIQVGGR.I
gi|21361331|r	4	6	4.90%	1500	164939	6.7	carbamoyl-phosphate synthetase 1, mitochondrial [Homo sapiens]				
*	HsSrcap_Ti_202.374	4.622	0.3998	1931.53	1931.24	5235.3	1	566.3	52.6	2	K.EPLFGISTGNLITGLAAGAK.T
*	HsSrcap_Ti_202.452	2.8381	0.2094	2310.6	2310.695	3414.4	6	183.2	36.8	1	K.QADTVYFLPITPQFVTEVIK.A
*	HsSrcap_Ti_202.354	3.9706	0.3946	1591.8	1590.814	4271.8	1	920.8	75	2	K.IAPSFAVESIEDALK.A
*	HsSrcap_Ti_206.265	4.0345	0.4575	2013.98	2014.375	7282	1	884.3	55.9	1	K.HLPTLDHPIIPADYVAIK.A
gi|20806097|r	2	7	4.90%	800	92548	9.2	nucleolar complex associated 3 homolog [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.9511	0.3325	2280.11	2280.589	6241.5	1	1517.1	42	6	R.FAAHLIAGAPSEGSGALKPELSR.R
*	HsFLAG-UTX1_Ti_2	3.7293	0.3516	1830.75	1830.989	8704.1	1	1614.2	66.7	1	K.RYSSEVATESPLDFTK.Y
gi|14211927|r	2	2	4.90%	817	89451	5	protein phosphatase 1, regulatory subunit 9B [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	3.7604	0.3217	2081.51	2082.326	6102.6	1	663.4	34.2	1	R.FDSKPAPSAQPAPPPHPPSR.L
*	HsFLAG-Lin9_Ti_20	4.0542	0.2592	2361.86	2362.527	5737.3	1	1235.3	42.1	1	K.LEGYWGEAQSLCQAVDEHLR.E
gi|8922388|re	3	4	4.90%	759	85766	9.2	RNA binding motif protein 28 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.4315	0.3843	1750.24	1749.979	8445.5	1	676.9	50	1	R.GFGYVTFSMLEDVQR.A
*	HsFLAG-p53-DNA-D	3.6367	0.2417	2556.6	2555.755	8230.4	1	781.2	45.2	2	R.NLSFDSEEEELGELLQQFGELK.Y
*	HsFLAG-FLJ20729_	3.7504	0.2789	2556.63	2555.755	6789.2	1	1125.1	38.1	1	R.NLSFDSEEEELGELLQQFGELK.Y
gi|45331215|r	1	2	4.90%	669	72759	6.5	leucine zipper, putative tumor suppressor 2 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.5986	0.3128	3349.19	3348.691	5629.3	1	886.9	28.1	2	K.AGQLDAEAAGLREPPVPPATADPFLLAESDEAK.V
gi|8922532|re	1	3	4.90%	470	52118	5.1	family with sequence similarity 82, member C [Homo sapiens]				
*	HsSrcap_Ti_202.570	6.2825	0.5063	2405.81	2406.736	6819.2	1	1766.2	61.4	3	K.TATALLESPLSATVEDALQSFLK.A
gi|20149592|r	1	2	4.90%	350	38452	5.1	serine/threonine kinase receptor associated protein [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.4928	0.45	1798.83	1799.978	7538.8	1	907.5	56.2	2	K.SFEAPATINSASLHPEK.E
gi|18379334|r	1	4	4.90%	305	34208	11.8	RNA-binding protein S1, serine-rich domain [Homo sapiens]				
gi|6857826|re	1	4	4.90%	305	34208	11.8	RNA-binding protein S1, serine-rich domain [Homo sapiens]				
	HsFlag-DPCD_Ti_20	4.2031	0.4649	1760.94	1761.839	7704.8	1	1604	71.4	4	K.GYAYVEFENPDEAEK.A
gi|9506689|re	1	5	4.90%	245	26383	6.5	exosome component 4 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.6042	0.3508	1325.33	1325.553	5748.1	1	1052.8	77.3	5	K.ALAVVYGPHEIR.G
gi|22538465|r	1	4	4.90%	205	22949	6.5	proteasome beta 3 subunit [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.3616	0.1904	1147.78	1146.258	6580.9	1	1229.3	88.9	4	K.NCVAIAADRR.F
gi|21361861|r	3	3	4.80%	1471	166461	6.2	Fanconi anemia complementation group D2 isoform a [Homo sapiens]				
gi|66528888|r	3	3	4.90%	1451	164128	5.9	Fanconi anemia complementation group D2 isoform b [Homo sapiens]				
	HsARP6-FLAG_Ti_1	4.347	0.3875	1520.2	1520.94	8354.5	1	2059	80.8	1	K.LLLGIDILQPAIIK.T
	HsFLAG-Lin9_Ti_20	2.8824	0.1222	2643.11	2642.062	8319.9	7	284.6	28.3	1	K.ELSDLLIENTSLTVPILDVLSSLR.L
	HsFLAG-Lin9_Ti_20	3.6133	0.3269	3557.43	3560.038	4935.8	4	253.4	18	1	K.YLAVTPDYVPPLGNFDVETLDITPHTVTAISAK.I
gi|29029559|r	2	5	4.80%	971	110417	5.8	CSE1 chromosome segregation 1-like protein [Homo sapiens]				
	HsFLAG-ARP8_Ti_2	3.6661	0.3851	2435.14	2434.835	7971.9	1	817.7	47.5	4	K.FLESVEGNQNYPLLLLTLLEK.S
*	HsFLAG-Lin9_Ti_20	4.0296	0.314	2806.6	2806.274	6799.3	1	687.1	40	1	R.GPNNATLFTAAEIAPFVEILLTNLFK.A
gi|20127460|r	3	5	4.80%	940	105953	8.9	xeroderma pigmentosum, complementation group C [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.5698	0.3136	2120.7	2121.479	5091.5	1	487.2	50	2	R.SLLPVKPVEIEIETPEQAK.T
*	HsH2AZ-FLAG_293_	4.1511	0.403	1431.14	1430.598	5873.9	1	1224.1	81.8	2	R.DVDTYYLSNLVK.W
*	HsFlag-FLJ90652_2	3.5821	0.292	1586.85	1584.874	8276.4	1	1168.7	69.2	1	K.HMDQPLPTAIGLYK.N
gi|38327039|r	3	6	4.80%	840	94331	5.2	heat shock 70kDa protein 4 isoform a [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.0338	0.2211	1904.07	1904.214	5366.4	1	630	50	1	K.SNLAYDIVQLPTGLTGIK.V

	HsFLAG-ARP6_Ti_1	5.0602	0.396	1537.59	1536.744	7693	1	1948.6	80.8	4	R.GCALQCAILSPAFK.V
	HsFlag-FLJ90652_2	2.0861	0.2198	871.37	871.971	2993.4	2	294.8	78.6	1	K.NHAAPFSK.V
gi|13129068|r	2	3	4.80%	516	58468	7.5	nucleolar complex associated 4 homolog [Homo sapiens]				
gi|89036504|r	2	3	4.80%	520	58322	7.3	PREDICTED: similar to nucleolar complex associated 4 homolog isoform 2 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	3.3629	0.3043	1425.29	1425.671	6079	1	868.2	62.5	2	R.LGELLGHPSFQVK.E
	HsFlag-NUFIP_Ti_2	3.7609	0.1683	1368.24	1368.575	6769.9	1	1456.2	81.8	1	K.FVQLEGAHPLEK.S
gi|13540531|r	1	2	4.80%	392	42907	7.1	integrin-linked kinase-associated protein phosphatase 2C isoform 1 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.2122	0.3851	2241.09	2241.466	6581.2	1	910.4	52.8	2	K.VFTPEEAVNFILSCLEDEK.I
gi|33598968|r	4	10	4.70%	1349	153670	7.8	LIM domain only 7 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	5.8219	0.3822	2741	2740.987	6107.6	1	1836.8	40.4	3	K.RTPNNVVSTPAPSPDASQLASSLSSQK.E
*	HsFlag-VPS71_Ti_1	3.2364	0.1871	1226.51	1226.418	7497.5	1	1464.4	94.4	3	K.KPQDQLVIER.E
*	HsYL1_Ti_101.1526.	2.9484	0.3208	1375.98	1374.401	5013	1	750.3	68.2	2	R.STTELDDYSTNK.N
*	HsFlag-VPS71_Ti_1	3.7875	0.4726	1505.69	1505.625	6935.8	1	1210.1	71.4	2	K.TSTTGVATTQSPTPR.S
gi|57863269|r	2	3	4.70%	758	84428	9.8	hypothetical protein LOC23076 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.2128	0.2944	2335.53	2335.455	7295.5	1	969.9	52.6	1	R.GRDDCGTFEDTGPLLQFDYK.A
*	HsFLAG-FLJ20309_	3.1271	0.4	1605.52	1605.791	4423.5	2	331.6	46.7	2	K.SSTATHPPGPAVQLNK.T
gi|50959085|r	3	5	4.70%	683	78508	6.9	Fms-interacting protein [Homo sapiens]				
gi|50959115|r	3	5	4.70%	683	78508	6.9	Fms-interacting protein [Homo sapiens]				
gi|50959110|r	3	5	4.70%	683	78508	6.9	Fms-interacting protein [Homo sapiens]				
gi|50959102|r	3	5	4.70%	683	78508	6.9	Fms-interacting protein [Homo sapiens]				
	HsFLAG-p53-DNA-D	2.5717	0.192	1221.42	1221.399	7630.7	2	695.5	72.2	1	K.KEYLSSLQPR.L
	HsARP6-FLAG_Ti_1	3.8131	0.2736	2544.3	2544.996	5768.1	1	695.7	32.1	1	K.VGILTLSDYVLELGHPYLWVQK.L
	HsFlag-VPS71_Ti_1	4.1432	0.3863	2546.07	2544.996	9428.9	1	1127.6	45.2	3	K.VGILTLSDYVLELGHPYLWVQK.L
gi|19923521|r	2	4	4.70%	682	76852	9.4	cytoskeleton associated protein 2 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.0249	0.3655	1556.9	1557.787	3927.2	1	447.8	60.7	2	K.ATKPQPVNTSSVTVK.S
*	HsFLAG-ARP6_Ti_1	3.2235	0.3491	2003.94	2005.158	4868.7	1	567.3	56.2	2	K.DHYPCVSSLEQLTELGR.E
gi|61744475|r	2	4	4.70%	661	71123	5	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform a [Homo sap				
gi|65506891|r	2	4	4.90%	630	67994	5	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform c [Homo sap				
gi|61744483|r	2	4	5.90%	529	57945	5.3	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform f [Homo sapi				
gi|61744481|r	2	4	5.50%	568	61816	5.2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform e [Homo sap				
gi|61744479|r	2	4	5.20%	599	64873	5.1	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform d [Homo sap				
gi|61744477|r	2	4	4.90%	631	68101	5	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2 isoform b [Homo sap				
	HsFLAG-ARP6_Ti_1	3.561	0.3261	1866.76	1868.103	8456.4	1	902.8	50	1	R.IGDLQAFQGHGAGNLAGLK.G
	HsFLAG-ARP6_Ti_1	3.0944	0.2796	1374.06	1372.694	4754.2	2	481.1	63.6	3	R.LLTSFLPAQLLR.L
gi|17402907|r	2	3	4.70%	570	63844	7	tripartite motif protein TRIM29 isoform beta [Homo sapiens]				
gi|17402909|r	2	3	4.60%	588	65835	7.1	tripartite motif protein TRIM29 isoform alpha [Homo sapiens]				
	HsYL1_Ti_104.1343.	2.6712	0.1219	1173.37	1172.327	5300.9	5	664.1	68.2	1	K.SLGSALKPGEGR.S
	HsYL1_Ti_101.1790.	4.3973	0.3318	1656.6	1655.688	4403.6	1	1119.9	71.4	2	K.SGSEEVLCDSCIGNK.Q
gi|42475941|r	3	9	4.60%	1370	152379	6.4	zinc finger protein 261 [Homo sapiens]				
gi|4827067|re	3	9	4.60%	1370	152379	6.4	zinc finger protein 261 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	2.9519	0.3485	2433.5	2434.708	5273.6	4	290.9	35.4	1	R.GWAPPGPSPSSGALDLLDTPAGLEK.D
	HsFlag-VPS71_Ti_1	6.6424	0.4484	2003.78	2002.315	8005	1	3438.8	78.9	6	K.DPGVLDGATELLGLGGLLYK.A
	HsFLAG-Lin9_Ti_20	3.1668	0.3362	1750.07	1750.007	5577.7	1	835.5	61.8	2	R.SAPTAPTPPPPPPPATPR.K

gi|21327715|r	4	7	4.60%	1098	123901	8.6	transcription elongation regulator 1 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.0074	0.3667	2032.58	2033.164	8988	1	812.7	46.9	2	K.SDFFELLSNHHLDSQSR.W
*	HsFLAG-ARP6_Ti_1	2.9019	0.2609	1314.56	1315.512	7478.2	2	834.8	75	2	K.LFNEHIEALTK.K
*	HsFLAG-p53-DNA-D	4.4975	0.2153	1338.96	1339.535	9720.4	1	1938.5	90	2	K.KLIQESDQHLK.D
*	HsFlag-VPS71_Ti_1	3.6878	0.2387	1550.02	1549.733	5971.4	1	1444.3	86.4	1	K.RYLVLDCVPEER.R
gi|41327773|r	3	5	4.60%	1031	117362	9.3	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46 [Homo sapiens]				
*	HsFLAG-FLJ20309_	1.8333	0.0844	846.64	847.043	7197.1	3	531.2	78.6	1	K.VVTVVTTK.K
*	HsFLAG-FLJ20729_	5.2384	0.3437	2529.38	2529.783	5239.6	1	1386.2	44.7	3	K.HLILVVNYSCPNHYEDYVHR.A
*	HsFlag-VPS71_Ti_1	2.9719	0.3699	2101.84	2102.37	10627.2	1	904.2	47.2	1	K.NLGIESQDVMQQATNAILR.G
gi|23097292|r	3	3	4.60%	1024	114681	9.2	processing of precursor 1, ribonuclease P/MRP subunit [Homo sapiens]				
*	HsYL1_Ti_106.2400.	2.5402	0.2651	1594.2	1592.919	4982.8	2	456.6	60.7	1	R.LIGPLSHSILTEAIK.A
*	HsARP6-FLAG_Ti_1	3.187	0.1659	1221.08	1220.541	6584.9	1	800.1	75	1	K.IPILLIQQPGK.V
*	HsSrcap_Ti_202.425	2.5098	0.2242	2595.75	2595.803	7274	5	200.9	30	1	K.LGTLAPFCCPWEQLTQDWESR.V
gi|7662128|re	2	4	4.60%	697	78292	7.6	zinc finger and BTB domain containing 24 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.4308	0.3917	1755.97	1754.915	6594.9	1	966.1	69.2	3	K.KPFSCPECNLQFAR.L
*	HsFLAG-ARP6_Ti_2	5.0667	0.4901	1834.4	1834.851	6601.6	1	1398.1	70.6	1	K.HASDASSISGSSNTEEVR.N
gi|4506387|re	1	4	4.60%	409	43171	4.8	UV excision repair protein RAD23 homolog B [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.9875	0.4735	2131.13	2131.526	6238	1	759.1	55.6	4	R.QIIQQNPSLLPALLQQIGR.E
gi|5902060|re	1	2	4.60%	350	39642	5.1	XRP2 protein [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.8258	0.3603	2131.08	2132.391	6249.8	1	1129.9	63.3	2	K.FGCFQWYYPELAFQFK.D
gi|7661790|re	1	2	4.60%	241	28660	9.9	hypothetical protein LOC29080 [Homo sapiens]				
*	HsYL1_Ti_101.1504.	3.5406	0.2732	1337.69	1337.429	5453	2	1300.3	80	2	K.AQEEYEQIQAK.R
gi|51493127|r	5	21	4.50%	2140	240735	6.6	PREDICTED: YLP motif containing 1 isoform 1 [Homo sapiens]				
gi|89037741|r	5	21	4.50%	2140	240735	6.6	PREDICTED: similar to YLP motif containing protein 1 (Nuclear protein ZAP3) (ZAP113) isoform 16 [Homo sa				
gi|89037739|r	5	21	4.60%	2067	232369	6.5	PREDICTED: similar to YLP motif containing protein 1 (Nuclear protein ZAP3) (ZAP113) isoform 15 [Homo sa				
gi|89037737|r	5	21	4.60%	2078	233330	6.6	PREDICTED: similar to YLP motif containing protein 1 (Nuclear protein ZAP3) (ZAP113) isoform 14 [Homo sa				
gi|89037731|r	5	21	4.70%	2061	231704	6.5	PREDICTED: similar to YLP motif containing protein 1 (Nuclear protein ZAP3) (ZAP113) isoform 11 [Homo sa				
gi|89037729|r	5	21	4.70%	2057	231141	6.6	PREDICTED: similar to YLP motif containing protein 1 (Nuclear protein ZAP3) (ZAP113) isoform 10 [Homo sa				
gi|89037727|r	5	21	4.50%	2146	241643	6.6	PREDICTED: similar to YLP motif containing protein 1 (Nuclear protein ZAP3) (ZAP113) isoform 9 [Homo sap				
gi|89037372|r	5	21	4.60%	2067	232369	6.5	PREDICTED: YLP motif containing 1 isoform 8 [Homo sapiens]				
gi|89037370|r	5	21	4.60%	2078	233330	6.6	PREDICTED: YLP motif containing 1 isoform 7 [Homo sapiens]				
gi|89037364|r	5	21	4.70%	2061	231704	6.5	PREDICTED: YLP motif containing 1 isoform 4 [Homo sapiens]				
gi|89037362|r	5	21	4.70%	2057	231141	6.6	PREDICTED: YLP motif containing 1 isoform 3 [Homo sapiens]				
gi|89037360|r	5	21	4.50%	2146	241643	6.6	PREDICTED: YLP motif containing 1 isoform 2 [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.1542	0.1735	1989.84	1989.26	10464.2	1	1049.5	56.7	1	R.EQHLAQLQQLQQMHQK.Q
	HsFLAG-ARP6_Ti_1	3.2123	0.2396	1570.97	1571.817	3098.8	2	547.9	60	4	K.SQLLAPPPPSAPPGNK.T
	HsFLAG-Lin9_Ti_20	4.0311	0.3954	2882.75	2884.126	6296.3	1	588.8	35.7	1	K.SALPYSSFSSDQGLGESSAAPSQPITAVK.D
	HsFLAG-ARP6_Ti_1	2.865	0.2475	2060.13	2058.29	11436.4	2	442.8	37.5	1	R.VLSLDDYFITEVEKEEK.D
	HsFLAG-p53-DNA-D	4.2342	0.413	2082.66	2083.348	4649	1	796.5	61.8	14	K.TLDDGFFPFIILDAINDR.V
gi|6005784|re	2	3	4.50%	644	72758	4.9	suppressor of S. cerevisiae gcr2 [Homo sapiens]				
	HsFlag-ZnF-HIT2_Ti_	2.81	0.3114	1202.41	1201.429	4544.6	1	598.5	77.3	2	K.GGVPAHMFGVTK.F
*	HsFlag-ZnF-HIT2_Ti_	2.9673	0.4048	1849.34	1850.165	6633.6	1	821.4	59.4	1	K.SLVTASPLWASFLESLK.K
gi|7706501|re	2	4	4.50%	641	69998	8.4	WW domain binding protein 11 [Homo sapiens]				

*	HsFLAG-p53-DNA-D	3.6912	0.3556	1430.81	1429.749	3528.9	1	847.4	80.8	2	R.AVSILPLLGHGVPR.L
*	HsFLAG-FLJ20729_	3.0693	0.1217	1541.21	1541.788	6535.8	1	662.5	57.1	2	K.ATATISAKPQITNPK.A
gi|13899354|r	1	2	4.50%	359	40150	6.7	RNA binding motif protein 4B [Homo sapiens]				
gi|89034901|r	1	2	11.20%	143	16173	6	PREDICTED: similar to RNA binding motif protein 4 isoform 4 [Homo sapiens]				
gi|89034899|r	1	2	9.00%	177	20044	7.8	PREDICTED: similar to RNA binding motif protein 4 isoform 3 [Homo sapiens]				
gi|89034897|r	1	2	9.00%	177	20044	7.8	PREDICTED: similar to RNA binding motif protein 4 isoform 2 [Homo sapiens]				
gi|4506445|re	1	2	4.40%	366	40940	8.2	RNA binding motif protein 4 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	4.2613	0.4182	1898.57	1898.129	7115.7	1	1551.2	70	2	R.AKFEEYGPVIECDIVK.D
gi|29826335|r	1	3	4.50%	333	38388	5.8	eukaryotic translation initiation factor 2 beta [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.7924	0.3597	1758.5	1757.808	8740.9	1	1955.7	75	3	K.DASDDLDDLNFFNQK.K
gi|5729939|re	1	2	4.50%	269	30255	8.3	cleavage and polyadenylation specific factor 4, 30kD subunit [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	3.4613	0.1435	1447.97	1448.628	8192.7	1	1150.9	68.2	2	R.GPRPLEQVTCYK.C
gi|4507857|re	3	3	4.40%	1102	128272	5.6	ubiquitin specific protease 7 (herpes virus-associated) [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.4297	0.3165	2489.17	2486.684	8276.3	1	614.8	42.1	1	K.SFGWETLDSFMQHDVQELCR.V
*	HsFLAG-Lin9_Ti_20	3.4668	0.2101	1814.57	1813.98	7263.4	1	747.7	60.7	1	R.SLNYCGHIYTPISCK.I
*	HsFlag-VPS71_Ti_1	3.5354	0.2921	1498.62	1496.792	5439.5	1	496.1	62.5	1	K.EVFGTFGIPFLLR.I
gi|73747829|r	3	6	4.40%	1009	112907	9	ligase III, DNA, ATP-dependent isoform alpha precursor [Homo sapiens]				
gi|73747844|r	3	6	4.60%	949	106018	9.2	ligase III, DNA, ATP-dependent isoform beta precursor [Homo sapiens]				
	HsFLAG-FLJ20729_	4.1116	0.3816	1702.92	1703.892	4872.2	1	984.2	71.4	1	K.HVLDALDPNAYEAFK.A
	HsFLAG-p53-DNA-D	4.7876	0.3283	1734.51	1734.91	8936.5	1	1518	67.9	2	R.VLHNAQEVEKEPGQR.R
	HsFLAG-p53-DNA-D	3.802	0.3249	1453.43	1452.74	4274.8	1	855.5	73.1	3	K.TGKPLPFGTLGVHK.K
SHUFFLED_	1	2	4.40%	641	68454	7.5	FALSE POSITIVE				
*	HsFlag-ZnF-HIT2_Ti_	4.9199	0.1122	3016.47	3017.461	6901.9	6	559.1	27.8	2	K.QQRPVVYFSGVVNLGAGALLSSNSPWLR.G
gi|16579828|r	1	2	4.40%	570	63445	7.4	zinc finger protein 91 isoform 1 [Homo sapiens]				
gi|25777701|r	1	2	4.70%	529	59571	8.2	zinc finger protein 91 isoform 2 [Homo sapiens]				
	HsYL1_Ti_103.1375.	3.0933	0.2031	2489.9	2490.692	4622.8	2	246.9	33.3	2	K.AAPEEPQQRPPEAVAAAPAGTTSSR.V
gi|51477359|r	1	2	4.40%	409	45080	7.4	PREDICTED: similar to Transcription factor Dp-1 (E2F dimerization partner 1) (DRTF1-polypeptide-1) (DRTF1				
gi|89060602|r	1	2	4.40%	409	45080	7.4	PREDICTED: similar to Transcription factor Dp-1 (E2F dimerization partner 1) (DRTF1-polypeptide-1) (DRTF1				
gi|89060600|r	1	2	4.40%	409	45080	7.4	PREDICTED: similar to Transcription factor Dp-1 (E2F dimerization partner 1) (DRTF1-polypeptide-1) (DRTF1				
gi|89059461|r	1	2	4.40%	409	45080	7.4	PREDICTED: similar to Transcription factor Dp-1 (E2F dimerization partner 1) (DRTF1-polypeptide-1) (DRTF1				
gi|6005900|re	1	2	4.40%	410	45070	6	transcription factor Dp-1 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	4.7989	0.4543	1774.72	1775.101	6618.8	1	1477.4	64.7	2	K.GVVSLVAVHPSTVNPLGK.Q
gi|73695475|r	3	4	4.30%	2144	242368	6.5	protein BAP28 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.4778	0.3003	4475.35	4473.944	8135	1	769	21.2	1	T
*	HsFLAG-Lin9_Ti_20	4.1357	0.1878	2830.24	2830.306	11378.2	1	1275.3	29	1	R.AAIQCLQALSGVASPFYLIIDHLISK.A
*	HsFLAG-p53-DNA-D	6.2708	0.3776	2862.35	2863.37	5228.2	1	1181.4	39.6	2	K.VVETLPHFISPYLEGILSQVIHLEK.I
gi|33946327|r	4	11	4.30%	2090	213618	7.5	nucleoporin 214kDa [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.5943	0.1412	1436.61	1436.654	6550.1	1	1127.8	77.3	1	R.LNHLVDSLQQLR.L
*	HsFLAG-p53-DNA-D	4.0847	0.2907	1775.72	1776.089	4764	1	728.3	62.5	3	R.TPSIQPSLLPHAAPFAK.S
*	HsFlag-VPS71_Ti_1	3.8087	0.4457	2252	2252.572	4175.4	1	521.4	50	4	K.LGELLFPSSLAGETLGSFSGLR.V
*	HsFlag-VPS71_Ti_1	4.9164	0.3919	3694.89	3693.921	10155.5	1	1301.2	24.3	3	T
gi|40789229|r	3	9	4.30%	1147	125869	9.6	splicing factor, arginine/serine-rich 15 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	3.5924	0.3269	1332.43	1331.598	6349.2	1	1174.9	81.8	4	K.VPGLYVIDSIVR.Q

*	HsFLAG-Lin9_Ti_20	4.0909	0.3082	2063.5	2064.265	8634.8	1	1621.7	65.6	1	K.NITATFQYLYLCPSEDK.S
*	HsFlag-DPCD_Ti_20	4.6013	0.4897	2113.73	2114.314	3605.9	1	712	63.2	4	K.TVEPPISQVGNVDTASELEK.G
gi|22027651|r	2	3	4.30%	949	104637	5.1	adaptor-related protein complex 1 beta 1 subunit isoform a [Homo sapiens]				
gi|22027653|r	2	3	4.40%	942	103921	5.1	adaptor-related protein complex 1 beta 1 subunit isoform b [Homo sapiens]				
	HsFLAG-p53-DNA-D	2.2043	0.2471	947.45	948.117	6345.2	1	649.3	75	1	R.KTAAVCVAK.L
	HsFLAG-Lin9_Ti_20	5.2532	0.2541	3617.56	3618.032	10707.7	1	1633.5	28.2	2	R.IDNADELLESFLEGFHDESTQVQLQLLTAIVK.L
gi|29826319|r	2	3	4.30%	737	80955	5.8	adducin 1 (alpha) isoform a [Homo sapiens]				
gi|29826325|r	2	3	4.80%	662	73333	6.5	adducin 1 (alpha) isoform d [Homo sapiens]				
gi|29826323|r	2	3	5.10%	631	69985	6.4	adducin 1 (alpha) isoform c [Homo sapiens]				
gi|29826321|r	2	3	4.20%	768	84303	6	adducin 1 (alpha) isoform b [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	2.6831	0.1224	1473.93	1474.7	4048.6	6	330.1	53.6	2	R.AAVVTSPPPTTAPHK.E
	HsFLAG-p53-DNA-D	3.1611	0.3588	1750.77	1750.035	7868.7	1	845.3	53.1	1	K.CVVHIHTPAGAAVSAMK.C
gi|4557871|re	2	3	4.30%	698	77050	7.1	transferrin [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.7192	0.3972	2171.04	2172.455	4177.6	1	747.8	58.3	2	R.SAGWNIPIGLLYCDLPEPR.K
*	HsFLAG-p53-DNA-D	3.6396	0.3432	1274.23	1274.419	8174.4	1	1345.9	85	1	K.HSTIFENLANK.A
gi|4503971|re	1	8	4.30%	447	50583	5.1	GDP dissociation inhibitor 1 [Homo sapiens]				
gi|6598323|re	1	8	4.30%	445	50663	6.5	GDP dissociation inhibitor 2 [Homo sapiens]				
	HsFLAG-ARP8_Ti_1	4.1773	0.5119	2142.57	2142.462	3891.3	1	662.7	58.3	8	K.SPYLYPLYGLGELPQGFAR.L
gi|21361144|r	1	2	4.30%	439	49204	5.2	proteasome 26S ATPase subunit 3 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.7723	0.22	2190.46	2190.519	7759.9	1	973.7	52.8	2	R.TMLELLNQLDGFQPNTQVK.V
gi|41393554|r	1	3	4.30%	371	43728	9.9	LUC7-like isoform b [Homo sapiens]				
gi|8922297|re	1	3	4.90%	325	38405	10	LUC7-like isoform a [Homo sapiens]				
	HsFlag-NUFIP_Ti_1	4.9638	0.4161	1865.98	1866.016	8362.3	1	2394	76.7	3	K.SHLLDCCPHDILAGTR.M
gi|42542392|r	2	3	4.20%	1054	120974	5.9	CCAAT/enhancer binding protein zeta [Homo sapiens]				
*	HsYL1_Ti_102.3623.	3.7343	0.396	2400.67	2401.679	7580.5	1	810.1	42.9	2	K.GAIDDLQQGELEAFIQNLNLAK.Y
*	HsFLAG-p53-DNA-D	5.792	0.4088	2481.88	2481.852	10600.8	1	2161.3	57.1	1	K.HLVAEFVQVLETLSHDTLVTTK.T
gi|17999535|r	3	5	4.20%	1007	116973	10.3	serine/threonine-protein kinase PRP4K [Homo sapiens]				
gi|28872759|r	3	5	4.20%	1007	116973	10.3	serine/threonine-protein kinase PRP4K [Homo sapiens]				
	HsFLAG-FLJ20729_	4.1927	0.2287	1386.98	1387.57	8747.6	1	1843.8	81.8	2	K.LDDLALLEDLEK.Q
	HsFLAG-FLJ20729_	4.0917	0.3182	1484.98	1485.779	7322	1	1552.8	83.3	2	K.DLLDQILMLDPAK.R
	HsFLAG-FLJ20729_	3.4577	0.2268	2010.53	2010.347	10127.6	1	842.9	50	1	K.RISINQALQHAFIQEKI.-
gi|29171734|r	3	3	4.20%	859	97208	9.2	eukaryotic translation initiation factor 2C, 2 [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	2.7288	0.286	1659.85	1659.794	5153.5	1	636.6	65.4	1	K.SIEEQQKPLTDSQR.V
*	HsFlag-FLJ90652_2	3.0476	0.2099	1408.27	1408.613	8706.6	2	769.5	63.6	1	K.KLTDNQTSTMIR.A
	HsFlag-Ies6_293_Ti_	3.2578	0.3108	1167.4	1167.31	5368.2	1	882.6	83.3	1	K.AVQVHQDTLR.T
gi|33356174|r	2	7	4.20%	717	81614	7.2	pinin, desmosome associated protein [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.7627	0.227	1316.57	1316.541	6608.2	1	1334.2	83.3	2	K.KPALQSSVVATSK.E
*	HsFLAG-p53-DNA-D	3.7013	0.3663	1875.16	1875.172	5077.1	1	588.8	56.2	5	K.LTEVPVEPVLTVHPESK.S
gi|5902034|re	1	3	4.20%	501	55828	4.8	periodic tryptophan protein 1 [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	5.0388	0.3576	2410.59	2410.689	5291	1	931	57.5	3	K.VQTLQFHPFEAQTLISGSYDK.S
gi|17511255|r	1	2	4.20%	479	53525	4.8	poly(A) binding protein interacting protein 1 isoform 1 [Homo sapiens]				
gi|89062167|r	1	2	4.30%	461	51942	4.8	PREDICTED: similar to poly(A) binding protein interacting protein 1 isoform 1 [Homo sapiens]				
gi|89041275|r	1	2	4.10%	488	54583	4.9	PREDICTED: similar to poly(A) binding protein interacting protein 1 isoform 1 [Homo sapiens]				

gi|34452730|r	1	2	5.40%	367	42007	4.5	poly(A) binding protein interacting protein 1 isoform 3 [Homo sapiens]				
gi|33386693|r	1	2	5.00%	400	45631	4.5	poly(A) binding protein interacting protein 1 isoform 2 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	4.3212	0.3548	2277.97	2278.592	6905.4	1	857.2	52.6	2	R.ELLNALFSNPMDDNLICAVK.L
gi|45356151|r	3	5	4.10%	1498	168890	7.5	KIAA0056 protein [Homo sapiens]				
*	HsYL1_Ti_101.1860.	3.89	0.3886	2107.56	2108.137	4643.5	1	660.8	55	2	R.SEPSGEINIDSSGETVGSGER.C
*	HsYL1_Ti_106.3087.	3.1587	0.0992	1783.6	1784.195	3371.4	8	274.5	50	2	K.RNFIENIIPIIISLK.T
*	HsYL1_Ti_105.2332.	3.8513	0.2979	2891.16	2889.207	5865.7	2	509.3	26	1	R.SQGNDILCLSLPDKPPPQPQQWNVR.S
gi|42476127|r	2	3	4.10%	1133	127819	8.5	polymerase (RNA) III (DNA directed) polypeptide B [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	3.5799	0.2956	1522.03	1521.841	9178.9	2	794.3	53.8	2	R.ELLASTILTHVPVK.E
*	HsFlag-NUFIP_Ti_1	3.5148	0.1731	3717.29	3718.132	5207.7	1	472.7	21.9	1	K.GVCGLIVPQEDMPFCDSGICPDIIMNPHGFPSR.M
gi|24638454|r	3	5	4.10%	1042	114757	5.3	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 1 [Homo sapiens]				
gi|4502285|re	3	5	4.30%	997	109691	5.4	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 2 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	4.1977	0.4155	1541.59	1540.754	4644.2	1	1158.2	82.1	1	K.DIVPGDIVEIAVGDK.V
	HsFLAG-ARP6_Ti_1	4.513	0.4218	1621.54	1621.791	7846.3	1	1985	78.6	2	K.VGEATETALTCLVEK.M
	HsFLAG-ARP6_Ti_1	3.4603	0.3038	1527.03	1527.702	7300.2	1	867	66.7	2	K.SMSVYCTPNKPSR.T
gi|55769550|r	2	3	4.10%	948	106986	5.3	PHD finger protein 14 isoform 1 [Homo sapiens]				
	HsH2AZ-FLAG_293_	4.4668	0.413	2446.63	2447.623	9371.9	1	1692.4	57.1	2	K.EGLLSEAAAEEDIADPFFAYCK.Q
*	HsFLAG-TIP49b_Ti_	2.7116	0.1803	2063.67	2061.364	8942.6	9	371.5	43.8	1	R.LCYHFGCLDPPLKKSPK.Q
gi|6912400|re	2	6	4.10%	822	92001	6.7	general transcription factor IIIC, polypeptide 4, 90kDa [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	4.9334	0.3643	2126.64	2126.371	8733.6	1	2009.1	63.9	5	K.TFEEAAAQLLESSVQNLFK.Q
*	HsFLAG-p53-DNA-D	3.3846	0.2355	1726.63	1726.883	7794.4	1	990.2	64.3	1	K.TPSEALWKPTHEDSK.I
gi|13376204|r	2	4	4.10%	491	54503	8.3	Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1 [Homo sapiens]				
*	HsSrcap_Ti_204.207	3.7234	0.3131	2164.6	2165.454	5863.4	1	625.1	52.6	2	R.ASLENVHPPIAPPPTEIPER.F
*	HsFLAG-UTX1_Ti_2	4.1029	0.1439	2166.16	2165.454	6712.6	1	1421.7	42.1	2	R.ASLENVHPPIAPPPTEIPER.F
gi|7661892|re	1	3	4.10%	482	53028	7	REST corepressor 1 [Homo sapiens]				
gi|8922733|re	1	3	4.00%	495	55581	8.3	REST corepressor 3 [Homo sapiens]				
	HsFlag-VPS71_Ti_1	4.5966	0.4157	2321.92	2322.533	4602.7	1	802	60.5	3	K.SLADLPNFTPFPDEWTVEDK.V
gi|29727992|r	1	2	4.10%	315	35165	7.3	PREDICTED: similar to CG17293-PA [Homo sapiens]				
gi|88970733|r	1	2	4.10%	315	35165	7.3	PREDICTED: similar to CG17293-PA [Homo sapiens]				
	HsFLAG-FLJ20729_	3.2763	0.344	1513.18	1513.703	6715.6	1	865.1	70.8	2	K.HTGPITCLQFNPK.F
gi|28559039|r	3	4	4.00%	1581	168477	8.7	MEDIATOR_TRAP220 {peroxisome proliferator-activated receptor binding protein; PPARG binding protein; th				
*	HsFlag-VPS71_Ti_1	4.514	0.4495	2576.81	2576.874	7923.7	1	860.7	45.5	2	K.WTPSFSSITSANSVDLPACFFLK.F
*	HsFLAG-Lin9_Ti_20	4.1142	0.42	1745.38	1745.717	8332.6	1	1269	58.8	1	K.SHHSHSSSSSSSASTSGK.M
*	HsFlag-VPS71_Ti_1	5.6551	0.4143	2013.69	2014.146	9548.6	1	1986.4	59.5	1	K.SPISSGSGGSHMSGTSSSSGMK.S
gi|15987121|r	3	11	4.00%	1297	143732	8.8	hypothetical protein LOC23223 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	2.9323	0.2586	1272.45	1272.45	5087.7	1	693.4	66.7	2	K.APAHHPAAISTAK.F
*	HsFLAG-p53-DNA-D	3.5293	0.3265	1846.55	1847.207	6935.3	1	650.6	53.3	6	R.LGFFTTYFLPLANTLK.S
*	HsFLAG-p53-DNA-D	4.873	0.5093	2471.29	2472.849	6168.6	1	887.9	54.5	3	K.NFLPILFNLYGQPVAAGDTPAPR.R
gi|89037890|r	2	5	4.00%	600	64322	7.4	PREDICTED: similar to Ig gamma-1 chain C region [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.8632	0.1415	1808.66	1809.118	7769	1	1530.5	70	3	R.VVSVLTVLHQDWLNGK.E
	HsFLAG-p53-DNA-D	2.1089	0.1664	838.46	839.023	2475.3	8	276.6	71.4	2	K.ALPAPIEK.T
gi|27363457|r	1	2	4.00%	544	60070	7.2	aarF domain containing kinase 4 [Homo sapiens]				
*	HsSrcap_Ti_202.566	4.1491	0.2063	2400.64	2399.793	8427.2	1	786.3	45.2	2	K.IQYPGIAQSIQSDVQNLLAVLK.M

gi|48255889|r	1	3	4.00%	528	59425	4.4	protein kinase C substrate 80K-H isoform 1 [Homo sapiens]				
gi|48255891|r	1	3	4.00%	525	59178	4.4	protein kinase C substrate 80K-H isoform 2 [Homo sapiens]				
	HsFlag-VPS71_Ti_1(	4.0703	0.4669	2169.57	2169.358	6940.9	1	1133.5	55	3	K.LGGSPTSLGTWGSWIGPDHDK.F
gi|21361875|r	1	2	4.00%	475	54855	4.9	hypothetical protein LOC84946 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.0418	0.4325	2082.62	2082.315	9799.4	1	1266	55.6	2	K.LPSSVFASEFEEDVGLLNK.A
gi|5031631|re	1	3	4.00%	478	54290	5.1	scavenger receptor class B, member 2 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.0263	0.3751	2266.59	2266.691	9076.6	1	920.2	50	3	R.TLNIPVLTVIEWSQVHFLR.E
gi|14861834|r	1	4	4.00%	423	46321	8.1	cat eye syndrome chromosome region, candidate 5 isoform 2 precursor [Homo sapiens]				
gi|21914862|r	1	4	4.30%	393	43588	6.9	cat eye syndrome chromosome region, candidate 5 isoform 1 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	5.3109	0.4387	1823.39	1824.133	7979.8	1	2369.5	78.1	4	R.VPVVFVTNAGNILQHSK.A
gi|4506145|re	1	6	4.00%	247	26558	6.5	protease, serine, 1 preproprotein [Homo sapiens]				
	HsFLAG-ARP6_Ti_2	3.3391	0.1063	1175.49	1175.429	3327.3	1	569.8	83.3	6	K.TLNNDIMLIK.L
gi|24430146|r	3	6	3.90%	1475	153938	8.7	nucleoporin 153kDa [Homo sapiens]				
*	HsYL1_Ti_106.1714.	3.3796	0.2201	1372.13	1371.45	5821.6	3	642.3	66.7	2	R.SHSLSQHTATSSK.K
*	HsYL1_Ti_102.2444.	4.034	0.3835	2515.86	2515.698	4404.7	1	475.3	42.3	2	R.ESGFSYPNFSLPAANGLSSGVGGGGGK.M
*	HsYL1_Ti_101.1638.	4.9252	0.4481	1754.49	1754.761	7441.8	1	1630.7	67.6	2	K.GFDTSSSSSNSAASSSFK.F
gi|52630449|r	2	2	3.90%	1035	119032	6.1	ubiquitin specific protease 48 isoform a [Homo sapiens]				
	HsFLAG-Lin9_Ti_20:	4.4629	0.4232	1836.87	1836.953	9632.9	1	1247.4	59.4	1	K.ALGLDTGQQQDAQEFSK.L
*	HsFLAG-Lin9_Ti_20:	3.1104	0.3886	2429.16	2428.835	8337.5	1	798.8	43.2	1	K.ILSDDCATLGTLGVIPESVILLK.A
gi|41281437|r	1	2	3.90%	819	93557	5.8	nucleoporin 93kDa [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.9649	0.3759	3414.67	3416.723	7352.4	1	778.2	25	2	R.ILHTLLASGEDALDFTQESEPSYISDVGPPGR.S
gi|11496978|r	1	2	3.90%	335	37194	5	nuclear transcription factor Y, gamma [Homo sapiens]				
*	HsFLAG-FLJ20729_	4.1382	0.3145	1625.77	1625.864	9532.9	1	1772.3	75	2	K.FDQFDFLIDIVPR.D
gi|41149143|r	1	3	3.90%	203	23619	10.9	PREDICTED: similar to ribosomal protein L13a isoform 1 [Homo sapiens]				
gi|89037072|r	1	3	4.50%	178	20680	10.9	PREDICTED: similar to ribosomal protein L13a isoform 3 [Homo sapiens]				
gi|89037070|r	1	3	3.90%	203	23443	10.8	PREDICTED: similar to ribosomal protein L13a isoform 1 [Homo sapiens]				
gi|89037068|r	1	3	4.40%	181	21017	10.9	PREDICTED: similar to ribosomal protein L13a isoform 2 [Homo sapiens]				
gi|89035384|r	1	3	3.90%	203	23299	10.3	PREDICTED: similar to ribosomal protein L13a isoform 7 [Homo sapiens]				
gi|89035382|r	1	3	3.90%	203	23299	10.3	PREDICTED: similar to ribosomal protein L13a isoform 6 [Homo sapiens]				
gi|89035380|r	1	3	3.90%	203	23299	10.3	PREDICTED: similar to ribosomal protein L13a isoform 5 [Homo sapiens]				
gi|89035378|r	1	3	4.70%	171	20142	10.5	PREDICTED: similar to ribosomal protein L13a isoform 4 [Homo sapiens]				
gi|89035375|r	1	3	4.40%	181	20847	10.4	PREDICTED: similar to ribosomal protein L13a isoform 3 [Homo sapiens]				
gi|89035373|r	1	3	9.30%	86	10191	10.3	PREDICTED: similar to ribosomal protein L13a isoform 2 [Homo sapiens]				
gi|89033544|r	1	3	5.60%	142	16773	10.8	PREDICTED: similar to ribosomal protein L13a isoform 3 [Homo sapiens]				
gi|89033542|r	1	3	4.40%	181	21167	11.1	PREDICTED: similar to ribosomal protein L13a isoform 2 [Homo sapiens]				
gi|89033540|r	1	3	3.90%	203	23619	10.9	PREDICTED: similar to ribosomal protein L13a isoform 1 [Homo sapiens]				
gi|89031570|r	1	3	3.90%	203	23619	10.9	PREDICTED: similar to ribosomal protein L13a isoform 5 [Homo sapiens]				
gi|89031568|r	1	3	5.60%	142	16773	10.8	PREDICTED: similar to ribosomal protein L13a isoform 4 [Homo sapiens]				
gi|89031566|r	1	3	4.50%	178	20803	10.9	PREDICTED: similar to ribosomal protein L13a isoform 3 [Homo sapiens]				
gi|89031563|r	1	3	4.40%	181	21167	11.1	PREDICTED: similar to ribosomal protein L13a isoform 2 [Homo sapiens]				
gi|6912634|re	1	3	3.90%	203	23577	10.9	ribosomal protein L13a [Homo sapiens]				
gi|41202038|r	1	3	3.90%	203	23299	10.3	PREDICTED: similar to ribosomal protein L13a isoform 1 [Homo sapiens]				
	HsFLAG-TCF3_Ti_1(	2.1667	0.128	939.49	940.09	3537	2	439.2	71.4	3	R.LAHEVGWK.Y

gi|32967603|r	3	3	3.80%	1556	178702	6.6	bromodomain adjacent to zinc finger domain, 1A isoform a [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.4348	0.3257	2367.54	2367.676	7733.8	1	1100.5	31.8	1	K.SALSAVASLAAAWPQLHQGCSLK.S
	HsFlag-DPCD_Ti_20	3.1236	0.2924	1807.84	1806.889	6106.5	1	851.1	60	1	K.SANNTPENSPNFPNFR.V
	HsFlag-DPCD_Ti_20	4.0585	0.3315	2031.71	2032.304	7664.6	1	1268.8	57.9	1	K.LGLHVTPSNVDQVSTPPAAK.K
gi|18644728|r	2	2	3.80%	1146	127593	7.6	nucleolar RNA-associated protein alpha isoform [Homo sapiens]				
gi|21218436|r	2	2	4.30%	1007	112304	7.7	nucleolar RNA-associated protein beta isoform [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	2.8461	0.1778	2164.95	2166.439	9645.5	3	454.6	39.5	1	R.VPSVPETELTDQAWLPAGVR.V
	HsFLAG-p53-DNA-D	4.1111	0.3054	2426.38	2427.895	4136.6	1	356.7	43.2	1	R.LLWGLEGLPLTVSAVQGAHPVLR.Y
gi|20149524|r	3	3	3.80%	1087	121000	5.1	suppressor of Ty 5 homolog [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.2776	0.25	1135.5	1135.355	4997.3	1	1299.2	90	1	R.HLVLAGGSKPR.D
*	HsFLAG-FLJ20729_	2.5854	0.1617	1645.59	1645.776	7397.5	4	399.6	46.2	1	R.VELHSTCQTISVDR.Q
*	HsFlag-VPS71_Ti_1	4.2451	0.4388	1737.8	1737.991	7107.1	1	933.8	56.7	1	K.VVSISSEHLEPITPTK.N
gi|51873036|r	2	2	3.80%	1023	115935	6.9	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) isoform 1 precursor [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.5488	0.2591	2107.01	2106.343	5559.8	1	713.8	47.5	1	R.GSLAAVAHAQSLVEAQPNVDK.L
*	HsFLAG-p53-DNA-D	2.6482	0.2568	2155.99	2157.395	10594.9	1	674.4	47.1	1	K.HWLDSPWPGFFTLDGQPR.S
gi|7669501|re	1	2	3.80%	416	44773	9.1	lysosomal-associated membrane protein 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.393	0.316	1846.52	1847.167	6756.4	1	1009.5	63.3	2	R.FFLQGIQLNTILPDAR.D
gi|58761500|r	1	5	3.80%	396	44744	7.8	GTP-binding protein PTD004 isoform 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.3156	0.3082	1569.11	1569.928	7454.6	1	1653	75	5	K.IPAFLNVVDIAGLVK.G
gi|18379349|r	1	2	3.80%	393	41920	6.3	vesicle amine transport protein 1 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.6897	0.3123	1443.42	1443.689	3333.3	1	639.8	67.9	2	R.PAAPPAPGPGQLTLR.L
gi|5453591|re	3	3	3.70%	1197	135780	8.6	structural maintenance of chromosomes 2-like 1 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	3.3304	0.2734	2250.17	2250.566	9429.8	1	632.8	44.7	1	K.SNILDSICFLLGISNLSQVR.A
*	HsFLAG-Lin9_Ti_20	3.2252	0.3939	1624.97	1625.822	10538.3	1	1224	64.3	1	K.KITDGLHALQEASNK.D
*	HsYL1_Ti_101.1492.	2.5129	0.16	1003.85	1003.097	3323	1	1050.3	93.8	1	K.DQEALEAVK.R
gi|24797086|r	3	4	3.70%	1115	125545	4.9	RAN binding protein 5 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.792	0.2986	1830.97	1831.125	8870.9	1	1248.5	59.4	2	R.ATAAFILANEHNVALFK.H
*	HsMRGBP-FLAG_Ti	3.3593	0.1398	1783.07	1783.124	7950	2	822.9	57.1	1	K.YLRPHLEATLQLSLK.L
*	HsFlag-FLJ90652_2	2.6538	0.181	1038.12	1038.192	5608.9	1	640.5	81.2	1	K.HIVENAVQK.E
gi|50980301|r	2	3	3.70%	1025	116533	6.2	myosin phosphatase-Rho interacting protein isoform 2 [Homo sapiens]				
gi|50980307|r	2	3	3.70%	1038	118103	6.4	myosin phosphatase-Rho interacting protein isoform 1 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	3.4661	0.299	1946.95	1946.124	6798.4	7	468.8	50	1	K.HVHPTTAPDVTSSLPEEK.N
	HsFLAG-Lin9_Ti_20	5.3448	0.5533	1830.57	1830.99	8940.1	1	1207.5	52.6	2	R.TLLTGDGGGEATGSPLAQGK.D
gi|73747799|r	1	2	3.70%	723	82221	6	suppressor of actin mutations 2-like [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	4.6043	0.3847	2760.18	2760.244	5347.6	1	914.6	46.2	2	K.LGELVDGLVVPSALVTAILEAPVTEPR.F
gi|21361376|r	1	6	3.70%	464	49256	9.6	splicing factor 3a, subunit 2 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	5.377	0.3406	2075.5	2075.43	9034.1	1	2068.8	71.9	6	R.WQYLLMAAEPYETIAFK.V
gi|48255898|r	4	11	3.60%	1572	179280	7.3	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a2 isoform b [Homo sapiens]				
gi|48255900|r	4	11	3.60%	1590	181278	7.2	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a2 isoform a [Homo sapiens]				
	HsFLAG-FLJ20729_	3.1258	0.2775	1562.69	1563.8	6271.8	1	522.7	57.7	1	R.GPSPFSPVQLHQLR.A
	HsARP6-FLAG_Ti_1	4.3946	0.2088	1618.2	1617.926	5797.2	1	1207.8	79.2	3	K.FNVLLTTYEYIIK.D
	HsARP6-FLAG_Ti_1	3.4162	0.2719	1512.2	1512.752	7683.9	1	1469.3	70.8	6	K.LTQVLNTHYVAPR.R
	HsFLAG-Lin9_Ti_20	3.0111	0.1977	2028.36	2029.516	8605	1	667.2	46.9	1	K.LPELWALLNFLLPTIFK.S

gi|4504555|re	3	5	3.60%	1262	144480	6.1	isoleucine-tRNA synthetase [Homo sapiens]				
gi|7770072|re	3	5	3.60%	1262	144480	6.1	isoleucine-tRNA synthetase [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.3501	0.262	2165.87	2165.382	9384.8	1	795.6	50	1	K.ILEFWTEFNCFQECLK.Q
	HsFLAG-ARP6_Ti_1	4.4777	0.532	1999.2	2000.273	6797	1	937.3	56.7	2	R.LLVATTFTHSYPFCWR.S
	HsFLAG-ARP6_Ti_1	2.8649	0.2379	1399.26	1399.63	3839.3	3	437.7	62.5	2	K.APLKPYPVSPSDK.V
gi|8923040|re	1	3	3.60%	580	61125	9	collaborates/cooperates with ARF (alternate reading frame) protein [Homo sapiens]				
*	HsFLAG-FLJ20729_	4.7879	0.4971	1959.13	1959.031	6024.7	1	1397.6	60	3	R.SVSSQSSSSVSSQVTTAGSGK.A
gi|7705853|re	1	8	3.60%	523	56627	6.6	dynein light chain-A [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	4.2695	0.4173	1927.74	1927.164	7230.7	1	766.8	50	8	K.AGATSEGVLANFFNSLLSK.K
SHUFFLED_	1	2	3.60%	364	40315	9.5	FALSE POSITIVE				
*	HsFLAG-TIP49b_Ti_	3.4627	0.1018	1414.64	1414.645	10380.8	3	1361	70.8	2	K.IERVPSAKELGSK.L
gi|33946282|r	5	6	3.50%	1812	202023	5	hypothetical protein LOC25962 isoform 1 [Homo sapiens]				
	HsARP6-FLAG_Ti_1	3.2212	0.2109	1396.51	1396.595	8028.9	1	984.1	70	1	R.FPCVVYINEVR.V
	HsARP6-FLAG_Ti_1	3.3777	0.2448	1613.08	1612.95	7728.7	1	1205	65.4	1	K.WVTALEEIPSLIIK.G
	HsARP6-FLAG_Ti_1	4.3111	0.1876	1426.34	1426.74	8448.4	1	1961.6	86.4	1	K.LLELILLDQTVR.V
*	HsARP6-FLAG_Ti_1	3.2527	0.3396	1551.25	1551.826	5959.9	1	946.8	70.8	2	R.YAEIFQDLLALVR.S
*	HsARP6-FLAG_Ti_1	2.873	0.3019	1604.22	1603.787	9472.7	1	1239.8	65.4	1	K.DTGELASSFLEFMR.Q
gi|20336290|r	2	2	3.50%	1155	129438	8.5	DEAH (Asp-Glu-Ala-His) box polypeptide 30 isoform 2 [Homo sapiens]				
gi|20336294|r	2	2	3.40%	1194	133938	8.8	DEAH (Asp-Glu-Ala-His) box polypeptide 30 isoform 1 [Homo sapiens]				
	HsFlag-NUFIP_Ti_1	4.0428	0.2401	2584.05	2583.898	8349	1	684.4	28.3	1	K.DSGPLSDPITGKPYVPLLEAEEVR.L
	HsFlag-NUFIP_Ti_1	4.3429	0.2683	1900.84	1900.305	6756.3	1	1783.3	76.7	1	K.YLILPVHSNIPMMDQK.A
gi|62244004|r	2	2	3.50%	1016	115409	8.1	modulator of estrogen induced transcription isoform b [Homo sapiens]				
gi|63176611|r	2	2	3.50%	1034	117149	7.9	modulator of estrogen induced transcription isoform a [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	2.7849	0.2592	2273.5	2274.239	9379.7	3	485.5	44.4	1	K.DCELENQEAHEQDGNDELK.D
	HsFLAG-p53-DNA-D	3.9914	0.2528	1979.79	1980.106	7650.1	1	656.1	53.1	1	R.KEWHGPPSQGPSYHDTR.R
gi|31541941|r	2	6	3.50%	839	94512	5.9	heat shock 70kDa protein 4-like [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.062	0.4363	1913.1	1913.013	5146.7	1	1298.3	78.6	2	R.NFDEALVDYFCDEFK.T
	HsFLAG-ARP6_Ti_1	5.0602	0.396	1537.59	1536.744	7693	1	1948.6	80.8	4	R.GCALQCAILSPAFK.V
gi|7705765|re	1	2	3.50%	521	57708	7.5	WD repeat domain 50 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.3171	0.4184	1660.58	1660.83	5607.4	1	714.7	58.8	2	K.AGAGPGGPPQKPAPSSQR.K
gi|4503265|re	1	3	3.50%	482	53487	8.5	dihydrolipoamide branched chain transacylase [Homo sapiens]				
*	HsFlag-NUFIP_Ti_1	3.2761	0.2627	1830.11	1830.236	6847.7	3	480.8	46.9	3	K.DMTVPILVSKPPVFTGK.D
gi|4502005|re	2	2	3.50%	367	39325	5.7	alpha-2-HS-glycoprotein [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	3.9277	0.3722	1338.33	1338.293	5104.3	1	1187.1	86.4	1	K.CDSSPDSAEDVR.K
*	HsFLAG-TCF3_Ti_1	3.6924	0.2984	1466.3	1466.467	7544.7	1	1153.4	70.8	1	K.CDSSPDSAEDVRK.V
gi|46430495|r	2	2	3.40%	1021	113357	6.7	basonuclin 2 [Homo sapiens]				
*	HsFlag-NUFIP_Ti_2	3.632	0.2666	2562.77	2562.773	8372.3	1	736.5	29.8	1	K.VLMNSERPDENHSEPSHQDVIK.V
*	HsFlag-NUFIP_Ti_2	2.7356	0.0929	1457.31	1457.69	5881.2	1	1238.1	79.2	1	K.IYGAQHPMGLDVR.E
gi|12746590|r	1	2	3.40%	985	106208	8	C-terminal binding protein 2 isoform 2 [Homo sapiens]				
gi|4557499|re	1	2	7.40%	445	48945	6.9	C-terminal binding protein 2 isoform 1 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	4.5245	0.2496	3532.05	3530.889	5511.2	1	484.5	23.4	2	K.AAGELGIAVCNIPSAAVEETADSTICHILNLYR.R
gi|11415036|r	2	3	3.40%	794	88992	6.5	zinc finger protein 148 (pHZ-52) [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	2.6254	0.1553	1740.59	1741.084	9447.1	7	466.6	43.3	1	R.LPQGLQYALNVPISVK.Q

*	HsYL1_Ti_105.1144.	3.1649	0.3345	1282.5	1280.386	4391.9	1	824	80	2	K.RYLQAASNNSR.E
gi|20149698|r	2	7	3.40%	705	79110	6.9	l(3)mbt-like 2 isoform a [Homo sapiens]				
	HsFLAG-TIP49b_Ti_	3.2666	0.302	1158.71	1159.219	6353.3	1	734.3	81.2	5	K.RFCSVSCSR.S
*	HsFlag-DPCD_Ti_20	3.3245	0.2633	1596.15	1595.88	4692.4	8	491.4	57.1	2	R.KISSEPVPGEIIAVR.V
gi|21361171|r	1	3	3.40%	415	46974	6.1	brain and reproductive organ-expressed (TNFRSF1A modulator) isoform 1 [Homo sapiens]				
gi|40353761|r	1	3	3.70%	383	43552	5.8	brain and reproductive organ-expressed (TNFRSF1A modulator) isoform 2 [Homo sapiens]				
gi|40353759|r	1	3	3.70%	376	42697	5.4	brain and reproductive organ-expressed (TNFRSF1A modulator) isoform 3 [Homo sapiens]				
gi|40353757|r	1	3	3.70%	383	43552	5.8	brain and reproductive organ-expressed (TNFRSF1A modulator) isoform 2 [Homo sapiens]				
gi|40353755|r	1	3	3.70%	376	42697	5.4	brain and reproductive organ-expressed (TNFRSF1A modulator) isoform 3 [Homo sapiens]				
	HsSrcap_Ti_202.366	4.2079	0.2955	1620.95	1620.929	6702.6	1	1239.5	73.1	3	K.LPVDFSNIPTYLLK.D
gi|4759172|re	2	6	3.30%	1148	128875	8.3	splicing factor, arginine/serine-rich 2, interacting protein [Homo sapiens]				
*	HsYL1_Ti_101.1842.	5.0637	0.4922	2326.62	2327.328	7585.5	1	1905.3	61.9	2	K.SSSNDSVDEETAESDTSPVLEK.E
*	HsYL1_Ti_104.1178.	3.6561	0.3952	1626.66	1626.72	5885.8	1	1182.4	73.3	4	R.KPLSGNSNSSGSESFK.F
gi|4503525|re	2	6	3.30%	913	105344	5.7	eukaryotic translation initiation factor 3, subunit 8, 110kDa [Homo sapiens]				
gi|89040127|r	2	6	3.30%	914	105473	5.6	PREDICTED: similar to eukaryotic translation initiation factor 3, subunit 8, 110kDa isoform 16 [Homo sapiens]				
gi|89040125|r	2	6	3.30%	914	105473	5.6	PREDICTED: similar to eukaryotic translation initiation factor 3, subunit 8, 110kDa isoform 15 [Homo sapiens]				
gi|89040121|r	2	6	3.80%	782	90161	5.7	PREDICTED: similar to eukaryotic translation initiation factor 3, subunit 8, 110kDa isoform 13 [Homo sapiens]				
gi|89040101|r	2	6	3.30%	914	105473	5.6	PREDICTED: similar to eukaryotic translation initiation factor 3, subunit 8, 110kDa isoform 3 [Homo sapiens]				
gi|89040099|r	2	6	3.30%	914	105473	5.6	PREDICTED: similar to eukaryotic translation initiation factor 3, subunit 8, 110kDa isoform 2 [Homo sapiens]				
gi|89040097|r	2	6	3.30%	914	105473	5.6	PREDICTED: similar to eukaryotic translation initiation factor 3, subunit 8, 110kDa isoform 1 [Homo sapiens]				
	HsFlag-VPS71_Ti_1	5.5859	0.3467	1981.69	1980.179	7740.8	1	2796.1	80	5	R.ILADLEDYLNELWEDK.E
	HsARP6-FLAG_Ti_1	2.7713	0.1589	1496	1497.608	8345.9	1	839.2	57.7	1	K.DAHNALLDIQSSGR.A
gi|4557469|re	2	2	3.30%	937	104553	5.4	adaptor-related protein complex 2, beta 1 subunit isoform b [Homo sapiens]				
gi|71773106|r	2	2	3.30%	951	105692	5.3	adaptor-related protein complex 2, beta 1 subunit isoform a [Homo sapiens]				
	HsFLAG-p53-DNA-D	2.2043	0.2471	947.45	948.117	6345.2	1	649.3	75	1	R.KTAAVCVAK.L
	HsFlag-VPS71_Ti_1	2.7471	0.1869	2394.77	2394.86	8560.3	1	631.3	40.5	1	K.KLAPPLVTLLSGEPEVQYVALR.N
gi|18201911|r	1	2	3.30%	478	54336	5.8	vitronectin precursor [Homo sapiens]				
*	HsSrcap_Ti_204.188	2.6616	0.216	1666.58	1667.839	5348.9	9	369.1	46.7	2	R.DWHGVPGQVDAAMAGR.I
gi|55769546|r	1	2	3.30%	392	43964	8.9	PAK1 interacting protein 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.2877	0.2217	1371.34	1371.579	8523.6	1	1307.8	70.8	2	K.GQVTFLSIHPSGK.L
gi|7706549|re	2	4	3.20%	1490	164154	9.5	CDC2-related protein kinase 7 [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	3.4237	0.3057	1366.5	1365.616	7517.4	1	820.8	62.5	2	K.TQVSVTAAIPHLK.T
*	HsFlag-VPS71_Ti_1	4.1466	0.2425	3296.84	3295.506	4358.9	1	621	27.3	2	K.LQNYGELGPGTTGASSSGAGLHWGGPTQSSAYGK.L
gi|89034039|r	2	2	3.20%	747	85105	4.9	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein U [Homo sapiens]				
gi|89034820|r	2	2	2.70%	904	101753	5.4	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein U [Homo sapiens]				
	HsFlag-NUFIP_Ti_11	2.715	0.2767	1051.28	1051.284	3470	4	411.7	75	1	R.ALLPHVLCK.N
	HsFLAG-p53-DNA-D	3.2236	0.3644	1733.44	1733.929	11543.9	1	924.3	57.1	1	K.SRDLLVQQASQCLSK.L
gi|19923272|r	1	2	3.20%	696	81535	8.4	xenotropic and polytropic retrovirus receptor [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.2675	0.2059	2441.62	2442.611	4888.3	1	553.4	47.6	2	K.DMLYSAQDQAPSVEVTDEDTVK.R
gi|7657013|re	1	6	3.20%	560	63133	4.9	apoptosis antagonizing transcription factor [Homo sapiens]				
*	HsFLAG-UTX1_Ti_2	3.7131	0.2823	2045.02	2043.414	3704.6	1	388	52.9	6	K.ALLTTNQLPQPDVFPLFK.D
gi|26667180|r	1	2	3.20%	499	56369	7.2	calcium/calmodulin-dependent protein kinase II delta isoform 3 [Homo sapiens]				
gi|26667189|r	1	2	3.30%	478	54114	7.1	calcium/calmodulin-dependent protein kinase II delta isoform 2 [Homo sapiens]				

gi|26667186|r	1	2	3.30%	478	54128	7.3	calcium/calmodulin-dependent protein kinase II delta isoform 1 [Homo sapiens]				
gi|26667183|r	1	2	3.30%	478	54128	7.3	calcium/calmodulin-dependent protein kinase II delta isoform 1 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.4073	0.3434	1783.83	1784.782	8700.6	1	994.1	56.7	2	K.ESTESSNTTIEDEDVK.A
gi|88953910|r	3	3	3.10%	2354	265615	6.2	PREDICTED: hypothetical protein LOC57683 [Homo sapiens]				
gi|88959048|r	3	3	3.10%	2354	265615	6.2	PREDICTED: hypothetical protein LOC57683 [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.1873	0.2678	2711.96	2712.072	6322.6	2	608.7	29.2	1	K.SVFETSLDSDVPLQAATHKPEVIVK.E
	HsFLAG-TCF3_Ti_1(	3.6087	0.3765	2423.37	2422.781	8745.7	1	660.2	40.5	1	K.GYVPSDSEIIYVSNIPLQSVIK.Q
	HsFLAG-ARP6_Ti_1	4.9598	0.3905	2837.19	2837.158	8336.8	2	587.5	27	1	K.LGDFDVSYASHIPVQFVTDQSSVPVK.E
gi|40807477|r	2	2	3.10%	1906	203350	8.8	retinoic acid induced 1 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20(	4.0334	0.2822	3811.11	3812.35	11592.7	1	1207.2	24.3	1	K.LPENLLSDLSLQSLTALTSQVENISNTVQQLLLSK.A
*	HsH2AZ-FLAG_293_	3.8818	0.111	2303.52	2303.503	4737	5	466.5	30.4	1	K.GPECAAAATAGKPPRPDGPADPAK.Q
gi|54124343|r	2	3	3.10%	1341	147183	4.8	hypothetical protein LOC387680 [Homo sapiens]				
gi|89031067|r	2	3	3.60%	1148	125037	4.9	PREDICTED: hypothetical protein LOC55747 isoform 1 [Homo sapiens]				
gi|89031065|r	2	3	5.80%	709	77846	6.6	PREDICTED: hypothetical protein LOC55747 isoform 4 [Homo sapiens]				
	HsFlag-VPS71_Ti_1(	3.8375	0.4458	2458.12	2457.607	5107.6	1	654.1	47.7	2	K.LLEPSVGSLFGDDEDDDLFSSAK.S
	HsFlag-VPS71_Ti_1(	2.6276	0.1968	1959.05	1959.209	4972.2	8	265.6	41.2	1	K.GIWKPETPQDSSGLAPFK.T
gi|5453998|re	2	3	3.10%	1038	119516	4.8	importin 7 [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.9421	0.4179	1651.52	1652.051	6447.4	1	1319.5	71.4	2	R.SPLVAAMQHFLPVLK.D
*	HsSrcap_Ti_204.282	4.0146	0.389	2054.89	2056.245	6226.2	1	1246.3	68.8	1	R.NPVWYQALTHGLNEEQR.K
gi|39725634|r	2	2	3.10%	1019	116465	9.1	la related protein isoform 1 [Homo sapiens]				
gi|61102725|r	2	2	2.90%	1096	123510	8.8	la related protein isoform 2 [Homo sapiens]				
	HsFlag-NUFIP_Ti_1(	3.6559	0.4626	2024.1	2025.228	6780.2	2	543.8	44.4	1	K.VGDFGDAINWPTPGEIAHK.S
	HsFLAG-ARP6_Ti_1	2.9295	0.3268	1487.75	1488.6	6715.8	1	640.1	62.5	1	K.WTSQHSNTQTLGK.-
gi|7705365|re	2	2	3.10%	960	107305	6.4	RNA binding motif protein 19 [Homo sapiens]				
	HsFlag-NUFIP_Ti_11	2.9286	0.1659	1699.21	1699.108	4435.8	1	584.2	60.7	1	K.NVMEFLAPLKPVAIR.I
	HsFlag-NUFIP_Ti_11	2.9649	0.2782	1744.89	1743.076	7810.4	1	597.6	50	1	K.GFAFITFMFPEHAVK.A
gi|14150171|r	1	4	3.10%	351	38772	6.1	THO complex 3 [Homo sapiens]				
gi|89071798|r	1	4	6.10%	179	19963	5	PREDICTED: similar to THO complex subunit 3 (Tho3) [Homo sapiens]				
	HsARP6-FLAG_Ti_1	3.8224	0.3585	1306.89	1306.471	5866.2	1	1320.9	90	4	K.RPLLAFACDDK.D
gi|24415404|r	10	20	3.00%	5596	632827	5.7	MDN1, midasin homolog [Homo sapiens]				
*	HsSrcap_Ti_202.467	4.209	0.3603	1602.73	1602.878	6349	1	937.3	73.1	2	R.QCVLSTLAQLLLDK.D
*	HsH2AZ-FLAG_293_	4.4654	0.3327	1429.03	1429.61	9163.9	1	2592.7	90.9	2	R.LLEEAQLQDLEK.A
*	HsH2AZ-FLAG_293_	3.3034	0.3162	1378.49	1378.624	4220.1	1	1010.1	77.3	1	K.LICQHIVPGNVK.S
*	HsSrcap_Ti_204.562	4.0416	0.3329	2529.63	2529.896	6627.1	1	1060.6	52.4	1	K.GYWIILDELNLAPTDVLEALNR.L
*	HsFLAG-ARP6_Ti_1	3.0266	0.2715	1295.28	1295.565	6835.9	1	838.5	70.8	1	K.KPILLEGSPGVGK.T
*	HsSrcap_Ti_202.373	4.7238	0.3223	2435.03	2433.675	10352.5	1	1505.4	50	1	R.INLSEQTDITDLFGADLPVEGGK.G
*	HsH2AZ-FLAG_293_	3.4513	0.2572	1682.59	1682.958	4373.2	1	535.7	60	1	R.LNALLEPGGVLTISER.G
*	HsSrcap_Ti_202.486	5.6453	0.4397	2478.75	2479.787	6714.3	1	1408.7	54.5	7	R.LVEGLDQFTGEVISSVSELQSLK.V
*	HsFLAG-ARP6_Ti_1	4.098	0.3717	2081.1	2082.142	5929.7	1	1277	64.7	2	K.DVSDQIGNEEQVEDTFQK.G
*	HsH2AZ-FLAG_293_	3.2633	0.2403	1514.34	1514.676	3189.4	3	468.4	69.2	2	R.DVNALPETLSDALR.Q
gi|67782328|r	2	3	3.00%	1722	182686	7	trinucleotide repeat containing 6B isoform 1 [Homo sapiens]				
	HsFlag-NUFIP_Ti_1(	3.598	0.1211	3188.93	3187.534	9813.1	1	1133.4	26.6	1	K.VPEVTKPSLSQPTAASPIGSSPSPPVNGGNNAK.R
*	Hs293Flag-Ies2_Ti_1	3.6958	0.3885	1990.62	1990.111	5322.4	1	763.8	58.8	2	K.GHPLPENQGNAQAPCWGR.S

gi|8923609|re	1	3	3.00%	608	68183	6.3	nuclear protein localization 4 [Homo sapiens]					
*	HsFlag-VPS71_Ti_1	4.2854	0.4956	2024.61	2024.235	6022.3	1	1081.6	64.7	3	K.VFGAPNVVEDEIDQYLSK.Q	
gi|24430149|r	2	3	2.90%	1391	155199	6.2	nucleoporin 155kDa isoform 1 [Homo sapiens]					
gi|4758844|re	2	3	3.00%	1332	149016	6.3	nucleoporin 155kDa isoform 2 [Homo sapiens]					
	HsFLAG-Lin9_Ti_20	3.3754	0.3353	1730.16	1728.946	9757.9	1	758.3	47.1	1	R.VASVSQNAIVSAAGNIAR.T	
	HsFlag-VPS71_Ti_1	3.5335	0.3339	2488.97	2487.816	3020.9	2	223.3	40.5	2	R.EITAIESSVPCQLLESVLQELK.G	
gi|38201619|r	3	7	2.90%	1403	154804	5.2	eukaryotic translation initiation factor 4 gamma, 1 isoform 4 [Homo sapiens]					
gi|38201627|r	3	7	2.70%	1512	166588	5.2	eukaryotic translation initiation factor 4 gamma, 1 isoform 2 [Homo sapiens]					
gi|38201625|r	3	7	2.90%	1435	158516	5.2	eukaryotic translation initiation factor 4 gamma, 1 isoform 3 [Homo sapiens]					
gi|38201623|r	3	7	2.60%	1599	175460	5.3	eukaryotic translation initiation factor 4 gamma, 1 isoform 1 [Homo sapiens]					
gi|38201621|r	3	7	2.60%	1599	175460	5.3	eukaryotic translation initiation factor 4 gamma, 1 isoform 1 [Homo sapiens]					
	HsFlag-VPS71_Ti_1	3.7941	0.2511	1478.3	1478.605	6431.5	1	1178.6	75	2	K.IHNAENIQPGEQK.Y	
	HsFLAG-FLJ20729_	2.9905	0.278	1589.71	1589.832	6173.6	4	509.1	57.7	2	K.VPTTEKPTVTVNFR.K	
	HsFlag-VPS71_Ti_1	3.694	0.09	1515.54	1514.855	5990.4	1	1221.1	69.2	3	K.AASLLLEILGLLCK.S	
gi|50658063|r	4	10	2.90%	1288	147182	6.8	SMC4 structural maintenance of chromosomes 4-like 1 isoform a [Homo sapiens]					
gi|50658067|r	4	10	4.00%	925	105722	8.6	SMC4 structural maintenance of chromosomes 4-like 1 isoform b [Homo sapiens]					
gi|50658065|r	4	10	2.90%	1288	147182	6.8	SMC4 structural maintenance of chromosomes 4-like 1 isoform a [Homo sapiens]					
	HsSrcap_Ti_205.213	3.1936	0.3341	1758.6	1758.937	6771.6	1	644.1	62.5	1	K.NHVCQYYIYELQK.R	
	HsFlag-VPS71_Ti_1	3.1418	0.2791	1098.58	1099.232	5149	1	644.5	77.8	4	R.HNTAVSQLTK.A	
	HsYL1_Ti_104.1224.	3.0241	0.2609	1099.79	1099.232	5359.2	1	1088.7	83.3	4	R.HNTAVSQLTK.A	
	HsYL1_Ti_105.2040.	4.5614	0.3988	1534.01	1532.783	7857.4	1	1808.2	80.8	1	K.RQNIGVATFIGLDK.M	
gi|31083367|r	2	2	2.90%	974	110507	6.5	SEC8 protein [Homo sapiens]					
*	HsFlag-VPS71_Ti_1	3.6611	0.2581	1739.54	1738.759	9829.4	1	1578.7	67.9	1	R.TLSTSDDVEDRENEK.G	
*	HsFLAG-p53-DNA-D	2.7138	0.292	1551.13	1550.795	7880.6	1	900.4	70.8	1	K.HVLNLLDEIENIK.Q	
gi|25777730|r	1	3	2.90%	517	57249	7	aldehyde dehydrogenase 1B1 precursor [Homo sapiens]					
*	HsFLAG-TIP49b_Ti_	3.5126	0.2001	1716.96	1717.061	6959.7	1	765.7	57.1	3	R.IAKEEIFGPVQPLFK.F	
gi|4753161|re	3	6	2.80%	2109	238417	7.4	general transcription factor IIIC, polypeptide 1, alpha 220kDa [Homo sapiens]					
*	HsFLAG-p53-DNA-D	3.1665	0.128	2229.41	2227.577	6023.3	2	428	47.1	2	R.VPPFPLPLEPCTQEFLWR.A	
*	HsFLAG-Lin9_Ti_20	3.0388	0.1955	2121.31	2122.222	8813.5	2	536.8	42.5	1	R.AGVRPSSSGSAWEACSEAPSK.G	
*	HsFLAG-ARP6_Ti_1	6.0039	0.4305	2238.3	2239.132	9156.8	1	2175.6	62.5	3	K.DGSLEDDEDEEDDLDEGVGGK.R	
gi|18375626|r	4	6	2.80%	2157	228869	9.5	HLA-B associated transcript-2 isoform a [Homo sapiens]					
gi|18375628|r	4	6	2.80%	2145	227644	9.4	HLA-B associated transcript-2 isoform b [Homo sapiens]					
	HsFLAG-KIAA0515_	3.0827	0.1453	840.29	839.97	3998.2	1	991.8	100	1	R.HGLQSLGK.V	
	HsFLAG-KIAA0515_	2.466	0.0825	1164.3	1165.436	5127.9	9	530.4	65	2	R.MPPPANLPSLK.A	
	HsFLAG-p53-DNA-D	4.1439	0.322	1730.64	1731.005	4287.1	2	561.3	62.5	2	K.RPPAAPENTPLVPSGVK.S	
	HsSrcap_Ti_205.224	2.5188	0.2269	2318.6	2319.666	4129.8	1	243	34.8	1	K.EGTLTQVPLAPPPPGAPPSPAPAR.F	
gi|6005872|re	1	2	2.80%	760	87997	5.3	SEC63-like protein [Homo sapiens]					
*	HsSrcap_Ti_201.069	4.5549	0.3964	2291.37	2292.298	8923	1	719.4	45	2	K.EQSICAAEEQPAEDGQGETNK.N	
gi|21361437|r	2	3	2.80%	755	85853	4.4	HIV TAT specific factor 1 [Homo sapiens]					
*	HsFlag-VPS71_Ti_1	3.2171	0.1627	1714.27	1711.973	4188.2	1	426	53.8	1	K.FGIIMRDPQTEEFK.V	
*	HsFlag-VPS71_Ti_1	2.1066	0.0835	795.46	795.957	4078.7	7	453.8	75	2	K.LHVEVAK.F	
gi|29789006|r	1	2	2.80%	680	77861	6.7	pleckstrin homology domain containing, family C (with FERM domain) member 1 [Homo sapiens]					
*	HsFLAG-FLJ20729_	3.8096	0.3655	2051.44	2051.342	5120.2	1	609.2	52.8	2	K.TSTILGDITSIPELADYIK.V	

gi|71979932|r	1	2	2.80%	507	55010	7.7	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.9493	0.4009	1456.27	1456.596	5326.1	1	1227.7	80.8	2	R.ALAAPAAEEKEEAR.E
gi|33563340|r	4	5	2.70%	1995	228000	5.9	myosin, heavy polypeptide 14 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	3.8076	0.3868	2125.48	2126.205	8110.7	1	708	44.7	1	R.EDQSILCTGESGAGKTENTK.K
	HsFLAG-ARP6_Ti_1	2.9294	0.2075	1543.17	1543.806	4525.3	2	644.1	70.8	1	R.QRYEILTPNAIPK.G
	HsFLAG-ARP6_Ti_1	3.1298	0.1302	1258.36	1258.417	6831.5	4	1016.2	80	1	R.KEEELQAALAR.A
	HsFLAG-Lin9_Ti_20	3.416	0.1163	1220.85	1221.396	6427.8	2	1186.2	83.3	2	R.KFDQLLAEEK.A
gi|54112392|r	2	3	2.70%	1145	129269	5.7	calcium channel, voltage-dependent, alpha 2/delta subunit 2 isoform a [Homo sapiens]				
gi|54112394|r	2	3	2.70%	1143	129085	5.7	calcium channel, voltage-dependent, alpha 2/delta subunit 2 isoform b [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	4.8294	0.4389	1690.12	1690.672	5790	1	1896.3	82.1	1	K.ADAELDDPESEDVER.G
	HsFLAG-ARP6_Ti_1	3.783	0.4157	1828.62	1828.047	6286.4	1	910.6	63.3	2	K.AQPVSCFTHLVQANVR.N
gi|13259508|r	2	2	2.70%	1144	127404	5.4	dynactin 1 isoform 2 [Homo sapiens]				
gi|13259510|r	2	2	2.40%	1278	141694	5.8	dynactin 1 isoform 1 [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.2002	0.3398	1661.04	1660.914	8039.2	1	1872.6	80.8	1	R.LHISQLQHENSILK.G
	HsFlag-VPS71_Ti_1	2.6181	0.1731	1753.58	1754.94	4832.1	1	345.1	53.1	1	K.LSHEGPGSELPAGALYR.K
gi|4505933|re	2	2	2.70%	1107	123635	7	polymerase (DNA directed), delta 1, catalytic subunit 125kDa [Homo sapiens]				
*	HsFLAG-FLJ20729_	2.8563	0.0924	1594.55	1594.948	8717.6	2	887.5	57.1	1	R.LALTLRPCAPILGAK.V
*	HsMRGBP-FLAG_Ti_	2.5744	0.0962	1924.87	1927.214	4151.3	2	312.7	53.6	1	K.KVRKDLEDQEQLLRR.F
gi|30181238|r	1	2	2.70%	733	81790	8	N2,N2-dimethylguanosine tRNA methyltransferase-like [Homo sapiens]				
*	HsFLAG-FLJ20729_	3.8968	0.3831	2182.27	2182.524	7281.8	1	705.8	47.4	2	K.TAIELGPLWSSSLFNTGFLK.R
gi|24497603|r	1	3	2.70%	522	53255	5.3	nucleoporin 62kDa [Homo sapiens]				
gi|24497609|r	1	3	2.70%	522	53255	5.3	nucleoporin 62kDa [Homo sapiens]				
gi|24497607|r	1	3	2.70%	522	53255	5.3	nucleoporin 62kDa [Homo sapiens]				
gi|24497605|r	1	3	2.70%	522	53255	5.3	nucleoporin 62kDa [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.1648	0.2086	1627.65	1627.872	4767.1	1	1305.1	84.6	3	K.ELEDLLSPLEELVK.E
gi|17505234|r	1	2	2.70%	440	49324	9.9	nucleolar and spindle associated protein 1 isoform 2 [Homo sapiens]				
gi|7705951|re	1	2	5.30%	226	24980	10.8	nucleolar and spindle associated protein 1 isoform 1 [Homo sapiens]				
	HsFlag-VPS71_Ti_1	2.7546	0.3285	1140.55	1141.269	4969.7	1	627.3	72.7	2	K.SAHVTVSGGTPK.G
gi|89041101|r	1	3	2.70%	375	40778	8.7	PREDICTED: hypothetical protein XP_944530 [Homo sapiens]				
	HsFLAG-TIP49b_Ti_	1.8805	0.159	1094.3	1094.256	3958.4	1	310.5	66.7	3	R.SAYATQLALR.M
gi|14790190|r	5	7	2.60%	3664	402251	7.6	spen homolog, transcriptional regulator [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.0665	0.3964	1767.01	1767.079	8080.7	1	945.6	56.2	2	K.TPVQAAAVSIVEKPVTR.K
*	HsFlag-NUFIP_Ti_2	3.5599	0.2618	1833.46	1833.996	4672	4	350.7	46.9	2	K.NSAADLEHPEPSLPLSR.T
*	HsFlag-NUFIP_Ti_2	3.4112	0.3211	1968.38	1969.202	8348.9	1	858.3	50	1	K.VDATRPEATTEVGPQIGVK.E
*	HsFLAG-Lin9_Ti_20	3.7595	0.3671	2775.22	2774.317	6243.4	1	691.8	27.8	1	K.PAPQTLTGLVSALTGLVNVSLVPVNALK.G
*	HsFLAG-ARP6_Ti_1	3.2327	0.1129	1478.22	1478.553	5942.5	1	901.8	70.8	1	R.DQEDVVSQTESLK.A
gi|33620775|r	2	3	2.60%	1357	156275	5.6	kinectin 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.8752	0.2863	1512.06	1510.731	6093.8	2	520.4	62.5	1	K.GELTTLIHQLQEK.D
*	HsFLAG-ARP6_Ti_1	4.6941	0.475	2266.33	2267.319	5538	1	927.5	54.8	2	K.AAGDTTVIENSDVSPETESSEK.E
gi|15451892|r	2	5	2.60%	1220	138929	5.5	translation initiation factor IF2 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	2.6235	0.1442	1750.96	1750.061	8080.9	1	545.3	53.3	1	K.LRAPIICVLGHVDTGK.T
*	HsFLAG-p53-DNA-D	4.5071	0.4003	1915.13	1916.227	7412.2	1	1795.1	73.3	4	R.IFSAEIIYHLFDAFTK.Y
gi|24496789|r	2	2	2.60%	1176	134411	7.2	leucyl-tRNA synthetase [Homo sapiens]				

*	HsFLAG-FLJ20729_	2.8876	0.1765	1926.11	1925.105	6277.2	3	426	46.7	1	R.SFITTDVNPYYDSFVR.W
*	HsARP6-FLAG_Ti_1	3.08	0.2217	1509.54	1509.7	7460.1	1	629.5	53.8	1	K.STGNFLTLTQAIDK.F
gi|8922557|re	1	2	2.60%	796	88945	5.2	solute carrier family 4 (anion exchanger), member 1, adaptor protein [Homo sapiens]				
*	HsFlag-VPS71_Ti_1(	3.6743	0.3658	2155.75	2156.317	6366.3	2	369.8	40	2	R.SLQEEQSRPTTAVSSPGGPAR.A
gi|4503131|re	2	3	2.60%	781	85497	5.9	catenin (cadherin-associated protein), beta 1, 88kDa [Homo sapiens]				
gi|88968770|r	2	3	2.80%	702	77207	6.6	PREDICTED: similar to Beta-catenin isoform 10 [Homo sapiens]				
gi|88968766|r	2	3	2.60%	770	84277	6	PREDICTED: similar to catenin (cadherin-associated protein), beta 1, 88kDa isoform 9 [Homo sapiens]				
gi|88968756|r	2	3	3.10%	653	71424	6.7	PREDICTED: similar to Beta-catenin isoform 6 [Homo sapiens]				
gi|88968752|r	2	3	2.60%	781	85497	5.9	PREDICTED: similar to catenin (cadherin-associated protein), beta 1, 88kDa isoform 5 [Homo sapiens]				
gi|88968749|r	2	3	2.60%	781	85497	5.9	PREDICTED: similar to catenin (cadherin-associated protein), beta 1, 88kDa isoform 4 [Homo sapiens]				
gi|88968746|r	2	3	2.60%	781	85497	5.9	PREDICTED: similar to catenin (cadherin-associated protein), beta 1, 88kDa isoform 2 [Homo sapiens]				
gi|88968743|r	2	3	2.90%	694	75927	6.6	PREDICTED: similar to catenin (cadherin-associated protein), beta 1, 88kDa isoform 3 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.3002	0.271	1084.4	1084.322	5502.2	1	1307.5	83.3	1	K.AAVMVHQLSK.K
	HsFLAG-ARP6_Ti_1	3.463	0.25	1303.54	1303.513	7930	1	1399.4	88.9	2	R.LVQNCLWTLR.N
gi|4758786|re	1	3	2.60%	463	52546	7.6	NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kDa (NADH-coenzyme Q reductase) [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.8608	0.4233	1197.2	1197.379	7728	1	1952.6	86.4	3	K.APGFAHLAGLDK.M
gi|55741641|r	2	4	2.50%	1771	196541	6.6	kinase D-interacting substance of 220 kDa [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.7103	0.2967	2308.7	2307.445	10506.7	1	977.4	45	2	K.NGANCNLEDLDNWTALISASK.E
*	HsFLAG-ARP6_Ti_1	2.8465	0.2986	2399.18	2398.611	10210.3	1	729.1	40.9	2	R.LSSVGGETSLAEMIATLSDACER.E
gi|32490572|r	2	3	2.50%	1087	120677	5.2	erythrocyte membrane protein band 4.1-like 3 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.5489	0.2137	1280.61	1280.428	10611.4	6	778.1	60	1	R.SGAWHFSFNVK.F
*	HsFLAG-ARP6_Ti_1	4.2028	0.403	1886.35	1886.114	7545.7	1	843.3	56.7	2	K.IRPGEFEQFESTIGFK.L
gi|30410720|r	1	4	2.50%	894	101982	6.6	Sec3 isoform 1 [Homo sapiens]				
gi|67944634|r	1	4	2.50%	894	101982	6.6	Sec3 isoform 1 [Homo sapiens]				
	HsFlag-VPS71_Ti_1(	3.9547	0.4545	2413.42	2414.803	7284.4	1	1167.3	52.4	4	K.VGILPFVAEFEEFAGLAESIFK.N
gi|21361397|r	1	2	2.50%	632	71027	8.9	Rac GTPase activating protein 1 [Homo sapiens]				
*	HsFLAG-FLJ20729_	2.8565	0.3197	1733.07	1733.061	7249.1	1	440	43.3	2	K.VSLLGPVTTPEHQLLK.T
gi|15150805|r	1	3	2.50%	522	56688	5.6	transducin beta-like 1Y [Homo sapiens]				
gi|5032159|re	1	3	2.30%	577	62496	6.6	transducin beta-like 1X [Homo sapiens]				
gi|19913371|r	1	3	2.50%	514	55595	5.6	nuclear receptor co-repressor/HDAC3 complex subunit [Homo sapiens]				
gi|19913367|r	1	3	2.50%	522	56688	5.6	transducin beta-like 1Y [Homo sapiens]				
gi|19913365|r	1	3	2.50%	522	56688	5.6	transducin beta-like 1Y [Homo sapiens]				
	HsFlag-VPS71_Ti_1(	3.6623	0.3194	1459.71	1459.602	9459.2	1	1484.1	70.8	3	K.TFQGHTNEVNAIK.W
gi|61676188|r	5	8	2.40%	4374	481896	5.2	HECT, UBA and WWE domain containing 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.8769	0.4843	1960.42	1961.235	4726	1	354.9	47.1	3	R.EVLGSLPNVFSALCLNAR.G
*	HsFLAG-ARP6_Ti_1	3.7654	0.2935	1632.45	1631.875	7563.6	2	878	64.3	2	K.LPGGVQNFPQFSALR.F
*	HsFLAG-ARP6_Ti_1	3.2818	0.361	1817.73	1818.207	3874.8	1	488.6	62.5	1	K.TTPLKPSPLPVIPDTIK.E
*	HsFLAG-ARP6_Ti_1	3.6156	0.2742	2238.55	2238.59	5113.3	1	760.5	38.1	1	R.LLGPSAAADILQLSSSLPLQSR.G
*	HsFLAG-ARP6_Ti_1	4.5921	0.2303	3544.17	3544.986	9250	1	747.7	23.4	1	R.ESQLAHIKDEPPPLSPAPLTPATPSSLDPFFSR.E
gi|12229217|r	1	2	2.40%	1102	123563	7.3	activity-dependent neuroprotector [Homo sapiens]				
gi|31563503|r	1	2	2.40%	1102	123563	7.3	activity-dependent neuroprotector [Homo sapiens]				
	HsSrcap_Ti_205.150	4.8169	0.4439	2439.81	2440.673	6143.8	1	690.5	42	2	R.VLGQSSSKPAAAATGPPPGNTSSTQK.W
gi|21071058|r	2	5	2.40%	1052	121933	8.1	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin a5 [Homo sapiens]				

*	HsFLAG-p53-DNA-D	3.5544	0.2747	1729.16	1729.976	7398.2	1	955.3	67.9	3	K.QTELFAHFIQPAAQK.T
	HsFLAG-Lin9_Ti_20	3.289	0.3611	1054.8	1055.181	9211.4	1	1677.8	88.9	2	R.HGATHVFASK.E
gi|5453660|re	1	7	2.40%	907	103571	8.1	spindle pole body protein [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	5.2868	0.5067	2354.57	2355.477	8131.4	1	1985.8	61.9	7	K.SAESPQDAADLFTDLENAFQGK.I
gi|33356547|r	1	4	2.40%	904	101896	5.5	minichromosome maintenance protein 2 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	5.3056	0.3681	2539.52	2539.635	7238.8	1	1177	50	4	R.ATEDGEEDEEMIESIENLEDLK.G
gi|26051278|r	1	2	2.40%	984	99037	9.8	nuclear pore membrane protein 121 [Homo sapiens]				
*	HsSrcap_Ti_205.168	4.5321	0.4688	2363.91	2361.657	5646.3	1	787.6	52.2	2	K.APPTLQAETATKPQATSAPSPAPK.Q
gi|45439306|r	1	2	2.40%	501	57136	6.5	aspartyl-tRNA synthetase [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.4348	0.3779	1399.99	1400.725	6576.6	1	1183.1	77.3	2	R.VTMLFLGLHNVR.Q
gi|22538461|r	3	5	2.30%	2440	270207	7.1	nuclear receptor co-repressor 1 [Homo sapiens]				
*	HsSrcap_Ti_204.202	3.7468	0.372	2564.13	2565.806	11078.6	1	1012.6	45.2	1	R.SSHLEVSQASQLLQQQQQQLR.R
*	HsYL1_Ti_106.2388.	3.1003	0.2946	1769.92	1769.14	4027.8	4	342.2	46.9	3	R.VSAAVLPLVHPLPEGLR.A
*	HsYL1_Ti_104.3378.	3.3388	0.3265	2129.14	2129.43	7347	1	1173.1	55.9	1	R.LITLADHICQIITQDFAR.N
gi|88953403|r	4	5	2.30%	1758	197486	6.3	PREDICTED: similar to RAN-binding protein 2-like 1 isoform 1 isoform 1 [Homo sapiens]				
gi|88953419|r	4	5	2.30%	1760	197624	6.5	PREDICTED: similar to RAN-binding protein 2-like 1 isoform 1 isoform 9 [Homo sapiens]				
gi|88953417|r	4	5	2.30%	1766	198381	6.5	PREDICTED: similar to RAN-binding protein 2-like 1 isoform 1 isoform 8 [Homo sapiens]				
gi|88953415|r	4	5	2.30%	1757	197284	6.4	PREDICTED: similar to RAN-binding protein 2-like 1 isoform 1 isoform 7 [Homo sapiens]				
gi|88953409|r	4	5	2.80%	1412	157861	6.2	PREDICTED: similar to RAN-binding protein 2-like 1 isoform 1 isoform 4 [Homo sapiens]				
	HsFlag-VPS71_Ti_1	3.2897	0.217	1788.65	1786.936	8271.5	1	833.8	50	1	K.SGQSALYDALFSSQSPK.D
	HsScrap_Ti_105.186	2.7444	0.1612	1335.54	1336.577	4894.7	1	431.7	70	1	R.LLVQHEINTLR.A
	HsFlag-VPS71_Ti_1	3.2882	0.2649	1336.77	1336.577	5684.3	1	918.2	80	2	R.LLVQHEINTLR.A
	HsARP6-FLAG_Ti_1	3.1594	0.1779	1388.03	1388.693	4109.2	7	557	72.7	1	R.LLLDIPLQTPHK.L
gi|42716280|r	2	3	2.30%	1268	141439	6.9	high density lipoprotein binding protein [Homo sapiens]				
gi|4885409|re	2	3	2.30%	1268	141439	6.9	high density lipoprotein binding protein [Homo sapiens]				
	HsFlag-VPS71_Ti_1	3.8773	0.3502	1727.81	1725.985	6091	1	809.4	57.1	2	K.ASVITQVFHVPLEER.K
	HsFlag-NUFIP_Ti_2	3.8892	0.3095	1616.23	1615.869	8648.9	1	1041.5	65.4	1	K.FPEVIINFPDPAQK.S
gi|28373117|r	1	2	2.30%	1018	113320	5.9	contactin 1 isoform 1 precursor [Homo sapiens]				
gi|28373119|r	1	2	2.30%	1007	111867	5.8	contactin 1 isoform 2 precursor [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	4.6126	0.3638	2594.89	2595.865	6244.1	1	810.9	47.7	2	K.GFGPIFEEQPINTIYPEESLEGK.V
gi|48762926|r	1	2	2.30%	919	102452	6.1	PWP2 periodic tryptophan protein homolog [Homo sapiens]				
*	HsFLAG-p53-DNA-D	3.4887	0.2029	2285.75	2285.629	12472.7	1	1117.6	45	2	R.LLDVLSGHEGPISGLCFNPMK.S
SHUFFLED_	1	2	2.30%	619	71527	5.9	FALSE POSITIVE				
*	HsFLAG-ARP5_Ti_1	4.4493	0.1137	1590.05	1591.684	8065.6	3	1581.3	51.9	2	K.DEQTLNTANGCLVR.E
gi|4506787|re	2	3	2.20%	1657	189251	6.5	IQ motif containing GTPase activating protein 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.7948	0.4099	1883.15	1884.137	7964.7	1	720.3	50	2	R.ILAIGLINEALDEGDAQK.T
*	HsFLAG-ARP6_Ti_1	3.6512	0.1219	1970.28	1970.274	10403.5	1	1498.7	55.9	1	K.SKVDQIQEIVTGNPTVIK.M
gi|38016947|r	2	5	2.20%	1676	188304	6.5	complement component 5 [Homo sapiens]				
*	HsSrcap_Ti_204.183	2.7056	0.2583	1253.45	1253.528	5629.9	3	717.1	75	2	K.TLLPVSKPEIR.S
*	HsSrcap_Ti_202.489	4.7611	0.3852	2840.55	2841.144	9112	1	1198.3	44	3	R.YGGGFYSTQDTINAIEGLTEYSLLVK.Q
gi|21735569|r	2	3	2.20%	1339	151093	4.8	claspin [Homo sapiens]				
*	HsSrcap_Ti_206.179	3.2349	0.2701	1368.45	1368.533	8708.9	1	1164.8	70.8	2	K.KLDGASHTKPGEK.L
*	HsSrcap_Ti_201.073	3.8992	0.3124	1683.33	1683.769	8357.1	1	912.7	60	1	K.FTSQDASTPASSELNK.Q

gi|53759103|r	1	2	2.20%	1037	119938	5.2	importin 8 [Homo sapiens]				
*	HsFlag-FLJ90652_2	3.3739	0.3397	2537.73	2538.813	7927	1	623.4	38.6	2	K.FDIFEDYASPTTAAQTLLYTAAK.K
gi|50582989|r	1	2	2.20%	963	108314	6.9	IQ motif and Sec7 domain 1 [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	5.0171	0.4955	2227.89	2227.346	7951.4	1	1294.8	57.5	2	K.SPAPSSDFADAITELEDAFSR.Q
gi|50658082|r	1	2	2.20%	597	69752	5.7	centrosomal protein 70 kDa [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.8955	0.2464	1484.12	1484.779	3863.2	3	733.7	75	2	K.TLSAELVPWLNLK.K
gi|46358364|r	1	2	2.20%	498	56581	7.8	beta 3-glycosyltransferase-like [Homo sapiens]				
*	HsFLAG-UTX1_Ti_2	2.8914	0.1636	1324.7	1324.65	4678.3	7	456.8	65	2	R.IQIPKLLETLR.R
gi|4557525|re	1	2	2.20%	509	54150	7.7	dihydrolipoamide dehydrogenase precursor [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.5707	0.404	1128.66	1128.36	7296.1	1	1190.9	80	2	K.ALTGGIAHLFK.Q
gi|50233868|r	2	4	2.10%	1460	164341	5.4	hypothetical protein LOC22897 [Homo sapiens]				
*	HsFlag-FLJ90652_2	4.288	0.4014	2150.35	2151.434	9111.6	1	1104.1	52.6	3	R.ISEHLLDVDVLSPVLGGACR.Q
*	HsFlag-FLJ90652_2	2.8442	0.091	1259.84	1260.39	5916.9	5	623.6	72.2	1	K.LREELESQQK.A
gi|62243696|r	2	2	2.10%	1258	144427	5.6	stromal antigen 1 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	2.5404	0.2239	2159.2	2156.419	11177.8	1	823.1	44.1	1	R.DIALLDLINFFIQCSGCR.G
	HsFlag-VPS71_Ti_1	1.8636	0.2099	959.5	960.136	5058.6	1	424.4	68.8	1	R.HTSTLAAMK.L
gi|42741679|r	1	2	2.10%	856	98082	6.6	ATPase, H+ transporting, lysosomal V0 subunit a isoform 2 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.1214	0.3425	1800.37	1800.062	6523.2	2	647.9	52.9	2	R.ADIPLPEGEASPPAPPLK.Q
gi|19743813|r	1	2	2.10%	798	88415	5.4	integrin beta 1 isoform 1A precursor [Homo sapiens]				
gi|19743823|r	1	2	2.10%	798	88415	5.4	integrin beta 1 isoform 1A precursor [Homo sapiens]				
gi|19743821|r	1	2	2.10%	819	91035	5.4	integrin beta 1 isoform 1C-2 precursor [Homo sapiens]				
gi|19743819|r	1	2	2.10%	801	88884	5.5	integrin beta 1 isoform 1D precursor [Homo sapiens]				
gi|19743817|r	1	2	2.10%	825	91620	5.4	integrin beta 1 isoform 1C-1 precursor [Homo sapiens]				
gi|19743815|r	1	2	2.20%	789	87446	5.5	integrin beta 1 isoform 1B precursor [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	4.6791	0.32	2020.52	2020.38	7086.8	1	1283.6	68.8	2	K.LKPEDITQIQPQQLVLR.L
gi|41281573|r	1	2	2.10%	780	84674	9.2	bromo adjacent homology domain containing 1 [Homo sapiens]				
*	HsH2AZ-FLAG_293_	2.8426	0.3296	1709	1709.899	2981.4	7	236.2	53.3	2	K.TALVPPSADYSTPPHR.T
gi|13376259|r	1	2	2.10%	656	75019	5.6	nucleoporin 85 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.8126	0.2381	1631.81	1631.875	9845.6	1	921.3	57.7	2	K.LFNESHGIFLGLQR.I
gi|4505055|re	1	2	2.10%	512	58574	7.1	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.2613	0.2637	1164.13	1164.211	4231.3	3	784.2	80	2	K.DSLSDDGVDLK.T
gi|56549668|r	2	4	2.00%	1835	197390	7.4	AT rich interactive domain 2 (ARID, RFX-like) [Homo sapiens]				
*	HsFlag-NUFIP_Ti_2	3.5887	0.3161	2055.55	2057.354	5619.4	1	815.5	55.3	3	R.AVVAQHVAPPPGIVEIDSEK.F
*	HsFLAG-p53-DNA-D	2.8624	0.0905	1869.54	1870.029	7928.4	4	518.5	50	1	K.RPAEDTDRETVAGIPNK.V
gi|54859722|r	2	2	2.00%	1436	162121	5.5	nucleoporin 160kDa [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.6432	0.2529	1217.54	1217.5	5706.9	1	1357.2	95	1	R.NPIHAIGLLIR.E
*	HsFLAG-ARP6_Ti_1	3.5412	0.4218	2061.56	2062.314	10280.5	1	512.4	44.1	1	R.MNLTQLYGSNTAGYIVCR.G
gi|44888822|r	2	4	2.00%	1424	152587	7.3	hypothetical protein LOC23248 [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	2.9359	0.2481	1561.94	1560.788	4249.3	1	613.1	64.3	2	R.ESFADVLPEAAALVK.D
*	HsARP6-FLAG_Ti_1	4.2568	0.2642	1488.54	1487.734	3924.5	2	773.6	76.9	2	K.VEITPESILSALSK.T
gi|40254967|r	1	2	2.00%	1315	143709	6.6	hypothetical protein LOC79832 [Homo sapiens]				
*	HsYL1_Ti_102.3831.	4.0061	0.3808	2664.63	2665.923	8975.7	1	913.2	40	2	R.NILSNVDDILAATAAACGVTPTDFSK.S
gi|24308033|r	1	3	2.00%	1015	110064	4.7	formin binding protein 4 [Homo sapiens]				

*	HsYL1_Ti_101.1274.	4.4932	0.4801	2050.29	2050.017	5992.5	1	788.3	50	3	K.TGTDSNSTESSETSTGSLCK.E
gi|17505907|r	1	2	2.00%	851	94087	10	DEAD (Asp-Glu-Ala-Asp) box polypeptide 31 isoform 1 [Homo sapiens]				
gi|20336298|r	1	2	2.90%	585	64137	9.9	DEAD (Asp-Glu-Ala-Asp) box polypeptide 31 isoform 2 [Homo sapiens]				
	HsFlag-VPS71_Ti_1(	3.7851	0.2895	1823.21	1823.097	8343.9	1	588.5	46.9	2	R.LADISLHDPVSISVLDK.S
gi|17999541|r	1	2	2.00%	796	91707	5.5	vacuolar protein sorting 35 [Homo sapiens]				
gi|89026254|r	1	2	4.40%	363	41504	6.2	PREDICTED: similar to vacuolar protein sorting 35 [Homo sapiens]				
	HsFLAG-p53-DNA-D	2.9998	0.3548	1856.39	1855.233	5358.6	1	512.9	56.7	2	R.FTLPPLVFAAYQLAFR.Y
gi|41281612|r	1	2	2.00%	812	89099	8.4	hypothetical protein LOC283489 [Homo sapiens]				
*	HsSrcap_Ti_203.235	3.1751	0.2642	1908.27	1910.18	9637.4	2	508.8	50	2	K.SSFFIEPQKPVFPETR.K
gi|4504957|re	1	2	2.00%	410	44961	5.6	lysosomal-associated membrane protein 2 precursor [Homo sapiens]				
gi|7669503|re	1	2	2.00%	410	44956	5.7	lysosomal-associated membrane protein 2 precursor [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.0644	0.0943	988.28	988.175	2920.8	3	833.7	92.9	2	R.IPLNDLFR.C
gi|62955803|r	2	3	1.90%	1749	196041	6.7	nucleoporin 188kDa [Homo sapiens]				
*	HsYL1_Ti_106.1807.	3.9435	0.2944	1541.98	1541.704	4473.7	1	690	63.3	2	R.VQRPPSAASAAPSSSK.Q
*	HsYL1_Ti_102.3914.	4.1494	0.4354	2013.4	2013.301	4633.3	1	889	64.7	1	K.ASPESQEPLIQLVQAFVR.H
gi|4503351|re	2	3	1.90%	1616	183164	7.8	DNA (cytosine-5-)-methyltransferase 1 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1(	4.3209	0.3427	1598.92	1598.883	6008.7	1	1136.8	75	1	K.LNLLHEFLQTEIK.N
*	HsFlag-VPS71_Ti_1(	5.0571	0.4568	2035.06	2034.235	7458.8	1	1875	70.6	2	K.NLGPINEWWITGFDGGEK.A
gi|28372493|r	1	2	1.90%	913	103982	7.4	cullin 4B [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.1573	0.3511	1655.77	1656.79	5958.8	1	562.1	50	2	K.SSTTVSSFANSKPGSAK.K
gi|42476007|r	1	2	1.90%	901	102903	7.7	hypothetical protein FLJ34922 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20:	3.2086	0.2631	1826.25	1825.125	5553.7	7	437.8	46.9	2	R.TADPAILPNVLICLASR.A
gi|4826960|re	1	2	1.90%	775	87799	7.2	glutaminyl-tRNA synthetase [Homo sapiens]				
*	HsFLAG-FLJ20729_'	3.1097	0.3727	1756.61	1758.076	3409.9	1	580	67.9	2	K.GFHQVPFAPIVFIER.T
gi|11079228|r	1	2	1.90%	744	82654	6.8	N-ethylmaleimide-sensitive factor [Homo sapiens]				
gi|89042743|r	1	2	4.40%	315	34944	7.7	PREDICTED: similar to N-ethylmaleimide sensitive fusion protein [Homo sapiens]				
	HsFLAG-p53-DNA-D	5.2058	0.3663	1571.53	1571.987	5946.1	1	1564.9	80.8	2	R.FSNLVLQALLVLLK.K
gi|4504327|re	1	2	1.90%	474	51294	9.4	hydroxyacyl dehydrogenase, subunit B [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.0518	0.2616	953.14	952.145	6411.5	1	819	81.2	2	R.AALTGLLHR.T
gi|16753233|r	2	2	1.80%	2541	269665	6	talin 1 [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1(	3.3838	0.3299	2094.66	2092.403	9221.9	1	959.3	47.5	1	R.GVGAAATAVTQALNELLQHVK.A
*	HsFLAG-TCF3_Ti_1(	2.8597	0.295	2470.15	2470.78	8829.7	2	332.3	31.2	1	R.GVAALTSDPAVQAIVLDTASDVLDK.A
gi|18497286|r	1	2	1.80%	1008	114776	7.7	DEAH (Asp-Glu-Ala-His) box polypeptide 36 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.7297	0.3158	2094.15	2095.181	7218	2	925.9	55.9	2	R.DSEYLLQENEPDGTLDQK.L
gi|14043022|r	1	2	1.80%	900	101116	6.2	methionine-tRNA synthetase [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.5543	0.2895	1804.52	1805	3824.1	1	282.5	53.3	2	R.TLPGSDWTPNAQFITR.S
gi|67782358|r	1	2	1.80%	764	85533	7.1	complement factor B preproprotein [Homo sapiens]				
*	HsSrcap_Ti_206.332	3.729	0.2563	1771.45	1771.115	6534.1	1	847.6	61.5	2	R.DFHINLFQVLPWLK.E
gi|11345460|r	1	3	1.80%	669	74266	8.5	hypothetical protein LOC60558 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20!	3.8091	0.3	1324.06	1324.482	7469.4	1	1118.8	77.3	3	R.NFSIVAHVDHGK.S
gi|67551265|r	2	3	1.70%	2266	252496	6.6	transcription factor ELYS [Homo sapiens]				
*	HsYL1_Ti_103.2080.	3.2838	0.2319	1552.22	1549.851	5652.9	3	831.4	61.5	1	R.ASELHLLETPLVVK.K
	HsYL1_Ti_102.2919.	2.93	0.257	2605.99	2606.935	4901.2	1	306.3	34.8	2	K.AILLPDLSEPNNEPLFSPASEVPR.K

gi|11496982|r	2	3	1.70%	2214	247704	7	supervillin isoform 2 [Homo sapiens]				
gi|4507323|re	2	3	2.10%	1788	200820	6.9	supervillin isoform 1 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	4.6328	0.3984	1992.17	1992.193	5336.1	1	1274	70.6	1	R.YQTQPVTLGEVEQVQSGK.L
	HsFLAG-Lin9_Ti_205	5.8107	0.4463	1842.6	1843.14	8199.6	1	2059.2	69.4	2	K.KGLASPTAITPVASAICGK.T
gi|44890068|r	2	2	1.70%	1548	172787	6.8	zinc finger protein 262 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_205	3.7465	0.3041	1517.44	1516.778	8137.3	1	798.8	57.7	1	K.KPIVTINTNSISTK.C
*	HsFLAG-Lin9_Ti_205	4.2075	0.3509	1285.21	1285.448	9001.1	1	1627	81.8	1	R.LAAQSQHVGFAR.S
gi|56243590|r	2	3	1.70%	1336	145891	9.2	WD repeat domain 33 isoform 1 [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	3.3566	0.173	1472.02	1472.687	9137.2	3	890.9	62.5	2	K.LNLNGNWLLTASR.D
*	HsFLAG-p53-DNA-D	3.1586	0.1541	1276.44	1276.478	6180.8	1	961.2	83.3	1	R.NLKEELQVFR.G
gi|4758084|re	1	2	1.70%	1321	142973	5.3	chondroitin sulfate proteoglycan 3 (neurocan) [Homo sapiens]				
*	HsFLAG-p53-DNA-D	2.9292	0.086	2234.18	2236.586	7962.9	2	577.5	40.5	2	K.KGTVLCGPPPAVENASLIGARK.A
gi|22748937|r	1	2	1.70%	1204	136311	5.8	exportin 5 [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	3.5591	0.3358	2152.12	2152.539	4556.5	1	379.3	47.4	2	K.SAILGLPQPLLELNDSPVFK.T
gi|41281518|r	2	4	1.70%	1159	134329	7.1	hypothetical protein LOC9897 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.7534	0.2866	2229.18	2230.609	10562.8	1	1266.8	35.5	1	K.IPEIPADVVGALLFLEDYVR.Y
*	HsFlag-VPS71_Ti_1	4.9696	0.4052	2231.6	2230.609	4451.7	1	1409.7	71.1	3	K.IPEIPADVVGALLFLEDYVR.Y
gi|30795220|r	1	2	1.70%	848	100551	8.1	crooked neck-like 1 protein [Homo sapiens]				
*	HsFlag-NUFIP_Ti_2	3.2128	0.2888	1674.4	1674.938	5794.2	1	598.8	57.7	2	K.ERELELLPPPPQQK.I
gi|4505917|re	1	2	1.70%	860	98089	8.4	exosome component 10 isoform 2 [Homo sapiens]				
gi|50301240|r	1	2	1.70%	885	100831	8.5	exosome component 10 isoform 1 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	2.9053	0.3435	1747.79	1747.827	3212.4	1	292.1	60.7	2	R.SFPGFQAFCETQGDR.L
gi|4503165|re	1	3	1.70%	768	88930	8.5	cullin 3 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.0471	0.2271	1430.22	1430.613	6781.3	1	970.6	70.8	3	R.ALQSLACGKPTQR.V
gi|34101288|r	1	5	1.70%	782	88487	5.1	cleavage and polyadenylation specific factor 2 [Homo sapiens]				
*	HsFLAG-FLJ20729_	4.4605	0.2529	1597.16	1597.898	8684.9	1	1978	79.2	5	R.VLELAQLLDQIWR.T
gi|61743954|r	5	16	1.60%	5890	629114	6.1	AHNAK nucleoprotein isoform 1 [Homo sapiens]				
	HsSrcap_Ti_204.271	3.5963	0.4552	2178.29	2178.456	7266.5	2	403.1	39.5	1	R.ELLLPNWQGSGSHGLTIAQR.D
*	HsMRGBP-FLAG_Ti	3.9207	0.3516	1639.72	1638.778	6182.7	1	1240.3	61.8	3	R.AGAISASGPELQGAGHSK.L
	HsFlag-VPS71_Ti_1	3.1039	0.2558	2028.43	2029.216	8360.6	1	848.1	52.9	5	K.VDIDAPDVDVHGPDWHLK.M
	HsMRGBP-FLAG_Ti	3.1504	0.2935	1268.4	1268.409	6684.2	2	1072.6	77.3	6	K.AEGPEVDVNLPK.A
*	HsFlag-VPS71_Ti_1	4.2548	0.3444	2582.91	2582.865	3453.8	1	425.3	45.8	1	K.SPSLDVTVPEAELNLETPEISVGGK.G
gi|21626468|r	2	4	1.60%	1978	220623	6.4	zinc finger protein 638 [Homo sapiens]				
gi|62526045|r	2	4	1.60%	1978	220623	6.4	zinc finger protein 638 [Homo sapiens]				
	HsFLAG-FLJ20309_	4.0465	0.2626	1577.7	1577.775	4916.2	1	607.9	60	3	K.TSSGTKPSVKPTSATK.S
	HsFLAG-ARP6_Ti_1	2.7597	0.3044	1884.31	1884.071	4380.8	1	673.7	60	1	K.AGFFCPICSLFYSGEK.A
gi|18375673|r	1	2	1.60%	1118	123036	6.7	regulator of nonsense transcripts 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.3971	0.3096	1862.67	1863.211	6818.7	1	767.6	52.9	2	K.TVLQRPLSLIQGPPGTGK.T
gi|10835055|r	1	2	1.60%	795	92707	5.6	cell division cycle 2-like 1 (PITSLRE proteins) isoform 1 [Homo sapiens]				
gi|16357498|r	1	2	1.70%	777	90661	5.5	cell division cycle 2-like 2 isoform 1 [Homo sapiens]				
gi|16357488|r	1	2	3.30%	397	45229	9.2	cell division cycle 2-like 2 isoform 2 [Homo sapiens]				
gi|16357486|r	1	2	1.70%	780	91063	5.4	cell division cycle 2-like 2 isoform 5 [Homo sapiens]				
gi|16357484|r	1	2	1.70%	767	89688	5.4	cell division cycle 2-like 2 isoform 4 [Homo sapiens]				

gi|16357482|r	1	2	1.70%	776	90698	5.4	cell division cycle 2-like 2 isoform 3 [Homo sapiens]				
gi|16357480|r	1	2	3.30%	397	45229	9.2	cell division cycle 2-like 2 isoform 2 [Homo sapiens]				
gi|16332372|r	1	2	1.70%	771	90047	5.4	cell division cycle 2-like 1 (PITSLRE proteins) isoform 9 [Homo sapiens]				
gi|16332370|r	1	2	1.70%	780	91009	5.4	cell division cycle 2-like 1 (PITSLRE proteins) isoform 8 [Homo sapiens]				
gi|16332366|r	1	2	2.30%	565	63937	4.7	cell division cycle 2-like 1 (PITSLRE proteins) isoform 6 [Homo sapiens]				
gi|16332364|r	1	2	1.70%	748	87138	5.4	cell division cycle 2-like 1 (PITSLRE proteins) isoform 5 [Homo sapiens]				
gi|16332362|r	1	2	1.80%	737	85906	5.3	cell division cycle 2-like 1 (PITSLRE proteins) isoform 4 [Homo sapiens]				
gi|16332360|r	1	2	2.50%	526	59273	4.6	cell division cycle 2-like 1 (PITSLRE proteins) isoform 3 [Homo sapiens]				
gi|16332358|r	1	2	1.70%	782	91332	5.5	cell division cycle 2-like 1 (PITSLRE proteins) isoform 2 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	3.88	0.3287	1367.38	1367.632	6156.7	1	1246.8	75	2	K.TSNLLLSHAGILK.V
gi|10947135|r	1	2	1.60%	807	91680	7.7	ATP-binding cassette, sub-family F, member 1 isoform b [Homo sapiens]				
gi|69354671|r	1	2	1.50%	845	95926	6.8	ATP-binding cassette, sub-family F, member 1 isoform a [Homo sapiens]				
	HsFLAG-p53-DNA-D	4.1117	0.3403	1614.65	1614.801	9835.4	1	1472.2	70.8	2	K.IGFFNQQYAEQLR.M
SHUFFLED_	1	5	1.60%	492	53132	9.4	FALSE POSITIVE				
SHUFFLED_	1	5	1.60%	492	53132	9.4	FALSE POSITIVE				
	HsFLAG-KIAA0515_	2.1559	0.1047	898.55	898.137	3680.8	9	439.6	71.4	5	K.PLTAVRLK.A
gi|21264565|r	2	2	1.50%	2285	242042	6.7	AT rich interactive domain 1A (SWI- like) isoform a [Homo sapiens]				
gi|21264575|r	2	2	1.70%	2068	218333	6.5	AT rich interactive domain 1A (SWI- like) isoform b [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	4.3844	0.2367	2516.76	2516.637	7624.6	1	1077	34.4	1	K.HVTTAEGTPGTTDQEGPPPDGPPEK.R
	HsFLAG-p53-DNA-D	2.4894	0.2871	1060.56	1061.356	4175.7	2	452.4	66.7	1	K.HPGLLLILGK.L
gi|89047143|r	2	2	1.50%	1848	213671	7.2	PREDICTED: myosin VB isoform 1 [Homo sapiens]				
gi|89047438|r	2	2	1.50%	1848	213641	7.2	PREDICTED: similar to Myosin-5B (Myosin Vb) isoform 5 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	2.7468	0.1547	1791.91	1792.132	9797.7	2	638.6	43.8	1	K.IIASILHLGSVAIQAER.D
	HsFLAG-ARP6_Ti_1	3.1134	0.2114	1453.28	1451.622	8922.1	1	1314.6	80	1	R.YNISQLEEWLR.G
gi|33620716|r	2	10	1.50%	1758	197286	9.6	retinoblastoma-binding protein 6 isoform 2 [Homo sapiens]				
gi|33620769|r	2	10	1.50%	1792	201563	9.6	retinoblastoma-binding protein 6 isoform 1 [Homo sapiens]				
	HsFLAG-Lin9_Ti_20	2.6361	0.0889	1616.82	1617.854	8459.5	1	832.7	65.4	1	K.KPLGPPPPSYTCFR.C
	HsFLAG-p53-DNA-D	3.7041	0.2846	1307.93	1308.52	5111	1	783	75	9	K.ILPAAALASEHSK.G
gi|39652628|r	1	2	1.50%	1118	121888	8.9	hypothetical protein LOC23196 [Homo sapiens]				
*	HsYL1_Ti_101.1190.	3.443	0.3404	1568.22	1567.607	4304	1	595.1	56.2	2	K.AEGSSTASSGSQLAEGK.G
gi|89040264|r	1	2	1.50%	869	96620	7.9	PREDICTED: zinc finger protein 629 [Homo sapiens]				
gi|89040817|r	1	2	1.50%	869	96620	7.9	PREDICTED: similar to zinc finger protein 629 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.644	0.1982	1489.41	1489.631	9214.7	1	1104.7	66.7	2	K.SFSVSSNLINHQR.I
gi|10834990|r	1	2	1.50%	848	93361	4.9	neural cell adhesion molecule 1 isoform 1 [Homo sapiens]				
gi|41281937|r	1	2	1.50%	858	94601	4.9	neural cell adhesion molecule 1 isoform 2 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.4493	0.177	1565.51	1564.513	5233	1	880.6	70.8	2	K.DGEQIEQEEDDEK.Y
gi|24308177|r	1	2	1.50%	819	91969	4.7	hypothetical protein LOC55677 [Homo sapiens]				
*	HsARP6-FLAG_Ti_1	3.5512	0.1828	1336.14	1335.734	3353.6	4	533.5	77.3	2	K.LTLLPAVVMHLK.K
gi|21040314|r	2	3	1.40%	2303	250386	5.6	SON DNA-binding protein isoform B [Homo sapiens]				
gi|38146099|r	2	3	1.40%	2386	259619	5.7	SON DNA-binding protein isoform G [Homo sapiens]				
gi|21040326|r	2	3	1.40%	2426	263827	5.6	SON DNA-binding protein isoform F [Homo sapiens]				
gi|21040322|r	2	3	1.40%	2325	252251	5.4	SON DNA-binding protein isoform C [Homo sapiens]				
gi|21040320|r	2	3	1.50%	2140	232307	6	SON DNA-binding protein isoform A [Homo sapiens]				

gi|21040318|r	2	3	1.60%	2108	228179	5.4	SON DNA-binding protein isoform E [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	2.9701	0.152	1857.36	1858.229	4041.2	8	299.2	44.1	1	K.ILDSFAAAPVPTTTLVLK.S
	HsFLAG-ARP6_Ti_1	3.6099	0.1713	1680.54	1679.87	5443.5	1	997.8	71.4	2	K.DIHLDLPSNNNLVSK.D
gi|26051235|r	1	2	1.40%	1156	128979	5.1	nucleoporin 133kDa [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.2135	0.4261	1909.53	1910.221	6996.5	1	1419.1	70	2	R.FLLHQETLPEQLLAEK.Q
gi|7662310|re	1	2	1.40%	1054	119888	8.8	FERM, RhoGEF and pleckstrin domain protein 2 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.2771	0.2979	1614.34	1613.718	6402.6	2	891.5	60.7	2	K.DSSSSLTDPQVSYVK.S
gi|31652264|r	1	2	1.40%	980	110666	9.1	cutaneous T-cell lymphoma tumor antigen se70-2 [Homo sapiens]				
*	HsFlag-VPS71_Ti_1	3.3279	0.3377	1410.8	1410.533	6985.6	1	610.8	57.7	2	K.TRAEAEAAAVHGAR.F
gi|55770844|r	1	2	1.40%	906	100071	6.3	catenin, alpha 1 [Homo sapiens]				
gi|55770846|r	1	2	1.40%	905	100447	6	catenin, alpha 2 [Homo sapiens]				
	HsFLAG-ARP6_Ti_1	3.1269	0.1791	1620.09	1620.821	5620.2	1	1060.4	79.2	2	R.IALYCHQLNICSK.V
gi|55769587|r	1	4	1.40%	857	97668	7.6	hypothetical protein LOC8602 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.0579	0.3068	1300.62	1300.46	6173.3	2	585.9	59.1	4	K.ASQGSTLVHPFR.A
gi|7662142|re	1	2	1.30%	1584	175322	7.1	centrosomal protein 170kDa [Homo sapiens]				
gi|88980705|r	1	2	2.80%	719	78666	9.2	PREDICTED: similar to KARP-1-binding protein [Homo sapiens]				
	HsFLAG-FLJ20729_	3.5715	0.3437	1950.43	1951.098	8905.6	1	647.4	42.1	2	K.ASVASEVSTTSSTSKPPTGR.R
gi|15559211|r	1	2	1.30%	1097	121888	6.7	RE1-silencing transcription factor [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	4.0973	0.2757	1543.05	1543.764	6358.7	1	1374.3	80.8	2	K.KPSNNVSVIQVTTR.T
gi|13470086|r	1	3	1.30%	980	110042	6.2	retinoic acid induced 14 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	5.3136	0.2628	1597.05	1597.852	10612	1	2824.3	87.5	3	R.IQQLQEILQDLQK.R
gi|42542379|r	1	9	1.30%	904	102335	11.8	serine/arginine repetitive matrix 1 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_20	4.012	0.2572	1439.62	1440.769	8241.3	1	1541	81.8	9	K.VNLEVIKPWITK.R
gi|4504951|re	1	2	1.20%	1786	198065	5	laminin, beta 1 precursor [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1	4.7361	0.4183	2393.03	2393.61	9409.4	1	1141.3	47.6	2	R.NFLTQDSADLDSIEAVANEVLK.M
gi|31982941|r	1	2	1.20%	1564	184854	9.5	KIAA0853 [Homo sapiens]				
*	HsFLAG-FLJ20729_	4.8634	0.3999	2028.4	2029.374	8010.6	1	2071.9	70.6	2	K.MPDPLDVIDVDWSGLMPK.H
gi|31543299|r	1	2	1.20%	1327	146269	7.8	neuropathy target esterase [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.5518	0.3406	1578.48	1578.812	8054.3	1	1013.6	63.3	2	R.AQPSVVLSAAHTVAAR.M
gi|41281483|r	1	4	1.20%	1282	145821	6.4	BMS1-like, ribosome assembly protein [Homo sapiens]				
*	HsFLAG-p53-DNA-D	4.9204	0.3076	1609.91	1609.907	8108.2	1	1433.2	67.9	4	K.ILALLDALSTVHSQK.M
gi|89056848|r	1	3	1.20%	1303	140256	6.3	PREDICTED: hypothetical protein LOC23211 isoform 1 [Homo sapiens]				
gi|89057535|r	1	3	1.20%	1303	140256	6.3	PREDICTED: similar to Zinc finger CCCH-type domain containing protein 6 isoform 4 [Homo sapiens]				
	HsSrcap_Ti_202.446	3.9211	0.356	1846.13	1846.22	5839.7	1	734.8	56.7	3	R.TVLWNPEDLIPLPIPK.Q
gi|18375637|r	1	3	1.20%	1210	132383	5.5	HLA-B associated transcript 8 isoform a [Homo sapiens]				
gi|18426879|r	1	3	1.20%	1176	129032	5.5	HLA-B associated transcript 8 isoform b [Homo sapiens]				
	HsSrcap_Ti_205.235	3.9156	0.3518	1708.72	1708.967	5805	1	811.8	61.5	3	R.FINHLCDPNIIPVR.V
gi|21702733|r	1	2	1.10%	1962	210270	6.7	trinucleotide repeat containing 6A isoform 2 [Homo sapiens]				
gi|21702742|r	1	2	1.20%	1709	182053	6.6	trinucleotide repeat containing 6A isoform 1 [Homo sapiens]				
	Hs293Flag-Ies2_Ti_1	4.0991	0.3719	2315.53	2314.522	6526.4	1	770.2	52.5	2	R.RGWGTPAQNTGTNLPSVEWNK.L
gi|51467601|r	1	2	1.10%	1337	145904	5.5	PREDICTED: hypothetical protein LOC23307 [Homo sapiens]				
gi|89030541|r	1	2	1.10%	1342	146529	5.6	PREDICTED: similar to Golgi autoantigen, golgin subfamily A member 6 (Golgin linked to PML) (Golgin-like pr				
	HsFlag-VPS71_Ti_1	4.8767	0.385	1705.92	1704.797	7109.2	1	1134.6	67.9	2	K.RNNSLQTATENTQAR.V

gi|19923597|r	1	2	1.10%	1048	110324	9.8	mSin3A-associated protein 130 [Homo sapiens]				
*	HsSrcap_Ti_205.154	3.0235	0.2831	1363.79	1363.56	3267	1	350.6	68.2	2	K.VVPQQITHTSPR.I
gi|19923790|r	1	4	1.00%	1393	155984	5.6	rab3 GTPase-activating protein, non-catalytic subunit [Homo sapiens]				
*	HsFlag-FLJ90652_29	4.1532	0.4037	1397.14	1397.574	9655.3	1	1749.9	76.9	4	K.VVSAAVQAQHSATK.V
SHUFFLED_g	1	2	1.00%	1147	124824	8.8	FALSE POSITIVE				
*	HsScrap_Ti_106.230	3.0242	0.1328	1167.57	1167.351	5709.4	2	1145.9	68.2	2	R.DPLATVAPGAVR.A
gi|33695086|r	1	2	1.00%	1086	113923	8	nicotinamide nucleotide transhydrogenase [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.3816	0.314	1155.41	1155.345	7264.2	1	1397	85	2	K.AVVLAANHFGR.F
gi|32967601|r	2	2	0.90%	4377	480416	6.5	ankyrin 3 isoform 1 [Homo sapiens]				
*	HsFLAG-Lin9_Ti_204	3.1592	0.2481	1676.85	1675.969	9353.6	3	885	53.1	1	K.VALLLLDQGASPHAAAK.N
	HsFLAG-p53-DNA-D	4.2811	0.2189	2294.42	2294.61	9094.4	1	752.9	42.5	1	R.IDIVTLLEGPIFDYGNISGTR.S
gi|57634534|r	1	2	0.90%	2012	227918	6.2	nucleoporin 205kDa [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	2.8582	0.2044	2164.71	2164.422	8621.8	8	473.9	41.2	2	R.TSQDFLFSQLQYLPFSNK.E
gi|32483416|r	1	2	0.90%	1020	111838	6.1	neurofilament, heavy polypeptide 200kDa [Homo sapiens]				
	HsH2AZ-FLAG_293_	3.083	0.0921	1134.32	1134.241	5037.5	1	845.6	81.2	2	R.KLLEGEECR.I
gi|89028962|r	1	2	0.80%	2951	322607	5.8	PREDICTED: similar to epiplakin 1 [Homo sapiens]				
*	HsFLAG-FLJ20729_	4.9785	0.2388	2514.57	2514.839	9228.9	1	2076.7	38.5	2	R.AGTLTVEELGATLTSLLAQAQAQAR.A
gi|4506355|re	1	2	0.80%	1482	163835	6.4	pregnancy-zone protein [Homo sapiens]				
*	HsFLAG-TCF3_Ti_1(	3.7058	0.3403	1493.95	1492.684	5756.7	1	867.3	72.7	2	K.DLFHCVSFTLPR.I
gi|24430139|r	1	2	0.80%	1393	152754	6.4	RNA polymerase II associated protein 1 [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.1219	0.226	1167.24	1167.354	6280.7	1	1039.7	80	2	R.ASLLASQALHR.G
gi|71044479|r	1	2	0.70%	2240	243840	7.9	death inducer-obliterator 1 isoform c [Homo sapiens]				
*	HsFlag-VPS71_Ti_1(	4.1735	0.469	1656.21	1655.935	7375.4	1	1000.1	60.7	2	K.TASPLEHILQTLFGK.K
gi|67190748|r	1	2	0.70%	1744	192784	7.1	complement component 4A preproprotein [Homo sapiens]				
*	HsSrcap_Ti_202.391	3.5796	0.2062	1368.35	1368.572	6090.6	1	1343.1	81.8	2	R.DSSTWLTAFVLK.V
SHUFFLED_g	1	2	0.70%	1036	113738	5.2	FALSE POSITIVE				
*	HsFLAG-FLJ20309_	2.2344	0.0829	755.43	755.933	3133	9	510.1	83.3	2	K.ELGVPLK.L
gi|56550039|r	1	2	0.50%	3969	431768	9.1	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila) [Homo sapiens]				
*	HsYL1_Ti_101.1778.	4.1108	0.4658	1970.68	1970.054	5364.8	1	889.4	57.9	2	R.NNVSSVSTTGTATDLESSAK.V
SHUFFLED_g	1	2	0.50%	3677	383851	7.3	FALSE POSITIVE				
*	HsFLAG-TIP49b_Ti_	3.2565	0.1432	1852.8	1853.153	5644.9	3	440.8	46.9	2	R.VGRPSKSMADPRALNPR.S
gi|21361116|r	1	2	0.50%	3396	372821	4.5	chondroitin sulfate proteoglycan 2 (versican) [Homo sapiens]				
*	HsFLAG-ARP6_Ti_1	3.5133	0.2168	1990.61	1991.047	9334.1	1	1203.9	56.2	2	R.NGFDQCDYGWLSDASVR.H

	Proteins	Peptide IDs	Copies
Redundant	1987	9657	69314
Nonredund	1287	8985	60474

Supporting Table 1C. List of Proteins after contaminant extraction and SVD ranking.

For each protein, Normalized spectral abundance factors (NSAF) are calculated for each run.

Contrast_Rank	Locus	Description	ARP5_NSAF	ARP6_1_NSAF	ARP6_2_NSAF	ARP6_3_NSAF	ARP8_1_NSAF	ARP8_2_NSAF	BC014022_NSAF	DPCD_NSAF	FLJ20309_NSAF	FLJ20436_NSAF	FLJ20643_NSAF	FLJ20729_NSAF	FLJ90652_NSAF	H2AZ_NSAF	Ies2_NSAF	Ies6_NSAF	KIAA0515_NSAF	Lin9_NSAF	MRGBP_1_NSAF	MRGBP_2_NSAF	NUFIP_1_NSAF	NUFIP_2_NSAF	RPB5MP_NSAF	SRCAP_1_NSAF	SRCAP_2_NSAF	TCF3-Amida_NSAF	TIP49a_NSAF	TIP49b_NSAF	UTX1_2_NSAF	YL1_1_NSAF	YL1_2_NSAF	ZnF-HIT1-VPS71_1_NSAF	ZnF-HIT1-VPS71_2_NSAF	ZnF-HIT2_NSAF	p53-DNA-DRP_NSAF	Length	MW	pI	Duplicate
8	gi|4506753|re	TATA binding protein interacting protei	0.038928	0.004956	0.034587	0.007173	0.079468	0.037222	0.003224	0.211878	0.132314	x	0.102249	0.000528	0.019158	0.132791	0.032003	0.013837	x	0.004591	0.044405	0.040873	0.037852	0.028166	0.009695	0.075011	0.038851	0.015473	0.288641	0.13225	0.039189	0.065964	0.235304	0.038272	0.140831	0.242142	0.011242	456	50228	6.4	N
15	gi|5730023|re	RuvB-like 2 [Homo sapiens]	0.055975	0.004659	0.035686	0.000785	0.032954	0.029328	x	0.122309	0.075445	x	0.058367	0.00052	0.01779	0.069133	0.028367	0.03407	x	0.002411	0.074045	0.027426	0.033515	0.017782	0.007638	0.049251	0.020753	0.010885	0.119167	0.296486	0.022778	0.062802	0.115211	0.034143	0.125859	0.243106	0.007103	463	51157	5.6	N
16	gi|27436929|	heat shock 70kDa protein 1-like [Homo	0.002769	0.008653	0.011716	0.006237	0.002975	0.005296	x	0.001442	0.004954	0.002341	0.01336	0.006015	0.013629	0.001729	0.01366	0.003691	0.040288	0.001524	0.002502	0.000959	0.00378	0.00411	0.005517	x	0.000937	0.008311	0.000622	0.00183	x	0.000782	0.003826	0.001184	0.000618	0.002545	0.001811	641	70405	6	N
17	gi|4885431|re	heat shock 70kDa protein 1B [Homo sa	0.016062	0.022595	0.019918	0.007938	0.010414	0.022243	0.006881	0.005048	0.007018	0.004683	0.023455	0.012782	0.073985	0.004107	0.038704	0.004922	0.10382	0.005443	0.001251	0.001598	0.010479	0.015927	0.013793	x	x	0.026956	0.003941	0.009884	0.000914	0.002737	0.001913	0.001381	x	0.008112	0.003622	641	70025	5.6	N
24	gi|16507237|	heat shock 70kDa protein 5 (glucose-re	0.000543	0.004084	0.003445	0.002223	x	x	0.002248	0.002121	0.000809	x	0.000873	0.001842	0.00916	0.000847	0.003347	x	0.0243	0.00128	0.002146	0.001566	0.00052	0.002014	x	0.003874	0.000918	0.002422	x	0.001435	x	0.00345	0.00375	0.003481	0.000606	0.000312	0.001627	654	72333	5.2	N
28	gi|4757718|re	actin-like 6A isoform 1 [Homo sapiens]	0.013241	0.001915	0.014005	x	0.006669	0.021365	x	0.001078	0.005552	x	x	0.001123	0.006982	0.014535	0.006803	0.005516	x	0.001952	0.008412	0.024826	x	0.000768	x	0.044296	0.015398	0.006377	0.008677	0.021332	0.002049	0.028046	0.024297	0.015919	0.03419	x	0.001578	429	47461	5.6	N
30	gi|14210536|	tubulin, beta 6 [Homo sapiens]	0.00398	0.003224	0.001684	0.000815	x	0.004567	x		0.00178	x	0.00128	0.004322	0.00056	0.001243	0.014724	x	0.006681	0.002503	0.001798	0.001837	0.002192	0.006646	0.000991	0.014202	0.019524	0.00904	x	0.003157	0.001971	0.00562	0.001375	0.000851	x	x	0.001518	446	49857	4.9	N
42	gi|89067014|	PREDICTED: similar to RuvB-like prote	0.103278	0.008404	0.013655	x	x	0.012344	x	0.180709	0.014434	x	0.00692	x	0.018153	0.128487	0.079601	x	x	0.005075	x	0.026067	0.030146	0.029939	x	x	0.032757	0.007854	0.418188	0.051197	0.042611	0.063806	x	0.029892	x	0.305864	0.005276	55	6231	6	N
43	gi|13654237|	protein kinase, DNA-activated, catalytic	8.60E-05	0.001281	0.000546	0.005106	x	0.000329	0.001425	0.000448	0.000577	x	x	0.001343	6.00E-05	x	x	0.000573	x	0.002434	0.000971	0.000695	x	x	x	0.000614	0.002473	3.50E-05	x	x	0.000568	0.005647	0.005644	0.004442	0.00048	x	0.001453	4128	469093	7.1	N
44	gi|4885375|re	H1 histone family, member 2 [Homo sa	0.010001	0.010368	0.024682	0.008531	x	0.014344	x	0.001085	0.011182	x	0.001787	0.007919	x	0.001952	x	0.022217	x	0.002621	0.003765	0.003846	0.004192	0.001546	0.008302	x	x	0.009464	x	x	0.002751	x	0.011514	0.003562	0.072583	x	0.010899	213	21365	10.9	N
45	gi|4885379|re	H1 histone family, member 4 [Homo sa	0.009727	0.009381	0.024005	0.008297	x	0.017051	x	0.001055	0.010875	x	0.001738	0.007702	x	0.001898	x	0.021609	x	0.003186	0.003662	0.003741	0.004077	0.001504	0.008074	x	x	0.00789	x	x	0.005351	x	0.011199	0.003465	0.072404	x	0.009275	219	21865	11	N
47	gi|10835063|	nucleophosmin 1 isoform 1 [Homo sapi	0.014491	0.001398	0.012773	0.003708	x	0.001155	x	0.004717	0.005401	x	x	0.010655	0.001698	0.001885	x	0.005365	x	0.001899	0.000682	0.000697	0.000289	0.004481	x	x	0.001021	0.005877	x	0.000798	0.004982	x	x	0.010324	0.002697	x	0.006251	294	32575	4.8	N
50	gi|24234688|	heat shock 70kDa protein 9B precursor	x	0.003101	0.001106	0.000535	0.004213	0.0035	x		x	x	0.001962	x	0.000735	0.000816	0.001075	0.001162	0.013165	0.000206	x	x	0.00119	x	x	0.005597	0.001327	0.000424	x	0.001382	x	0.000369	x	0.000186	x	0.0003	0.00114	679	73681	6.2	N
52	gi|89058472|	PREDICTED: similar to Ig kappa chain	0.013397		0.035426	0.006857	x	x	0.013869	0.008722	0.014979	0.056637	0.005386	0.015913	0.009419	x	0.089488	0.349715	0.028111	0.043446	x	x	x	0.059031	0.016682	x	x	0.004075	x	x	0.024873	x	x	0.003579	0.026178	x	0.001825	106	11497	4.6	N
57	gi|4503297|re	DEAH (Asp-Glu-Ala-His) box polypepti	0.000278	0.001847	0.005872	0.001421	x	x	0.001149	0.002349	0.008069	x	x	0.004145	x	0.000542	x	0.0037	x	0.007201	0.000157	x	0.01057	0.00309	x	0.006934	x	0.000901	x	0.000367	0.001603	x	x	0.001187	0.00031	x	0.004159	1279	142069	6.6	N
69	gi|34932414|	non-POU domain containing, octamer-	0.005276	0.001309	0.007973	0.008488	x	0.002883	x	0.00638	0.005057	x	x	0.007163	0.00371	0.000588	x	x	x	0.009185	x	0.00087	0.000722	0.004894	x	x	0.001913	0.000611	x	0.002989	0.008086	x	x	0.009666	x	x	0.006777	471	54232	8.9	N
70	gi|4826998|re	splicing factor proline/glutamine rich (p	0.002511	0.001235	0.004249	0.006169	x	0.00096	x	0.003596	0.00524	x	x	0.005453	0.000706	0.000196	x	x	x	0.002961	0.000284	0.000579	6.00E-05	0.004192	x	x	x	0.001222	x	0.001991	0.005801	x	x	0.00483	x	x	0.005199	707	76150	9.4	N
71	gi|4506003|re	protein phosphatase 1, catalytic subuni	x	0.001245	0.004552	0.003304	x	x	x	0.002802	0.000802	x	0.002883	0.003651	x	0.00042	x	x	x	0.004229	x	x	0.00438	0.000998	x	0.007678	0.009099	x	0.000806	x	0.018642	0.00076	x	0.002683	x	0.000309	0.005569	330	37512	6.3	N
72	gi|4506007|re	protein phosphatase 1, catalytic subuni	x	0.001113	0.00465	0.00225	x	x	x	0.002862	0.000819	x	0.002946	0.00373	x	0.000429	x	x	x	0.005617	x	x	0.003817	0.00102	x	0.007844	0.009296	x	0.000823	x	0.017232	0.000776	x	0.002349	x	0.000316	0.004492	323	36984	6.5	N
74	gi|4506005|re	protein phosphatase 1, catalytic subuni	x	0.001099	0.004593	0.002223	x	x	x	0.002827	0.000809	x	0.001746	0.003685	x	0.000424	x	x	x	0.004694	x	x	0.00312	0.002014	x	0.007748	0.011019	x	0.000813	x	0.017022	0.000767	x	0.00232	x	0.000312	0.00355	327	37187	6.2	N
79	gi|4504255|re	H2A histone family, member Z [Homo s	0.005547	0.004012	0.011735	x	x	0.010608	x		0.004135	x	x	0.003765	x	0.047632	x	x	x	0.004361	0.001566	0.0048	0.001993	x	x	x	x	x	0.003116	0.016499	0.002289	0.121416	x	0.021736	0.003097	x	0.00529	128	13553	10.6	N
80	gi|24638446|	H2A histone family, member Q [Homo	x	0.007166	0.023288	0.002817	x	0.010526	x		0.016411	x	x	0.003736	x	0.008593	x	x	x	0.010818	0.001554	0.003175	0.001977	x	0.003427	x	x	0.001116	0.003092	x	0.006813	x	0.009506	x	0.027657	x	0.006748	129	13988	10.9	N
86	gi|10800130|	histone 1, H2ad [Homo sapiens]	x	0.007111	0.023108	0.002796	x	0.005223	x		0.016285	x	x	0.003707	x	0.008527	x	x	x	0.010735	0.001542	0.003151	0.001962	x	0.003401	x	x	0.001108	0.003068	x	0.004507	x	0.009433	x	0.027444	x	0.006696	130	14107	10.9	N
92	gi|4503745|re	filamin 1 (actin-binding protein-280) [H	0.000805	0.000078	0.000851	0.001922	x	x	x	0.002096	0.0006	x	0.000288	0.001548	0.00132	x	x	x	x	0.003374	7.60E-05	0.000464	3.20E-05	0.001991	x	x	x	0.000272	x	x	0.00321	x	x	0.001529	x	x	0.00402	2647	280759	6.1	N
96	gi|7706254|re	nucleolar protein NOP5/NOP58 [Homo	0.000671	0.001165	0.00142	0.001374	x	x	0.005558	0.000874	0.0005	x	x	0.002278	x	x	x	x	x	0.001847	x	x	0.000241	0.008093	x	x	0.000568	x	0.010807	0.001774	0.001108	0.003317	x	0.000478	x	x	0.000731	529	59578	8.9	N
101	gi|4501955|re	poly (ADP-ribose) polymerase family, r	0.002451	0.000253	0.004444	0.007527	x	0.00067	0.013049	0.001596	0.001827	x	x	0.008555	0.000246	0.00205	x	x	x	0.005367	x	x	0.00021	0.001949	x	x	x	x	x	0.000231	0.002022	x	x	0.002245	x	x	0.005819	1014	113135	8.9	N
108	gi|11036646|	H2B histone family, member S [Homo	0.005635	0.009375	0.005961	x	x	0.018859	x		0.006301	x	x	0.003825	x	0.016496	x	x	x		x	0.006502	0.000675	x	x	x	x	x	0.003165	0.005587	0.00465	0.049735	0.029197	0.011041	0.066069	x	0.009212	126	13944	10.4	N
110	gi|20336754|	H2B histone family, member R [Homo	0.005635	0.007745	0.005961	x	x	0.016165	x		0.006301	x	x	0.003825	x	0.006598	x	x	x		x	0.006502	0.000675	x	x	x	x	x	0.003165	0.005587	0.00465	0.047746	0.029197	0.007026	0.053484	x	0.006909	126	13904	10.3	N
111	gi|5174449|re	H1 histone family, member X [Homo sa	0.001667	0.003376	x	0.003412	x	0.003187	x		0.003727	x	0.001787	0.002263	0.002344	0.001301	x	0.011109	x	0.00131	x	x	0.004591	x	x	x	x	x	x	0.002203	0.006877	x	x	0.001187	0.003722	x	0.003179	213	22487	10.8	N
112	gi|55956788|	nucleolin [Homo sapiens]	x	0.004702	0.003173	0.006654	x	0.002869	x	0.000651	0.005218	x	x	0.004752	x	0.002342	x	x	x	0.003145	x	0.001442	0.016706	0.001855	x	x	x	0.001622	x	x	0.000825	x	0.000864	0.002494	x	x	0.006267	710	76615	4.7	N
114	gi|5803225|re	tyrosine 3/tryptophan 5 -monooxygenas	x	0.003223	0.00589	0.00285	x	x	x		0.003113	x	x	0.002835	0.012725	0.00163	x	x	0.00779	0.002189	x	0.00241	0.001667	0.002583	0.003467	x	x	x	x	0.002761	x	x	x	0.001488	x	x	0.002655	255	29174	4.7	N
117	gi|14043072|	heterogeneous nuclear ribonucleoprote	0.001006	0.002764	0.004255	0.007207	x	x	x	0.002619	0.009746	x	x	0.009557	x	0.005103	x	x	x	0.01186	x	x	0.000602	0.010262	x	x	x	0.000408	x	0.003988	0.004149	x	x	0.00609	x	x	0.009864	353	37430	8.9	N
118	gi|7669492|re	glyceraldehyde-3-phosphate dehydrog	x	0.0023	x	0.00217	x	x	0.008777	0.00207	0.00079	x	x	0.009351	0.002235	0.004964	x	x	x	0.002916	x	x	0.000254	0.003932	0.003959	x	x	0.001719	x	x	0.001749	x	x	0.020385	x	x	0.007218	335	36053	8.5	N
122	gi|41152056|	U5 snRNP-specific protein, 116 kD [Ho	x	0.000211	x	0.004113	x	x	x	0.000238	0.000272	x	x	0.000992	0.000514	x	x	x	x	0.001436	x	x	x	0.001016	x	0.01173	0.003707	0.000148	x	x	0.002713	x	x	0.001561	x	0.018356	0.001095	972	109478	5	N
123	gi|40217847|	activating signal cointegrator 1 complex	x	0.000168	0.000352	0.005445	x	x	0.000688	0.000433	0.000124	x	x	0.000677	x	x	x	x	x	0.001241	x	x	x	0.000617	x	0.007117	0.003233	x	x	x	0.001783	x	x	0.001539	x	0.004248	0.000725	2136	244505	6.1	N
127	gi|31542947|	chaperonin [Homo sapiens]	0.002478	0.005199	0.005243	x	x	x	x	0.00121	0.000924	x	x	0.001262	x	0.000484	x	x	x	0.002435	x	x	0.00089	x	0.000772	x	x	0.001005	x	0.000819	0.000511	x	x	0.000441	x	x	0.003714	573	61055	5.9	N
128	gi|7657351|re	MYB binding protein 1a [Homo sapiens	x	0.000232	0.001697	0.004379	x	x	0.007749	0.001915	0.004384	x	x	0.003085	x	0.000626	x	x	x	0.007987	x	0.000154	x	0.000992	x	x	x	0.000108	x	x	0.004633	x	x	0.000286	x	x	0.003059	1328	148850	9.2	N
130	gi|12056465|	fibrillarin [Homo sapiens]	0.004424	0.00384	x	0.005661	x	0.001058	0.01374		x	x	x	0.001501	x	x	0.002273	x	x	0.004347	x	x	0.00053	0.004104	x	x	0.003742	0.001794	x	0.002193	0.002738	x	x	x	x	x	0.002712	321	33784	10.2	N
131	gi|4507955|re	YY1 transcription factor [Homo sapiens	0.004288		x	x	x	0.00082	x	0.001117	0.003196	x	x	0.001164	0.002412	x	0.00705	0.00381	x	0.000337	x	x	x	0.000795	x	x	x	x	0.000642	0.000567	x	0.002422	0.001481	0.000916	x	x		414	44713	6.3	N
132	gi|17999537|	U5 snRNP-specific protein [Homo sapi	x	0.000176	x	0.001401	x	x	x	0.000396	0.000227	x	x	0.000413	x	x	x	x	x	0.000657	x	x	1.80E-05	0.000141	x	0.005426	0.001543	x	x	x	0.000753	x	x	0.001246	x	0.00262	0.001118	2335	273686	8.8	N
152	gi|14043070|	heterogeneous nuclear ribonucleoprote	0.001909	0.001519	x	0.004885	x	x	x	0.002485	0.009248	x	x	0.009717	x	0.002607	x	x	x	0.009003	x	x	0.000114	0.013279	x	x	x	x	x	0.001892	0.00315	x	x	0.007139	x	x	0.0091	372	38747	9.1	N
156	gi|31542680|	ARP5 actin-related protein 5 homolog [	0.243893		x	x	0.01571	0.021811	x		0.02267	x	x	x	0.011925	x	0.015627	0.007796	x	0.00115	x	x	x	x	x	x	x	0.009014	0.002628	0.003866	x	0.003717	0.00202	x	0.000653	x		607	68241	5.2	N
157	gi|23346420|	nuclear factor related to kappaB bindin	0.010458		x	x	0.003601	0.012307	x		0.017788	x	x	0.000182	0.010746	x	0.00496	0.006553	x	0.000105	x	x	x	x	x	x	x	0.008048	0.001607	0.003367	x	0.00568	0.001389	x	x	x		1324	141860	9	N
161	gi|4758860|re	nucleolar and coiled-body phosphoprot	0.001016	0.001469	x	0.00052	x	x	x	0.001323	0.003407	x	x	0.001034	x	0.000198	x	x	x	0.002396	x	x	x	x	x	x	0.002148	x	x	x	0.001676	x	x	0.001266	0.001701	x	0.001937	699	73720	9.5	N
162	gi|72534660|	splicing factor, arginine/serine-rich 7, 3	x	0.000863	0.009467	0.006108	x	x	x	0.001942	0.008895	x	x	0.003037	x	x	x	x	x	0.002345	x	x	0.001786	0.002767	x	x	x	0.001815	x	x	0.007385	x	x	x	0.001666	x	0.001626	238	27367	11.8	N
163	gi|4504253|re	H2A histone family, member X [Homo s	x	0.007183	0.005252	0.005083	x	0.009496	x		0.003701	x	x	0.00337	x	0.003876	x	x	x	0.007807	0.001402	x	0.001487	x	x	x	x	x	x	x	0.008194	x	x	x	0.002772	x	0.002706	143	15145	10.7	N
165	gi|6678271|re	TAR DNA binding protein [Homo sapie	x	0.001489	x	0.006145	x	x	x	0.001675	0.001918	x	x	0.006403	x	0.000669	x	x	x	0.009438	x	0.000989	x	0.003182	x	x	x	x	x	x	0.000708	0.000605	x	0.002138	x	x	0.002804	414	44740	6.2	N
186	gi|52632383|	heterogeneous nuclear ribonucleoprote	0.001808	0.001221	0.001275	0.003085	x	x	x	0.001962	0.001797	x	x	0.011865	x	0.000235	x	x	x	0.007108	x	x	0.000361	0.002237	x	x	x	x	x	x	x	x	x	0.00408	x	x	0.00427	589	64133	8.2	N
190	gi|4506901|re	splicing factor, arginine/serine-rich 3 [H	x	0.001566	0.013738	0.019944	x	x	x	0.001409	0.006454	x	x	0.002939	x	x	x	x	x	0.005106	x	x	0.00337	0.008032	x	0.007725	x	0.000878	x	x	0.012504	x	x	x	x	x	0.004128	164	19330	11.6	N
191	gi|13123776|	DNA methyltransferase 1-associated p	x		0.012866	x	x	x	x		x	x	x	x	x	0.034122	x	x	x		0.015455	0.017104	x	x	x	0.043404	0.009002	x	0.007117	0.019094	x	0.023617	0.02232	0.014623	0.021221	x		467	52993	9.5	N
192	gi|5729838|re	glioma-amplified sequence-41 [Homo s	x	0.000679	x	x	x	x	x		x	x	x	x	x	0.025027	x	x	x		0.011481	0.023459	x	x	x	0.039066	0.007937	x	0.007028	0.017573	x	0.016564	0.013505	0.014485	0.012224	x		227	26499	8.4	N
193	gi|HsSRCAP	current presumptive full-length human	x	0.000243	0.003791	0.000115	x	x	x		x	x	x	x	x	0.012108	x	x	x		x	x	x	x	x	0.022779	0.005399	x	0.002223	0.005626	x	0.006484	0.011992	0.00758	0.009379	x		3170	337678	5.8	N
194	gi|27734727|	hypothetical protein LOC283899 [Hom	0.01164		x	x	0.011725	0.01113	x		0.008676	0.006151	x	x	0.318138	x	0.029905	x	x		x	x	x	x	x	x	x	0.008852	0.000545	0.003847	x	0.003082	0.020103	x	0.001625	x		244	26478	8.3	N
196	gi|39812115|	actin-related protein 8 [Homo sapiens]	0.018206		x	x	0.553216	0.3275	x		0.013995	x	x	x	0.006	x	0.003508	0.010112	x	0.000447	x	x	x	x	x	x	x	0.003692	0.002557	0.00188	x	0.00241	0.001965	x	x	x		624	70484	7.8	N
197	gi|4502643|re	chaperonin containing TCP1, subunit 6	0.012703	0.009188	x	0.002053	x	x	x	0.001306	x	x	x	0.000454	0.00141	x	x	x	x	0.000526	x	x	x	x	x	x	x	0.000271	x	x	0.000552	x	x	0.000714	x	0.000192	0.000546	531	58024	6.7	N
198	gi|48762932|	chaperonin containing TCP1, subunit 8	0.009718	0.009278	x	0.001326	x	x	x		x	x	x	0.000879	0.001366	x	x	x	x		x	x	0.000155	0.001803	x	x	x	0.000263	x	x	x	x	x	0.001154	x	0.000186	0.000353	548	59621	5.6	N
199	gi|14589951|	PolII_Rpb5 {DNA directed RNA polyme	x		x	x	x	x	0.042004	0.005503	0.00126	x	0.028999	x	x	x	x	x	x	0.000665	x	x	0.022674	x	0.018946	x	x	x	0.003165	0.002235	0.020925	x	x	x	x	0.004855	0.011515	210	24611	6	N
207	gi|24234747|	interleukin enhancer binding factor 2 [H	x	0.000263	x	0.001864	x	x	x	0.002371	0.001357	x	x	0.002472	x	0.000355	x	x	x	0.006441	x	x	x	0.004222	x	x	0.00077	x	x	x	0.002253	x	x	0.004864	x	x	0.003472	390	43062	5.3	N
208	gi|5902076|re	splicing factor, arginine/serine-rich 1 (s	x	0.002278	0.024227	0.013189	x	x	x	0.000932	0.001067	x	x	x	x	0.001117	x	x	x	0.003376	x	x	0.004114	0.002656	x	x	x	x	x	x	0.002363	x	x	0.00051	x	x	0.00351	248	27745	10.4	N
210	gi|50659095|	DEAD (Asp-Glu-Ala-Asp) box polypept	0.000453		0.000959	0.001857	x	x	x	0.003838	0.002028	x	x	0.004616	x	0.000354	x	x	x	0.004812	x	x	x	0.001262	x	x	x	x	x	x	0.000748	x	x	0.001454	x	x	0.002347	783	87344	9.3	N
213	gi|11968057|	ARP6 actin-related protein 6 homolog [	x	0.001816	0.017069	x	x	x	x		x	x	x	x	x	0.026943	x	x	x		x	x	x	x	x	0.019195	0.014407	x	0.006379	0.015407	x	0.01266	0.02787	0.022036	0.063066	x		396	45810	5	N
214	gi|5174715|re	transcription factor-like 1 [Homo sapien	x	0.000423	x	x	x	x	x		x	x	x	x	x	0.009517	x	x	x		0.004406	0.002251	x	x	x	x	0.006599	x	0.00073	0.010314	x	0.0303	0.084222	0.004864	0.018514	x		364	40594	6.5	N
215	gi|7019371|re	TCF3 (E2A) fusion partner (in childhoo	0.018242		x	x	0.003769	0.004025	x		0.012552	x	x	x	0.010852	x	0.01442	0.009352	x		x	x	x	x	x	x	x	0.180414	0.002102	0.00371	x	0.001982	0.002423	x	x	x		253	28278	5.2	N
216	gi|33469139|	yeast INO80-like protein [Homo sapien	0.009811		x	x	0.004903	0.008945	x		0.014626	x	x	x	0.006898	x	0.008441	0.004055	x	0.000179	x	x	x	x	x	x	x	0.003054	0.002222	0.002111	x	0.001289	x	x	x	x		1556	176752	9.5	N
218	gi|42822884|	hypothetical protein LOC125476 [Hom	0.048075		x	x	0.004967	0.019449	x		0.035835	x	x	x	0.0117	0.009382	0.019002	0.090374	x		x	x	x	x	x	x	x	0.012749	0.00554	0.009777	x	0.002611	x	x	x	x		192	20643	10	N
219	gi|24307939|	chaperonin containing TCP1, subunit 5	0.020343	0.009303	x	0.003359	x	x	x		x	x	x	0.001336	x	x	x	x	x	0.000516	x	x	0.000157	x	x	x	x	0.000798	x	x	0.000542	x	x	0.000468	x	0.000188	0.000894	541	59671	5.6	N
220	gi|5453607|re	chaperonin containing TCP1, subunit 7	0.012422	0.013431	x	0.001339	x	x	x		0.001949	x	x	0.000444	0.001379	x	x	x	x	0.000257	x	x	x	x	x	x	x	0.00053	x	x	x	x	x	0.000699	x	0.000188	0.000891	543	59367	7.6	N
221	gi|4758560|re	WD repeat domain 57 (U5 snRNP spe	0.001989	0.000144	x	0.003054	x	x	x		x	x	x	0.00135	x	x	x	x	x	0.000782	x	x	x	0.001845	x	0.003549	0.003364	x	x	x	x	x	x	0.000708	x	0.004569	0.000542	357	39299	8.1	N
222	gi|14591909|	ribosomal protein L5 [Homo sapiens]	x	0.003113	x	x	x	x	x		0.001782	x	x	x	x	x	x	0.010622	x	0.00094	x	0.00069	0.00501	0.002218	x	x	x	0.007757	x	x	x	x	x	0.000426	0.005339	x	0.000326	297	34363	9.7	N
223	gi|14211889|	dpy-30-like protein [Homo sapiens]	x	0.005707	x	0.022026	x	x	0.0594		0.013365	x	x	0.009736	x	x	x	x	x	0.005639	x	x	x	x	x	x	0.036396	0.002909	x	x	0.017755	x	x	0.006387	x	x	0.007816	99	11250	4.9	N
228	gi|13514822|	DEAH (Asp-Glu-Ala-His) box polypepti	x	0.002404	0.012783	0.006186	x	x	x	0.002951	0.015765	x	x	0.008203	x	x	x	x	x	0.003563	x	x	0.008684	x	x	x	x	x	x	x	0.00374	x	x	0.001076	x	x	0.004939	235	24336	10.1	N
234	gi|13775202|	high mobility group AT-hook 1-like 4 [H	0.009315		x	x	0.00278	0.009897	x		0.004629	x	x	x	0.003638	x	0.134022	0.004599	x		x	x	x	x	x	x	x	0.002519	0.000388	0.001368	x	0.002192	x	x	x	x		343	37218	9.4	N
235	gi|8923598|re	hypothetical protein LOC55011 [Homo	x		x	x	x	x	0.050695	0.006376	x	x	0.301869	x	x	x	x	x	x		x	x	0.060106	x	0.027439	x	x	x	0.002751	0.000809	0.029295	x	x	x	x	0.003867	0.009005	290	32363	5.1	N
236	gi|24308444|	hypothetical protein LOC116143 [Hom	x		x	x	x	x	0.177078	0.00259	x	x	0.051175	x	x	x	x	x	x		x	x	0.040728	x	0.047056	x	x	x	0.006703	0.000657	0.034465	x	x	x	x	0.005997	0.014631	357	39740	8.1	N
238	gi|19924159|	RPB5-mediating protein isoform a [Hor	x		x	x	x	x	0.02748	0.005616	x	x	0.048378	x	x	x	x	x	x		x	x	0.019231	x	0.056189	x	x	x	0.003479	0.003947	0.032854	x	x	x	x	0.004574	0.009944	535	59832	5	N
239	gi|18079254|	p53 and DNA damage-regulated protei	x		x	x	x	x	0.121592	0.006952	x	x	0.044358	x	x	x	x	x	x		x	x	0.030047	x	0.113011	x	x	x	0.004998	0.003529	0.11674	x	x	x	x	0.000767	0.057453	133	15511	6	N
240	gi|51460917|	PREDICTED: similar to 60S acidic ribo	x	0.001802	x	0.003188	0.008365	0.002978	x		x	x	x	x	x	0.002431	x	x	x	0.002448	x	0.001797	x	x	x	x	x	0.006315	x	x	x	x	x	x	0.003477	x	0.000848	114	11577	4.7	N
252	gi|5453603|re	chaperonin containing TCP1, subunit 2	0.010617	0.019392	x	0.004076	x	x	x	0.000432	0.000989	x	x	0.00045	x	x	x	x	x	0.000261	x	x	x	x	x	x	x	0.001077	x	x	x	x	x	0.001418	x	x	0.001085	535	57488	6.4	N
255	gi|34577110|	aldolase A [Homo sapiens]	x	0.000282	x	0.000998	x	x	x	0.000635	x	x	x	0.00331	0.000686	0.001142	x	x	x	0.001917	x	x	x	0.003619	x	x	x	x	x	x	x	x	x	0.014592	x	x	0.002392	364	39420	8.1	N
258	gi|16753227|	ribosomal protein L6 [Homo sapiens]	x	0.00428	x	x	x	x	x		x	x	0.000661	x	x	0.000481	x	0.01917	x	0.001938	x	0.000711	0.000443	x	x	x	x	0.008999	x	x	0.003052	x	x	x	x	x	0.001008	288	32728	10.6	N
262	gi|4502491|re	complement component 1, q subcompo	x	0.002914	x	x	x	0.001204	x	0.004098	x	x	x	0.001709	0.002655	x	x	x	x	0.001485	x	x	x	x	x	x	0.003194	0.002553	x	0.001664	x	x	x	x	x	x	0.000686	282	31362	4.8	N
271	gi|39725938|	polymerase (RNA) III (DNA directed) p	x		x	x	x	x	0.001058		x	x	0.004107	x	x	x	x	x	x		x	x	0.002692	x	x	x	0.000864	x	0.000191	0.000675	0.002529	x	x	x	x	0.000807	0.001461	1390	155641	8.5	N
272	gi|7657162|re	HLA class II region expressed gene KE	x		x	x	x	x	0.068379	0.005375	x	x	0.035406	x	x	x	x	x	x		x	x	0.041525	x	0.0891	x	x	x	x	0.001819	0.036335	x	x	x	x	0.001581	0.022494	129	14583	8.9	N
273	gi|13375809|	hypothetical protein LOC79657 [Homo	x		x	x	x	x	0.02874	0.003128	x	x	0.093008	x	x	x	x	x	x		x	x	0.024677	x	0.037892	x	x	x	0.002399	x	0.028634	x	x	x	x	0.003833	0.0096	665	75703	7.1	N
274	gi|12408675|	prefoldin 2 [Homo sapiens]	x		x	x	x	x	0.019093	0.004503	x	x	0.043252	x	x	x	x	x	x		x	x	0.047759	x	0.074636	x	x	x	0.00259	x	0.022827	x	x	x	x	0.004634	0.017586	154	16648	6.6	N
277	gi|15431306|	ribosomal protein L8 [Homo sapiens]	x	0.0006	x	x	x	x	x		0.00103	x	x	x	x	0.000539	x	0.018414	x	0.000543	x	0.001594	x	x	x	x	x	0.003362	x	x	x	x	x	x	0.007712	x	0.001129	257	28025	11	N
303	gi|5803102|re	MORF-related gene 15 isoform 1 [Hom	x		x	x	x	x	x	0.000716	x	x	x	x	x	0.00429	x	x	x		0.160759	0.139501	x	x	x	x	x	x	0.000823	0.003632	x	0.008537	0.001898	x	x	x	0.000299	323	37231	9.2	N
306	gi|38455427|	chaperonin containing TCP1, subunit 4	0.008563	0.011625	x	0.004046	x	x	x		x	x	x	0.000894	0.000926	x	x	x	x	0.000777	x	x	x	x	x	x	x	0.000534	x	x	x	x	x	0.000235	x	0.000189		539	57924	7.8	N
307	gi|4507691|re	transformation/transcription domain-as	x		x	x	x	x	x		x	x	x	x	x	0.004486	x	x	x	0.000073	0.007119	0.014171	x	x	x	x	x	x	0.001874	0.006188	x	0.006283	0.010726	x	0.000311	x		3830	434416	8.2	N
317	gi|7706753|re	ubiquitin C-terminal hydrolase UCH37	0.004316		x	x	0.011594	0.009286	x		0.012065	x	x	x	0.008345	x	x	x	x	0.000424	x	x	x	x	x	x	x	0.005252	0.001616	x	x	0.001524	x	x	x	x		329	37607	5.3	N
320	gi|58761486|	chaperonin containing TCP1, subunit 3	0.010442	0.007647	x	0.001336	x	x	x	x	x	x	x	x	0.001376	x	x	x	x	x	x	x	x	0.000605	x	x	x	x	x	x	x	x	x	0.000697	x	0.000187	0.000356	544	60463	6.5	N
323	gi|24041018|	ubiquitously-expressed transcript isofo	x		x	x	x	x	0.052195		x	x	0.018017	x	x	x	x	x	x		x	x	0.008302	x	0.049701	x	x	x	x	0.001388	0.019068	x	x	x	x	0.001207	0.00973	169	19597	7.1	N
376	gi|4504279|re	H3 histone, family 3A [Homo sapiens]	x	0.002266	x	x	x	0.004992	x	0.008498	x	x	x	x	x	0.003057	x	x	x	0.004105	x	x	0.002501	x	x	x	x	x	x	x	0.015078	x	x	x	x	x	0.007823	136	15328	11.3	N
385	gi|13904870|	ribosomal protein S5 [Homo sapiens]	x	0.003776	x	0.001782	x	0.006656	x	0.001133	0.001297	x	x	x	x	x	x	x	x		x	x	0.031677	x	x	x	x	0.005647	x	x	x	x	x	x	x	x	0.000948	204	22876	9.7	N
386	gi|5453617|re	zinc finger, HIT domain containing 1 [H	x		x	x	x	x	x		x	x	x	x	x	0.006298	x	x	x		x	x	x	x	x	x	x	x	0.00259	0.004571	x	0.009766	0.015926	0.00657	0.033464	x		154	17536	9.4	N
387	gi|56549696|	E1A binding protein p400 [Homo sapie	x		x	x	x	x	x		x	x	x	x	x	0.005637	x	x	x		0.010981	0.013842	x	x	x	x	x	x	0.002044	0.007817	x	0.007788	0.018264	x	0.000254	x		3122	339693	9.2	N
388	gi|34452705|	bromodomain containing 8 isoform 1 [H	x		x	x	x	x	x		x	x	x	x	x	0.003351	x	x	x		0.021292	0.029074	x	x	x	x	x	x	0.000979	0.004935	x	0.00659	0.007737	x	0.001251	x		951	102839	4.7	N
392	gi|4506691|re	ribosomal protein S16 [Homo sapiens]	x	0.004221	x	0.004978	x	x	x		x	x	0.005214	x	x	x	x	x	x		x	x	0.010483	0.002256	x	0.008677	0.002057	0.001972	x	x	x	x	x	x	x	x		146	16445	10.2	N
393	gi|38488718|	hypothetical protein LOC54891 [Homo	0.004043		x	x	0.001086	0.001933	x		0.003617	x	x	x	0.000853	x	0.004155	0.000898	x		x	x	x	x	x	x	x	0.000328	x	x	x	x	x	x	x	x		878	98172	8.2	N
394	gi|29893564|	microspherule protein 1 isoform 1 [Hon	0.005379		x	x	0.006192	0.000735	x		0.042959	0.250149	x	x	0.005403	x	0.001579	x	x		x	x	x	x	x	x	x	0.000935	x	x	x	x	x	x	x	x		462	51803	9.4	N
400	gi|4506693|re	ribosomal protein S17 [Homo sapiens]	x	0.002663	x	x	x	0.007544	x		x	x	x	x	x	x	x	0.017527	x		x	x	0.030862	x	x	x	x	0.008533	x	x	x	x	x	0.000937	x	x	0.002149	135	15550	9.8	N
457	gi|36287069|	HIV-1 Tat interactive protein, 60kDa iso	x		x	x	x	x	x		x	x	x	x	x	0.007613	x	x	x		0.006609	0.011629	x	x	x	x	x	x	0.001948	0.009025	x	0.007345	0.005615	x	x	x		546	61798	8.6	N
458	gi|21361489|	enhancer of polycomb homolog 2 [Hom	x		x	x	x	x	x		x	x	x	x	x	0.003269	x	x	x		0.005518	0.006174	x	x	x	x	x	x	0.000523	0.002768	x	0.005256	0.004822	x	x	x		763	86267	8.6	N
459	gi|13376810|	enhancer of polycomb 1 [Homo sapien	x		x	x	x	x	x		x	x	x	x	x	0.00116	x	x	x		0.004317	0.00784	x	x	x	x	x	x	0.000159	0.005894	x	0.004498	0.000733	x	x	x		836	93463	8.6	N
529	gi|10440560|	H3 histone family, member I [Homo sa	x	0.004154	x	x	x	0.009984	x	0.0017	x	x	x	x	x	x	x	x	x		x	x	0.001563	x	x	x	x	x	x	x	0.008616	x	x	x	x	x	0.004978	136	15404	11.1	N
531	gi|31742503|	H3 histone family, member M [Homo sa	x	0.001133	x	x	x	0.004992	x	0.003399	x	x	x	x	x	x	x	x	x		x	x	0.00125	x	x	x	x	x	x	x	0.008616	x	x	x	x	x	0.007112	136	15388	11.3	N
563	gi|8922764|re	MRG-binding protein [Homo sapiens]	x		x	x	x	x	x		x	x	x	x	x	0.004755	x	x	x		0.110069	0.098391	x	x	x	x	x	x	x	0.00115	x	0.006144	0.003006	x	x	x		204	22417	5.8	N
564	gi|40255020|	hypothetical protein LOC64769 [Homo	x		x	x	x	x	x		x	x	x	x	x	0.007583	x	x	x		0.007979	0.018341	x	x	x	x	x	x	x	0.008172	x	0.004988	0.030504	x	x	x		201	22755	8.3	N
565	gi|38201655|	inhibitor of growth family, member 3 iso	x		x	x	x	x	x		x	x	x	x	x	0.001657	x	x	x		0.009593	0.00539	x	x	x	x	x	x	x	0.001684	x	0.002399	0.010268	x	x	x		418	46743	6.3	N
653	gi|6912448|re	MORF-related gene X [Homo sapiens]	x		x	x	x	x	x		x	x	x	x	x	0.001925	x	x	x		0.159412	0.115207	x	x	x	x	x	x	x	x	x	0.001741	0.004258	x	x	x		288	32308	9.7	N
975	gi|7656936|re	zinc finger, HIT domain containing 2 [H	x		x	x	x	x	x		x	x	x	x	x	x	x	x	x		x	x	x	x	x	x	x	x	0.002309	0.001747	x	x	x	x	x	0.09057		403	42884	6	N

1029	gi|39930355|	DPCD protein [Homo sapiens]	x		x	x	x	x	x	0.060347	x	x	x	x	x	x	x	x	x		x	x	x	x	x	x	x	x	0.005894	0.00578	x	x	x	x	x	x		203	23240	9	N
1034	gi|4506711|re	ribosomal protein S27 [Homo sapiens]	x	0.003057	x	x	x	x	x		x	x	x	x	x	x	x	x	x		x	x	x	x	x	x	0.003575	x	x	0.005587	x	x	x	x	x	x		84	9461	9.5	N
1040	gi|4504345|re	alpha 2 globin [Homo sapiens]	x		x	x	x	x	x		x	x	x	x	x	x	0.005139	x	x		x	x	x	x	0.043585	x	x	0.002028	x	x	x	x	x	x	x	x		142	15258	8.7	N
1203	gi|21361918|	leucine proline-enriched proteoglycan (	x		x	x	x	x	x		x	x	x	x	x	x	x	x	x		x	x	x	x	x	x	x	x	x	x	x	x	x	0.000472	x	x		804	90544	5.8	N
1273	gi|13376798|	hypothetical protein LOC80304 [Homo	x		x	x	x	x	x		x	x	x	x	x	x	x	x	x		x	x	x	x	x	x	x	x	0.003688	0.005858	x	x	x	x	x	x		721	79136	6.7	N
1278	gi|10835165|	CD59 antigen p18-20 [Homo sapiens]	x	0.002407	x	x	x	x	x		x	x	x	x	x	x	x	x	x		x	x	x	x	x	x	x	x	x	0.0055	x	x	x	x	x	x		128	14177	6.5	N
1286	gi|6912542|re	nuclear fragile X mental retardation pro	x		x	x	x	x	x		x	x	x	x	x	x	x	x	x		x	x	x	0.02129	x	x	x	x	0.002686	x	x	x	x	x	x	x		495	56369	9.2	N
1287	gi|20149643|	hypothetical protein LOC54680 [Homo	x		x	x	x	x	x		x	x	x	x	x	x	x	x	x		x	x	x	0.008408	x	x	x	x	0.003677	x	x	x	x	x	x	x		470	53846	5.9	N
1490	gi|46367785|	hypothetical protein LOC54934 [Homo	x		x	x	x	x	x		x	0.242452	x	x	0.01024	x	x	x	x		x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x		390	43483	5.3	N
1642	gi|5174745|re	ubiquinol-cytochrome c reductase hing	x		x	x	x	x	x		x	x	x	x	x	x	x	x	x		x	x	x	x	x	x	0.052795	x	x	x	x	x	x	x	x	x		91	10755	4.4	N
1670	gi|4504349|re	beta globin [Homo sapiens]	x		x	x	x	x	x		x	x	x	x	x	x	x	x	x		x	x	x	x	0.072175	x	x	x	x	x	x	x	x	x	x	x		147	15998	7.3	N
1755	gi|89030033|	PREDICTED: hypothetical protein LOC	x		x	x	x	x	x		x	x	x	x	x	x	x	x	0.213484		x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x		442	47563	9.2	N
1758	gi|13569879|	acidic (leucine-rich) nuclear phosphopr	x		x	x	x	x	x		x	x	x	x	x	0.055322	x	x	x		x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x		268	30692	3.8	N
1764	gi|47824889|	hypothetical protein LOC388272 [Homo	x	x	x	x	x	x	x	x	x	x	x	x	x	0.008098	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x	x		154	17799	10.1	N