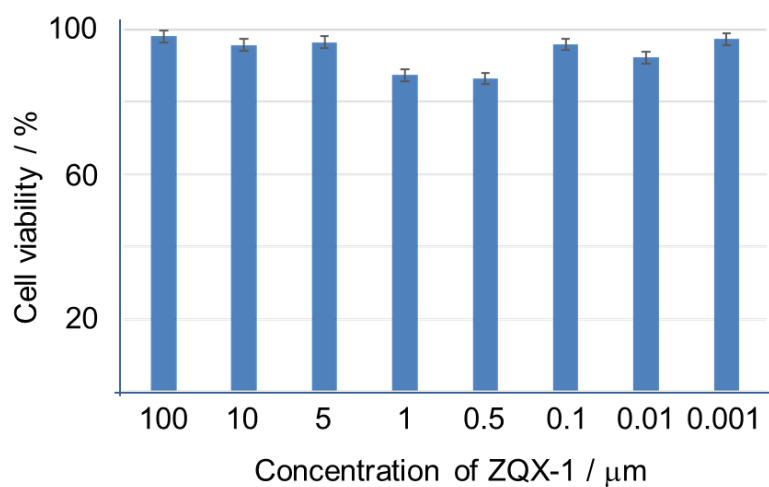


## **Supplementary Materials**

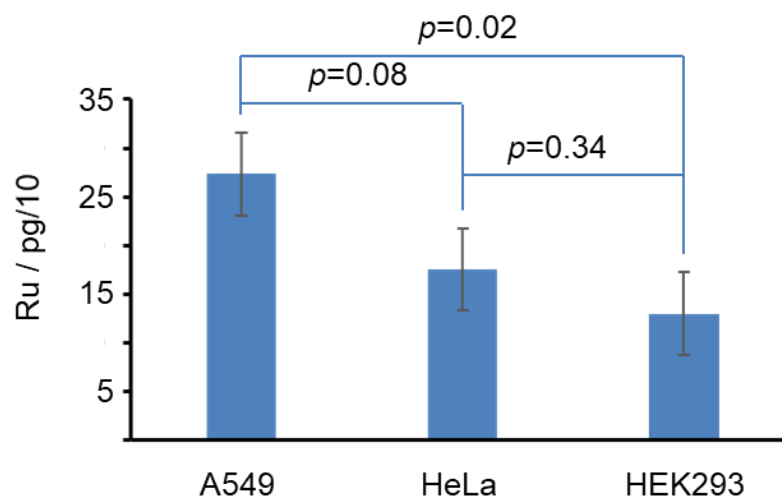
Figure S1 – S12

Table S1 – S5

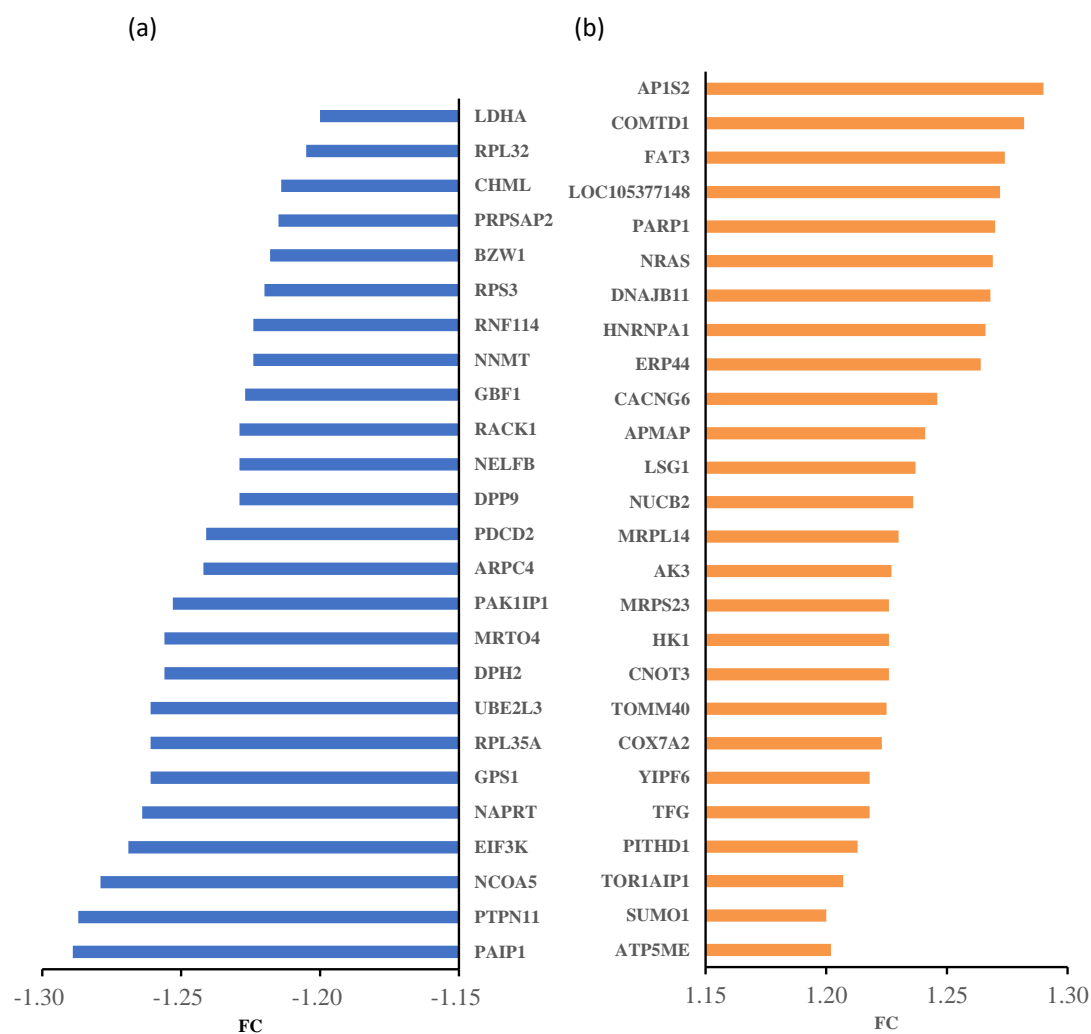
(a)



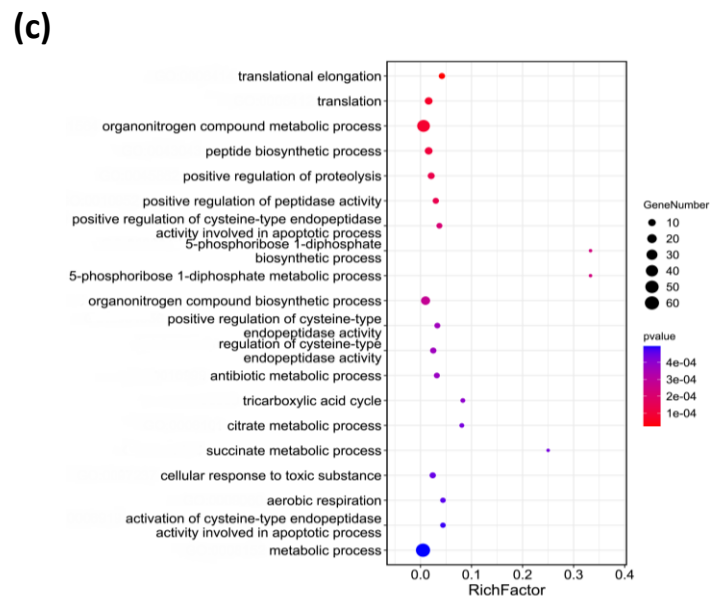
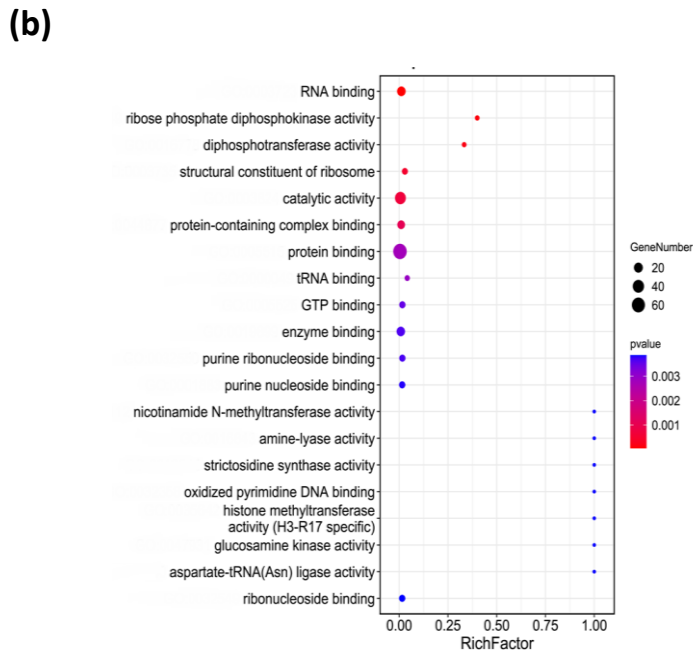
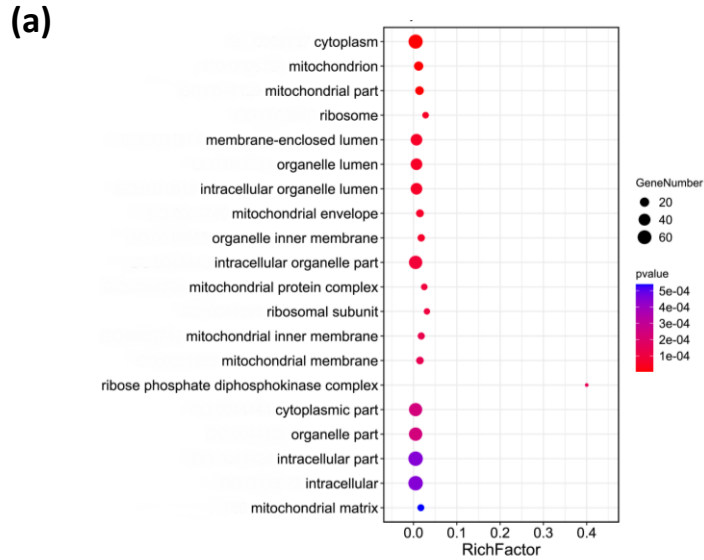
(b)



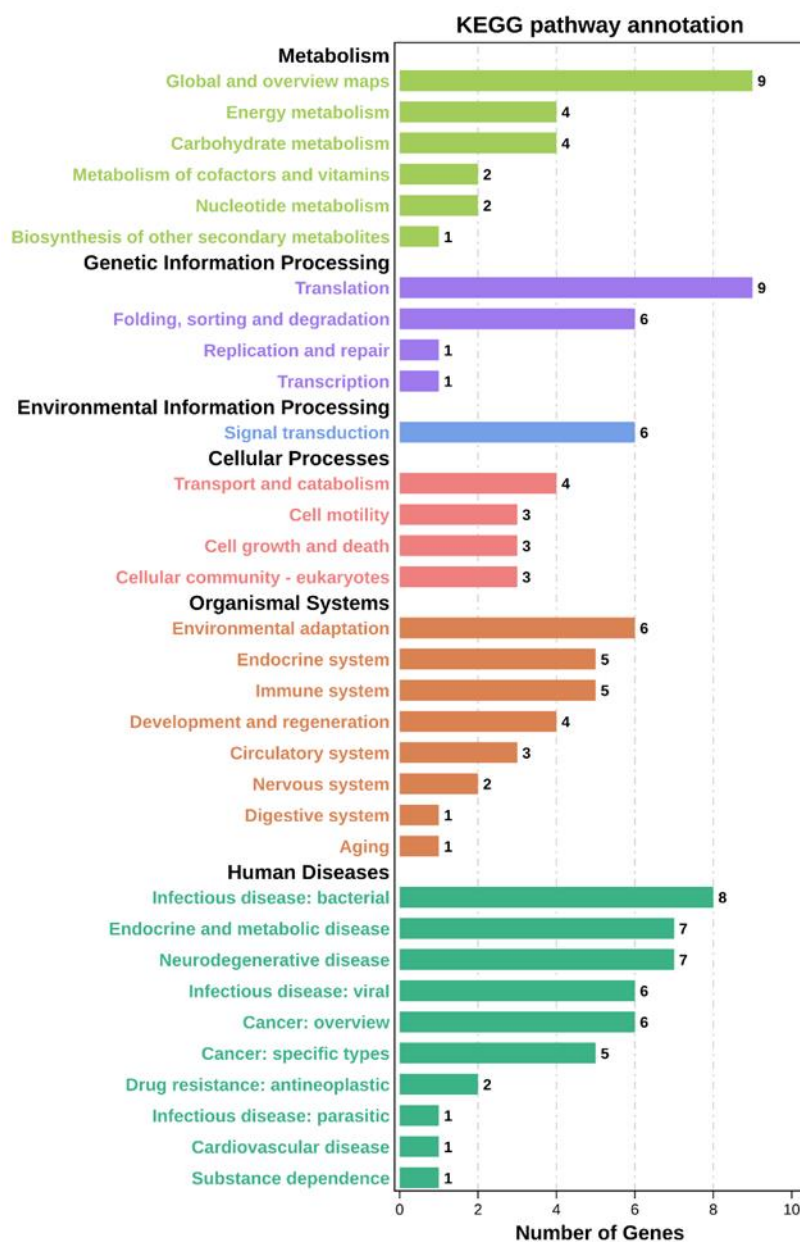
**Figure S1.** (a) The cell viability of HEK293 incubated with various concentrations of ZQX-1 in the dark for 4 h, followed by irradiation at 420 nm for 20 min and further incubation in the dark for 0.5 h. The cell viability (%) of HEK293T cells are present as mean  $\pm$  SD,  $n=6$ . (b) Ru concentrations determined by ICP-MS in A549, HeLa and HEK293T cells exposed to ZQX-1 (5  $\mu\text{M}$ ) for 4 h in the dark. All results are present as mean  $\pm$  SD,  $n=3$ .



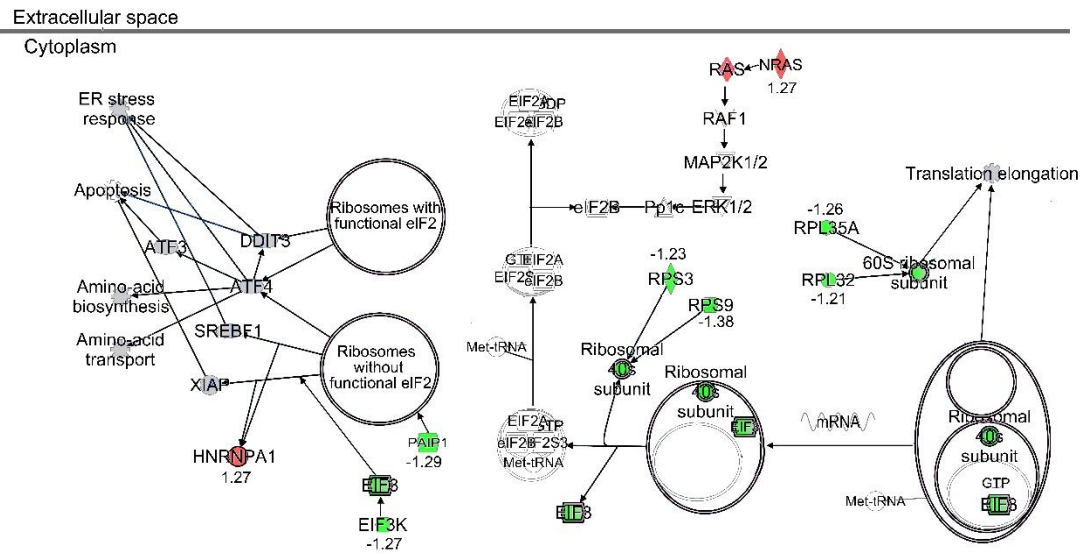
**Figure S2.** Differentially expressed proteins (DEPs) identified in A549 cells in LZ group with a fold changes (FC)  $\leq -1.2$  and  $\geq -1.3$  (a) or of  $\geq 1.2$  and  $\leq 1.3$  (b), compared to those in A549 cells in LB group.



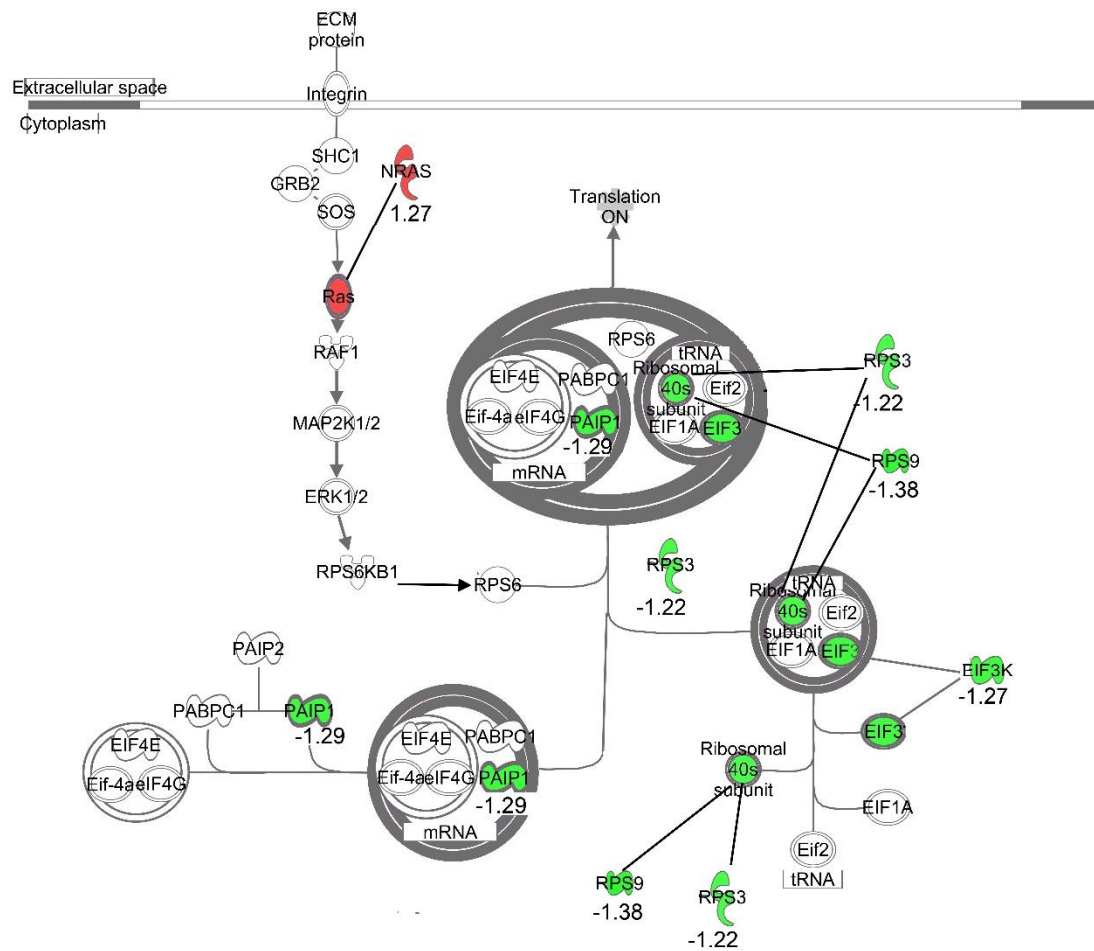
**Figure S3.** Bioinformatics analysis of the differentially expressed proteins (DEPs) with  $|FC| \geq 1.2$  identified in A549 cells exposed to 0.5  $\mu\text{M}$  of ZQX-1 under irradiation at 420 nm. Top 20 GO annotated (a) cellular component, (b) molecular functions and (c) biological process of the DEPs.



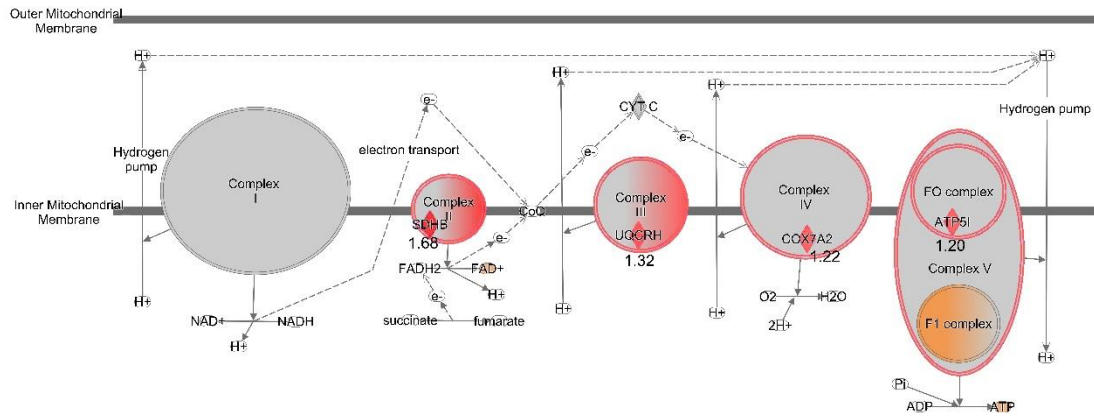
**Figure S4.** The KEGG pathway annotation of the differentially expressed proteins with  $|FC| \geq 1.2$  identified in A549 cells treated with 0.5  $\mu\text{M}$  of ZQX-1 under irradiation at 420 nm.



**Figure S5.** Schematic diagram generated by IPA of EIF2 signaling pathway with which the DEPs with  $|FC| \geq 1.2$ , identified in A549 cells exposed to 0.5  $\mu\text{M}$  of ZQX-1 under irradiation at 420 nm, are associated. The red color represents the protein (or complex) upregulated, green downregulated.

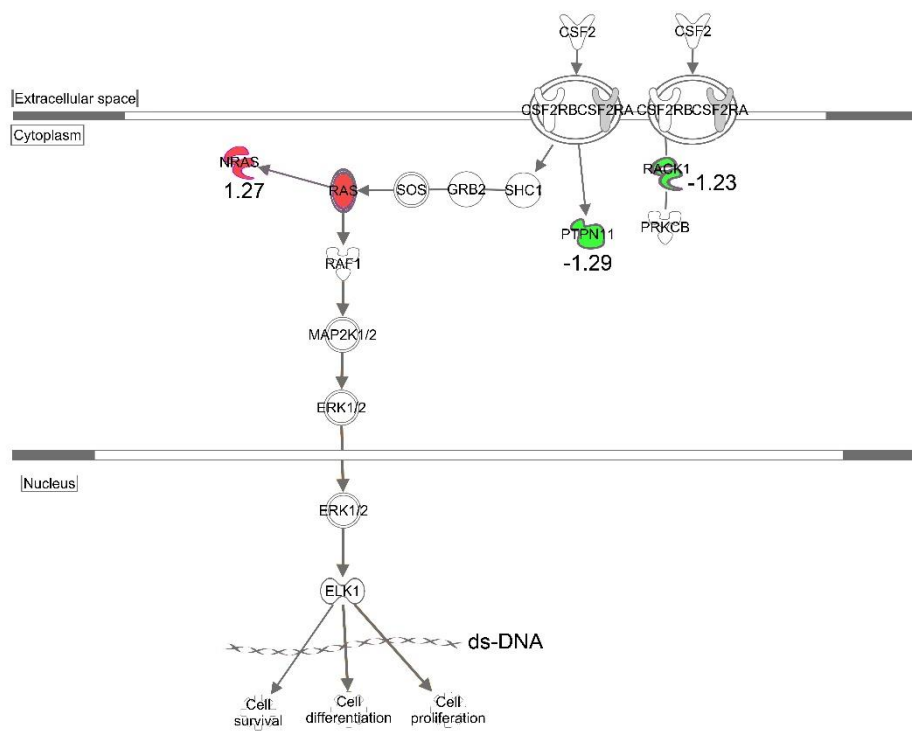


**Figure S6.** Schematic diagram generated by IPA of eIF4 and p70S6K signaling pathway with which the DEPs with  $|FC| \geq 1.2$ , identified in A549 cells exposed to 0.5  $\mu\text{M}$  of ZQX-1 under irradiation at 420 nm, are associated. The red color represents the protein (or complex) upregulated, green downregulated.

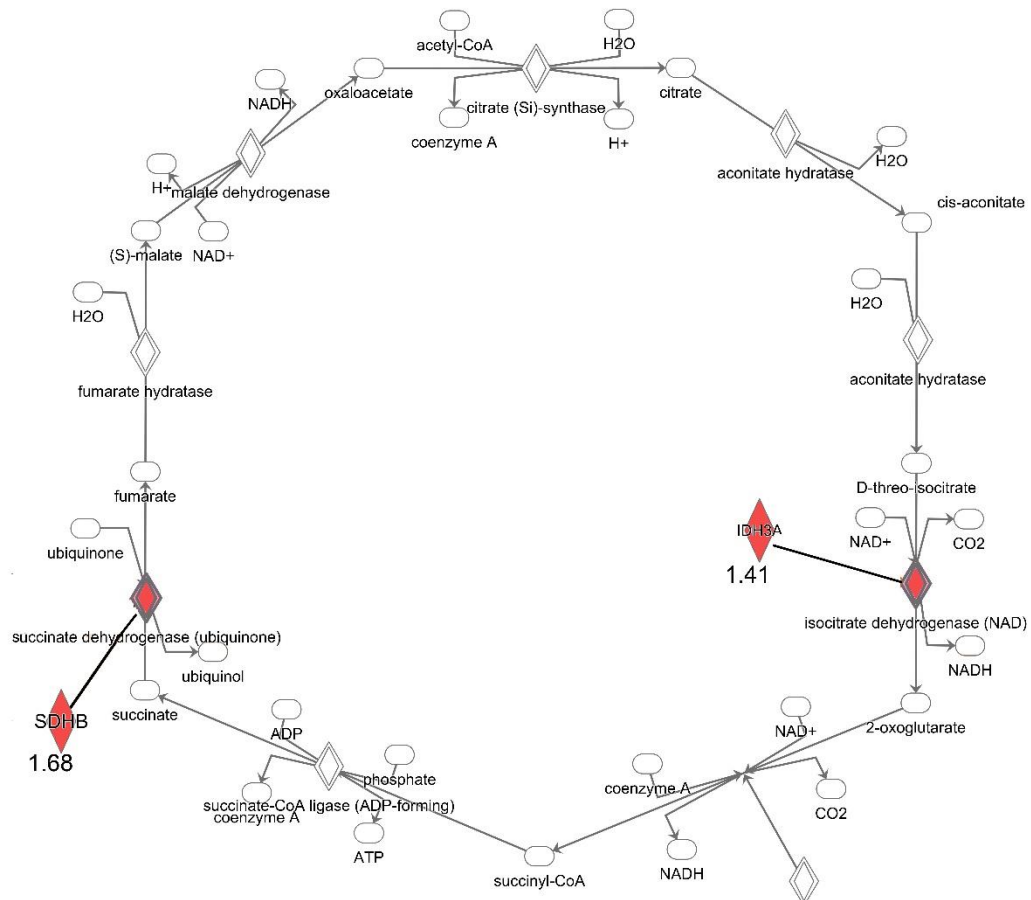


**Figure S7.** Schematic diagram generated by IPA of oxidative phosphorylation signaling pathway with which the DEPs with  $|FC| \geq 1.2$ , identified in A549 cells exposed to 0.5  $\mu\text{M}$  of ZQX-1 under irradiation at 420 nm, are associated. The red color represents the protein (or complex) upregulated, the orange represents the complex or compound predictively upregulated

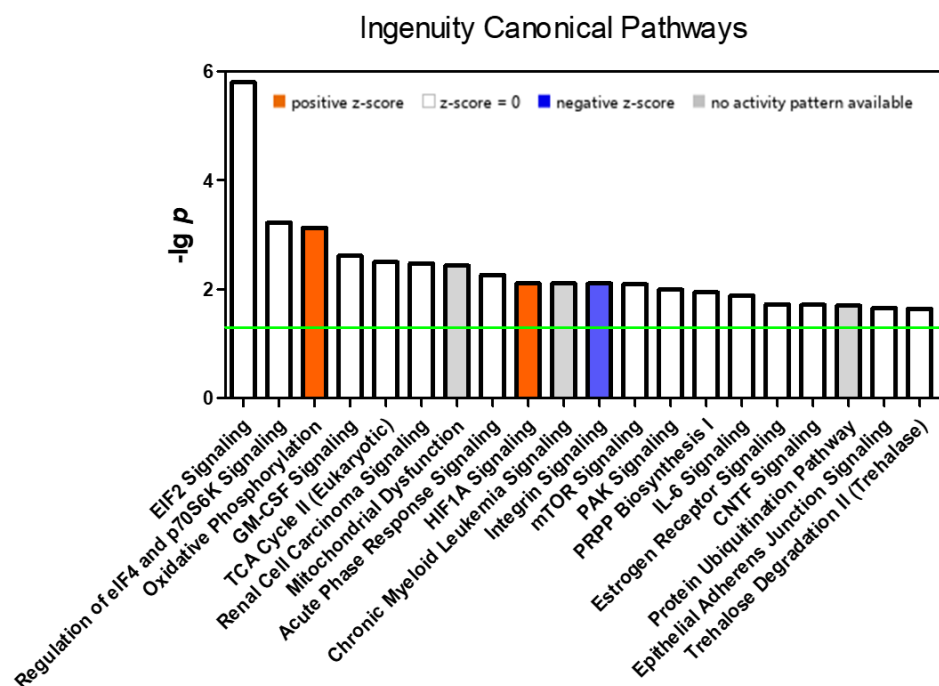




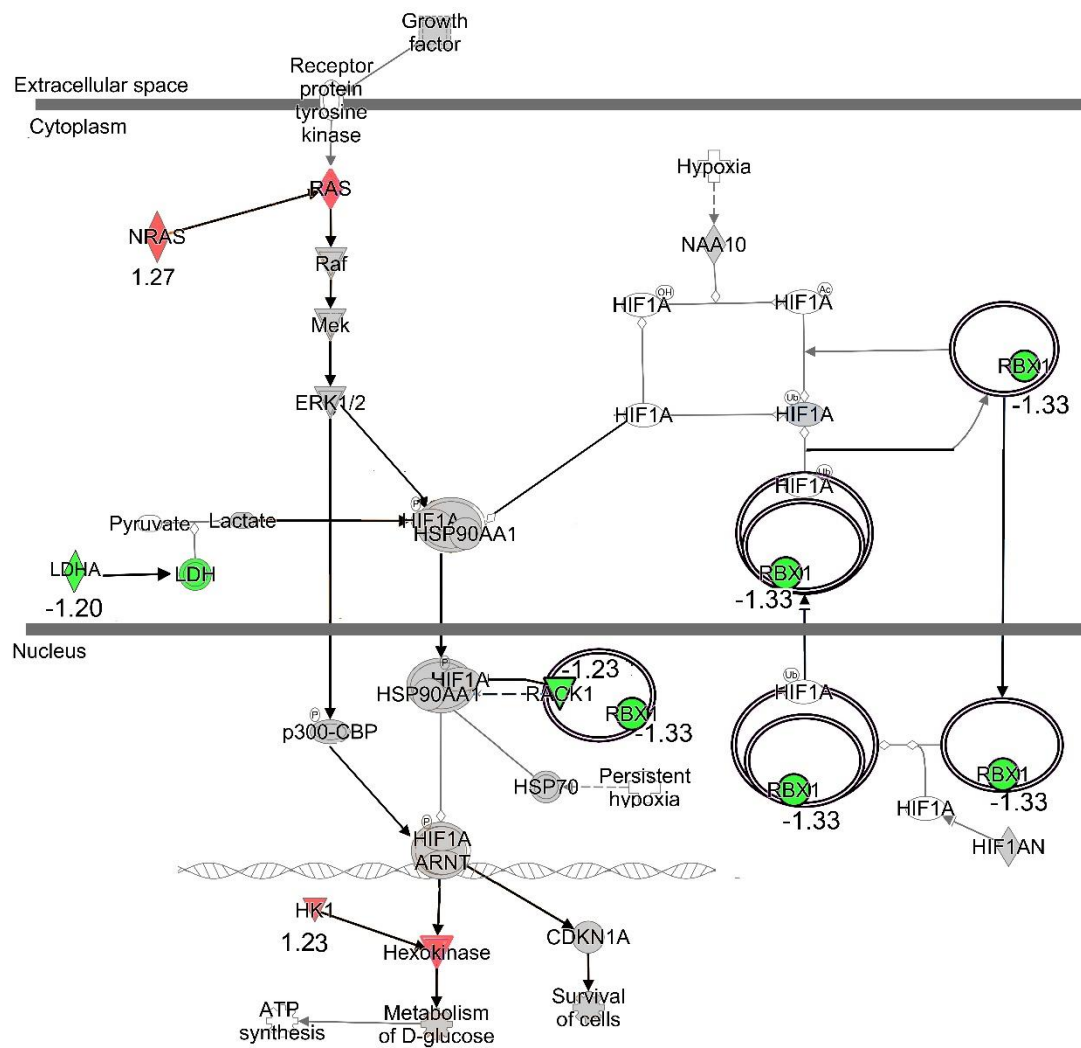
**Figure S8.** Schematic diagram generated by IPA of granulocyte-macrophage colony-stimulating factor (GM-CSF) signaling pathway with which the DEPs with  $|FC| \geq 1.2$  identified in A549 cells exposed to 0.5  $\mu$ M of ZQX-1 under irradiation at 420 nm. The red represents the protein (or complex) upregulated, green downregulated.



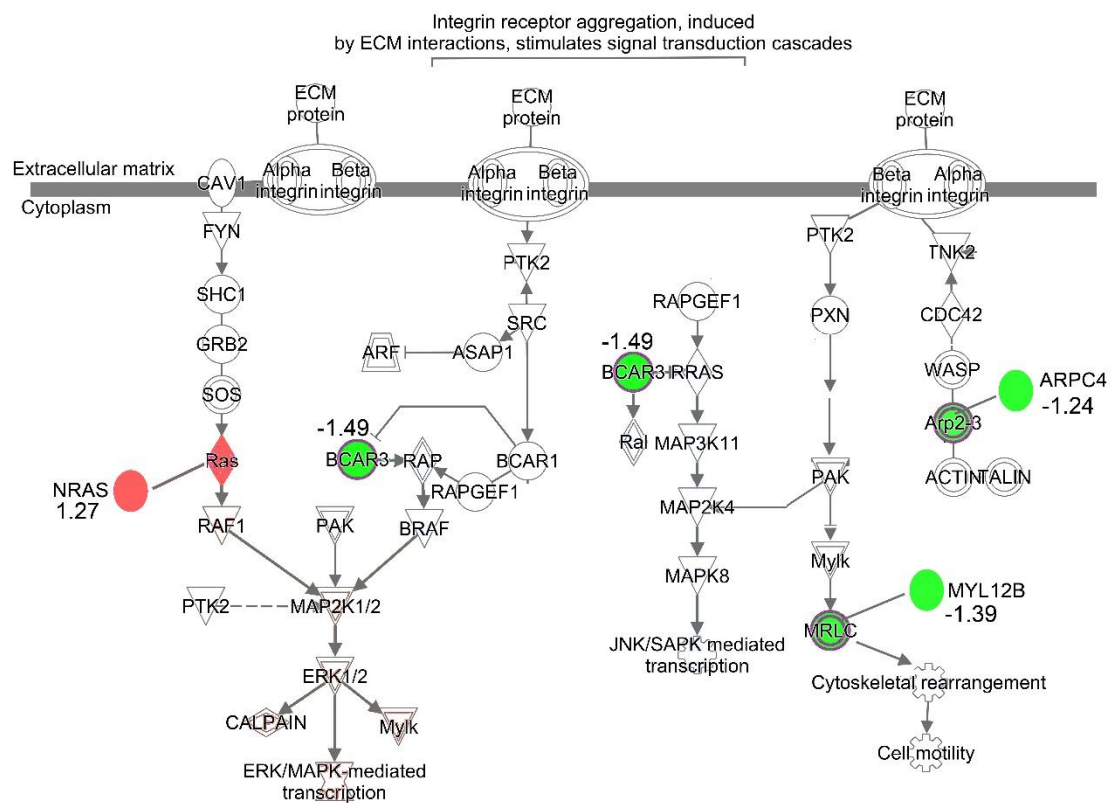
**Figure S9.** Schematic diagram generated by IPA of TCA cycle II signaling pathway with which the DEPs with  $|FC| \geq 1.2$ , identified in A549 cells exposed to 0.5  $\mu\text{M}$  of ZQX-1 under irradiation at 420 nm, are associated. The red color represents the protein (or complex) upregulated.



**Figure S10.** The Top 20 canonical pathways with which the DEPs with  $|FC| \geq 1.2$ , identified in A549 cells exposed to 0.5  $\mu\text{M}$  of ZQX-1 under irradiation at 420 nm, are associated. Green line indicates  $p \leq 0.05$ ; Orange represents activation of the pathway, blue inhibition of the pathway.



**Figure S11.** Schematic diagram generated by IPA of HIF1 $\alpha$  signaling pathway with which the DEPs with  $|FC| \geq 1.2$ , identified in A549 cells exposed to 0.5  $\mu$ M of ZQX-1 under irradiation at 420 nm, are associated. The red color represents the protein (or complex) upregulated, green downregulated.



**Figure S12.** Schematic diagram generated by IPA of integrin signaling with which the DEPs with  $|FC| \geq 1.2$ , identified in A549 cells exposed to 0.5  $\mu$ M of ZQX-1 under irradiation at 420 nm, are associated. The red color represents the protein (or complex) upregulated, green downregulated.

**Table S1.** MS/MS raw data for protein identification and quantification in A549 cells.

[illegible]



[illegible]



FALSE	High	Master Prc	P17480-1	Nuclear l	0.002	3.606	1	1	1	1	764	89.4	5.81	1.8	1	metabolic nucleus	DNA bindi	PI00505, F 7343	ENSG0000 UBTf	17		Ectoderm i RNA Polyr	12		High	High	High	High	High	High	1			
FALSE	High	Master Prc	Q17480-1	Cysteine/l	0.004	2.76	1	1	1	1	501	55.4	9.19	0	1	cell differe	cell surface protein bir	PD0324, F 73657	ENSG0000 SLCTA11	5		NR2F path	Basigin int	9		High	High	High	High	High	High	1		
FALSE	Low	Master Prc	P42702-1	Leukemia i	0.051	1.886	1	1	1	1	1097	123.7	5.72	1.72	1	regulation extracellul	protein bir	PI00041, 3977	ENSG0000 LIFR	5	Jak-STAT si	Physiologi	IL-6-type c	17		High	High	High	High	High	High	1		
FALSE	High	Master Prc	Q15103	rho guanin	0.002	3.526	1	1	1	1	1369	151.5	5.68	2.84	1	cell organi cytosol	protein bir	PI00621, 9639	ENSG0000 ARHGFE10	8; CHR_ HS	G alpha i1:	11		High	High	High	High	High	High	1				
FALSE	Low	Master Prc	P42763-1	Unconvent	0.05	1.196	2	1	1	1	135	59.8	5.05	0	1	metabolic cytoplasm;	enzyme re	PI02996, F 8725	ENSG0000 UR1I	19				0		High	High	High	High	High	High	1		
FALSE	High	Master Prc	Q96020	PRKC appo	0	7.939	4	1	1	1	340	36.5	5.41	3.04	1	cell death; cytoplasm;	protein bir	PI01544, F 5074	ENSG0000 PAWR	12				0		High	High	High	High	High	High	1		
FALSE	High	Master Prc	QGZM8	Nuclear dr	0.006	2.393	11	2	3	2	345	38.4	5.24	0	2	cell differe chromosom	catalytic a-	PI04880, F 81565	ENSG0000 NDEL1	17		Amplificati		16		High	High	High	High	High	High	1		
FALSE	Medium	Master Prc	Q96E15	Transcripti	0.026	1.474	4	1	1	1	215	24.6	5.2	0	1	metabolic nucleus	protein bir	PD4538, 79921	ENSG0000 TCCLA4	X				0		High	High	High	High	High	High	1		
FALSE	High	Master Prc	QB8Y6	Exocyt co	0.003	3.468	2	2	2	2	725	81.7	5.49	0	2	cell organi cytoplasm;	protein bir	PI00169, F 149371	ENSG0000 EXOC8	1	RALA down	Translocat	11		High	High	High	High	High	High	High	High	1	
FALSE	Medium	Master Prc	Q13287	N-myc-inte	0.031	1.421	3	1	1	1	307	35	5.34	0	1	defense res cytoplasm;	protein bir	PI07292, F 9111	ENSG0000 NM1	2	IL-2 Signali		0		High	High	High	High	High	High	High	High	1	
FALSE	Medium	Master Prc	Q95073-1	Fibrinogen	0.015	1.736	5	1	1	1	299	34.7	7.12	0	1	metabolic nucleus	catalytic a-	PI13873, 100861411	ENSG0000 FSBP; RAD	8				0		High	High	High	High	High	High	1		
FALSE	High	Master Prc	QB8T6M	E3 ubiquiti	0.005	2.563	3	2	2	2	617	67.6	6.95	1.74	2	metabolic endoplasm;	catalytic a-	PI00097, F 84447	ENSG0000 SYVN1	11	Protein prc	Hlt mutant	18		High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc	Q01658	Protein Dr	0	6.244	9	2	2	3	176	19.4	4.75	6.17	2	cell organi nucleus	DNA bindi	PI00808, 1810	ENSG0000 DR1	1	HAT3 acty	3			High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc	P07305	Histone H1	0.009	2.105	7	1	1	1	194	20.9	10.84	2.65	1	cell organi chromosom	DNA bindi	PI00538, 3005	ENSG0000 H1F0	22	Formation	10			High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc	QP64E1	Protein CA	0	6.686	6	2	2	2	433	48.8	5.82	2.74	2	Golgi;mern		PI04156, 113201	CASC4	15				0		High	High	High	High	High	High	High	High	1
FALSE	High	Master Prc	Q96K21	Abscission,	0	6.312	7	3	3	2	471	51.5	5.73	1.85	3	cell divisio cytoplasm;	metal ion	PI01363, 84936	ENSG0000 ZFYVE19	15				0		High	High	High	High	High	High	High	High	1
FALSE	High	Master Prc	P33121																															

FALSE	High	Master Prc	Q195394	phosphoc	0	7.904	8	4	4	4	542	59.8	6.25	1.82	4	metabolic	cytosol	catalytic	at	P100408, F	5238	ENSG00000	PGM3	6	Amino sug	Glucuronid	Synthesis c	9	High	High	High	High	High	High	1
FALSE	High	Master Prc	P32970	CD70 anti	0.003	2.84	6	1	1	1	193	21.1	8.53	1.72	1	cell comm	membrane	protein bir	PI00229	970	ENSG00000	CD70	19		Cytokine-c	TNFs bind	5	High	High	High	High	High	High	1	
FALSE	High	Master Prc	QBWY22	BR13-bind	0	5.726	10	2	2	2	251	27.8	9.44	1.7	2	membrane			P114965	140707	ENSG00000	BR13BP	12					High	High	High	High	High	High	1	
FALSE	High	Master Prc	QK4MQC2	Anoctamin	0.002	3.922	3	2	2	2	910	106.1	7.77	2.53	2	cell organ	cell surface	protein bir	PI04547	196527	ENSG00000	ANO6	12			Neurothril	6	High	High	High	High	High	High	1	
FALSE	High	Master Prc	QBQ800	ras-related	0.002	3.717	3	1	1	1	399	44.2	5.1	2.55	1	cell comm	cytoplasm;	catalytic	at	PI00025, F	64121	ENSG00000	RAGC	1	mTOR sign	Target Of f	Energy deg	17	High	High	High	High	High	High	1
FALSE	High	Master Prc	PL1978-2	Isomform 2	0	242.785	65	28	139	1	464	51.3	363.05		28	metabolic	cytoplasm;	DNA bindi	PI00013, F	31190	ENSG00000	HNRNPNC	9		mRNA Pro		12	High	High	High	High	High	High	1	
FALSE	Medium	Master Prc	P118850	Cyclic AMP	0.018	1.661	2	1	1	1	670	74.5	8.22		1	metabolic	cytosol;eni	DNA bindi	PI00170, F	22926	ENSG00000	ATF6	6	Protein prc	Sterol Res	ATF4 activ	1	High	High	High	High	High	High	1	
FALSE	High	Master Prc	Q15239	NADH deht	0.001	4.469	19	1	1	1	70	8.1	8.84	3.73	1	cell organ	cytosol;me	catalytic	at	4694	ENSG00000	NDUFA1	X	Metabolic	Electron Tr	Complex i	12	High	High	High	High	High	High	1	
FALSE	Medium	Master Prc	QBW181	Inositol 1,4	0.032	1.397	1	1	1	1	547	6.2	5.88	0	1	membrane			PI03281	85450	ENSG00000	ITPR1P	10					High	High	High	High	High	High	1	
FALSE	High	Master Prc	QBK64X	HEAT repe	0.008	2.199	1	1	1	1	2040	221.9	6.58	2.52	1					25938	ENSG00000	HEATRS1A	14					High	High	High	High	High	High	1	
FALSE	High	Master Prc	P48029-1	Sodium-ai	0	4.836	2	1	1	1	635	70.5	6.42	1.97	1	metabolic	membrane	transporte	PI00209	6535	ENSG00000	SLC6A8	X			NR1F2 path	Creatine m	5	High	High	High	High	High	High	1
FALSE	Medium	Master Prc	P101008	Antithrom	0.036	1.344	2	1	1	1	464	52.6	6.71	0	1	coagulation	extracellul	enzyme re	PI00079	462	ENSG00000	SERPINC1	1	Compleme	Compleme	Post-trans	10	High	High	High	High	High	High	1	
FALSE	High	Master Prc	Q14965	Aurora kin	0	6.171	5	1	1	1	403	45.8	9.39	3.49	1	cell divisio	cytoplasm;	catalytic	at	PI00069, F	6790	ENSG00000	AURKA	20	Oocyte me	Gastric Car	FBX17 down	27	High	High	High	High	High	High	1
FALSE	High	Master Prc	Q75717	WD repeat	0	12.296	5	4	5	4	1129	125.9	5.62	4.31	4	cytoplasm;	DNA bindi	PI00400, F	11169	ENSG00000	WDHD1	14		Mesoderm		1	High	High	High	High	High	High	1		
FALSE	High	Master Prc	Q13308-1	Inactive ty	0	11.169	4	2	2	2	1070	118.7	7.09	8.8	2	cell differe	membrane	catalytic	at	PI00047, F	5754	ENSG00000	PTK7	6					High	High	High	High	High	High	1
FALSE	High	Master Prc	QBWU90	Zinc finger	0	9.691	9	4	4	4	426	48.6	5.31	1.68	4	regulation	cytoplasm;	metal ion	PI00642	55854															

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FALSE	Medium	Master Prc QSNY71-1	elongation	0.024	1.503	3	1	1	1	299	35.3	9.42	1.87	1	metabolic	endoplasmic reticulum	catalytic	at	P01151	60481	ENSG000001	ELOVL5	6	Fatty acid	Synthesis	c	11	High	High	High	High	High	High	High	1
FALSE	High	Master Prc Q92922	SWI/SNF co	0	19.999	5	6	9	3	1105	122.8	5.76	11.12	6	cell organi	chromosome	DNA bindi	ng	P04433	6599	ENSG000001	SMARCC1	3		RUNX1	int	8	High	High	High	High	High	High	High	1
FALSE	High	Master Prc Q96C9	GRIP and c	0.001	4.264	1	1	1	1	775	87.8	5.45	0	1	metabolic	cytoplasm	protein bin		P01465	F 79571	ENSG000001	GC1	7		Retrigade	a	8	High	High	High	High	High	High	High	1
FALSE	High	Master Prc Q9NV23	Adaptin ec	0.003	3.133	4	1	1	1	263	28.3	8.38	2.21	1	transport	membrane			P07933	55707	ENSG000001	NECAP2	1		Cargo reco	d	4	High	High	High	High	High	High	High	1
FALSE	High	Master Prc P52732	Kinesin-III	0.002	9.852	3	3	3	3	1056	119.1	5.64	6.08	3	cell division	cytoplasm	catalytic	at	P00225	F 3832	ENSG000001	KIF11	10		COPII-depe	e	11	High	High	High	High	High	High	High	1
FALSE	Medium	Master Prc Q9UKU7	Isobutyryl-	0.016	1.714	2	1	1	1	415	45	7.85	1.79	1	metabolic	mitochondr	catalytic	at	P00441	F 27034	ENSG000001	ACAD8	11	Metabolic	Branched-c	5	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prc Q95989	Diphospho	0	5.148	5	1	1	1	172	19.5	3.64	0	1	cell commu	cytoplasm	catalytic	at	P00293	11165	ENSG000001	NUDT3	6		Synthesis c	3	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prc Q13033	Striatin-3	0	6.181	2	1	1	1	797	87.2	5.36	2.55	1	regulation	cytoplasm	protein bin		P00400	F 29966	ENSG000001	STRN3	14			0	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prc Q9P2W9	Syntaxin-1	0.003	2.976	6	1	1	1	335	38.7	4.29	2.3	1	cell organi	endoplasmic	protein bin		P10496	53407	ENSG000001	STX18	4	Phagosome	COPII-depe	7	High	High	High	High	High	High	High	High	1
FALSE	Medium	Master Prc Q2RRP1-1	neuroblast	0.026	1.468	0	1	1	1	2371	268.4	5.96	0	1	metabolic	cytoplasm	protein bin		P08314	F 51594	ENSG000001	NBAS	2		COPII-depe	5	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prc Q8WXG6	MAP kinase	0.003	3.11	1	1	1	1	1647	183.2	4.60	2.03	1	cell death	cytoplasm	enzyme re		P02141	F 8567	ENSG000001	MADD	11		Deregulat	2	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prc Q8NHG8	E3 ubiquiti	0.003	2.86	14	1	1	1	242	24.1	7.09	2.39	1	metabolic	cytoplasm	catalytic	at	P00097	F 223082	ENSG000001	ZNF82	7		Antigen pr	2	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prc Q5VZK9	F-actin-uni	0.006	2.519	1	2	2	2	1371	151.5	7.85	1.75	2	cell organi	cytoplasm	protein bin		P08542	55604	ENSG000001	LRC16A	16		Factors inv	4	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prc Q9NZJ6	Ubiquitin	0.004	2.7	5	1	1	1	369	41	7.42	0	1	metabolic	membrane	catalytic	at	P01209	F 51805	ENSG000001	CO3	6	Metabolic	Ubiquinol	6	High	High	High	High	High	High	High	High	1
FALSE	Medium	Master Prc P17540	Creatine kin	0.037	1.324	3	1	1	1	419	47.5	8.19	0	1	metabolic	membrane	catalytic	at	P00217	F 1160	ENSG000001	CKMT2	5	Metabolic	Creatine m	6	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prc Q43324-1	Eukaryotic	0.001	4.452</																														

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[illegible]

FALSE	High	Master PrC Q85R1	Polypeptid	0.009	2.114	1	1	1	1	603	68.9	8.59	2.49	1	metabolic	Golgi;mem	catalytic	ai	P00035, F	55568	ENSG0000	GALT10	5	Metabolic	O-linked gl	6	High	High	High	High	High	High	High	1	
FALSE	High	Master PrC Q9275	UBX doma	0	9.071	9	3	4	3	508	56.7	6.38	3.76	3	metabolic	cytosol;eni	protein bi	ai	P00789	23190	ENSG0000	UBXNA	2			0	High	High	High	High	High	High	High	1	
FALSE	High	Master PrC Q9P282	prostaglan	0.003	3.165	1	1	1	1	879	98.5	6.61	1.72	1	cell organi	cell surface	protein bi	ai	P007679	5738	ENSG0000	PTGFRN	1			0	High	High	High	High	High	High	High	1	
FALSE	High	Master PrC Q9UDT6-1	CAP-Gly d	0	7.613	4	4	4	4	1046	115.8	6.73	6.33	4	metabolic	cytoplasm;	catalytic	ai	P01302, F	7461	ENSG0000	CLIP2	7			0	High	High	High	High	High	High	High	1	
FALSE	High	Master PrC Q9UNU4	Transmem	0	7.933	8	2	2	2	274	31.1	6.99	4.38	2	cell organi	endosome	protein bi	ai	P007092	54664	ENSG0000	TMEM106	7			0	High	High	High	High	High	High	High	1	
FALSE	Medium	Master PrC Q9NW34	Nucleosul	0.048	1.217	2	1	1	1	567	64.5	9.74	0	1	developme	nucleus			P014780	25871	ENSG0000	Clorf17; N	3			0	High	High	High	High	High	High	High	1	
FALSE	High	Master PrC Q9EY1-1	DnaI hom	0.002	3.548	3	1	2	1	480	52.5	9.26	2.31	1	cell death;	cytoplasm;	enzyme re		P00226, F	9093	ENSG0000	DNAJ3	16; CHR_H	Viral carci	1	1	High	High	High	High	High	High	High	1	
FALSE	Medium	Master PrC P36402	Transcript	0.048	1.218	2	1	1	1	384	41.6	6.81	1.88	1	cell differe	nucleus	DNA bindi		P000505, F	6932	ENSG0000	TCF7	5	Wnt signal	Arrhythmic	RUNX3 reg	33	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q8N9E0	Protein FA	0.009	2.122	3	1	1	1	248	28.9	10.1	1.76	1			protein bi		286499		ENSG0000	FAM133A	X			0	High	High	High	High	High	High	High	1	
FALSE	High	Master PrC Q1ED39	Lysine-rich	0.002	3.943	4	1	1	1	458	51.6	9.86	3.19	1		nucleus	RNA bindi		P015477	400506	ENSG0000	C16orf88;	16			0	High	High	High	High	High	High	High	1	
FALSE	High	Master PrC Q9J324	rRNA-proc	0	5.471	6	1	2	1	198	23.4	9.7	2.48	1	metabolic	nucleus	RNA bindi		P004900	51077	ENSG0000	FCF1	14	Ribosome		Major patt	6	High	High	High	High	High	High	High	1
FALSE	Low	Master PrC P98196	Probable p	0.075	1.015	1	1	1	1	1134	129.7	6.6	0	1	cell organi	endoplasm	catalytic	ai	P00122, F	23250	ENSG0000	ATP11A	13		Lung fibro	Neutrophil	7	High	High	High	Not Found	High	High	1	
FALSE	High	Master PrC Q9B208	Protein N8	0	6.206	3	2	2	2	928	103.1	4.78	3.66	2	regulation	cytoplasm;	protein bi		116496		ENSG0000	FAM129A	1			0	High	High	High	High	High	High	High	1	
FALSE	High	Master PrC P82664	28S riboso	0.003	2.908	6	1	1	1	201	23	8	0	1	cell organi	membrane			P00338	55173	ENSG0000	MRPS10	6	Ribosome		Mitochondr	7	High	High	High	High	High	High	High	1
FALSE	Medium	Master PrC Q8BW13-1	Isomorf 6	0.018	1.662	1	1	1	1	1551	170.3	6.61	0	1	defense re	cytoplasm;	DNA bindi		P005729, F	84166	ENSG0000	NLRCS	16			0	High	High	High	High	High	High	High	1 [R1533]	
FALSE	Medium	Master PrC Q08378	Golgin sub	0.028	1.449	1	1	1	1	1498	167.3	5.44	0	1	metabolic	cytoplasm;	catalytic	ai	P00038, F	2802	ENSG0000	GOLGA3	12												

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FALSE	Medium	Master Prc Q9NYB-1	TGF-beta-1	0.011	2	2	1	1	1	693	76.4	8.54	0	1	metabolic	cytoplasm; metal ion	P100641, F 23118	ENSG000001TAB2	6	Epstein-Ba	Regulation	IRAK2 med	67	High	High	High	High	High	High	High	1			
FALSE	High	Master Prc P40188-1	Interleukin	0.002	4.115	1	1	1	1	918	103.5	5.95	1.93	1	metabolic	extracellular	protein	P100041, F 3572	ENSG000001LUST	5	Signaling p	Physiologic	IL-6-type c	26	High	High	High	High	High	High	High	1		
FALSE	Low	Master Prc Q8TCT1	Phosphoet	0.063	1.094	3	1	1	1	267	29.7	7.71	0	1	metabolic	cytosol	catalytic a	P100702, F 162466	ENSG000001PHOSPHO1	17	Glyceroph	Synthesis c		8	High	High	High	High	High	High	High	1 [Q233]		
FALSE	High	Master Prc Q96NU1	Sterile alga	0	5.207	2	1	2	1	681	72.7	7.59	5.01	1	nucleus	protein	P107647	148398	ENSG000001SAMD11	1				0	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc P62487	DNA-direct	0.002	3.528	5	1	2	1	172	19.3	5.54	1.88	1	cell death	nucleus	catalytic a	P100575, F 5436	ENSG000001POLR23	11	Pyrimidine	Eukaryotic	Signaling b	75	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc Q15643	Thyroid rec	0	6.469	1	1	1	1	1979	227.4	5.26	3.51	1	cell differe	cytoplasm; protein	P104111, F 9321	ENSG000001TRIP11	14			Intra-Golgi	7	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9UNK0	Syntaxin-8	0	0.016	6	1	1	1	236	26.9	4.98	2.9	1	cell organi	cytosol;en	protein	P105739	9482	ENSG000001STX8	17	SNARE int			1	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc Q9UL15-1	BAG family	0.002	3.927	3	1	1	1	447	51.2	6.05	4.48	1	cell death	cytosol;en	enzyme re	P102179	9529	ENSG000001BAG5	14			Regulation	4	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prc P49427	ubiquitin c	0.003	3.061	5	1	1	1	236	26.7	4.54	0	1	cell division	cytoplasm; catalytic a	P100179, F 997	ENSG000001CD-C34	19	Ubiquitin r		Synthesis c	17	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc Q9NPAD	ER membr	0	6.56	10	1	1	1	242	26.5	9.25	3.25	1	membrane		P109430	56851	ENSG000001EMC7	15				0	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc P13121	CAMP-dep	0.002	3.5	5	2	2	1	381	43	5.71	2.34	2	coagulation	cytosol;en	enzyme re	P100027, F 5575	ENSG000001PKRARI8	7	Insulin sig	miRs in M	Signaling b	32	High	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prc Q8X01-1	SURP and	0	7.612	3	3	3	3	1082	120.1	7.28	1.64	3	metabolic	nucleus	RNA bindi	P101585, F 10147	ENSG000001SUGP2	19			mRNA Pro	1	High	High	High	High	High	High	High	High	1	
FALSE	Medium	Master Prc Q8Y39-1	NADH deh	0.012	1.958	8	1	1	1	141	14.8	8.72	0	1	cell organi	membrane	catalytic a		126328	ENSG000001NDUAF1	19	Alzheimer	Oxidative	Complex I	12	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prc Q8N8W7	Retinol der	0.003	2.87	9	2	2	2	331	35.9	8.1	1.88	2	metabolic	membrane	catalytic a	P100106, F 112724	ENSG000001RDH13	19; CHR_H			RA biosynt	4	High	High	High	High	High	High	High	High	1	
FALSE	Medium	Master Prc P98172	ephriin-B1	0.016	1.073	5	1	1	1	346	38	8.94	0	1	cell commu	cytoplasm; protein	P100812	1947	ENSG000001EPN13	3	Axon guid		EPH-ephri	7	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc Q9H40-3	traB doma	0	6.255	6	2	2	2	376	42.3	8	4.05	2			P101963	80305	ENSG000001TRABD	22														

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FALSE	High	Master Prc P2020-2	isoform 2	0	119.099	67	12	49	1	162	17.7	7.5	132.42	12	metabolic; cytosol; metal protein	PR18449	689	ENSG000001	BT3F	5							0	1.385	0.333650044	1.37	1029.1	854.3	29.68	13.88	High	High	High	High	High	High	High	High	1	[K2]
FALSE	High	Master Prc Q7609-1	Protein ITI	0	9.137	9	1	2	1	146	16.3	8.28	5.46	1	cell death; cytoplasm; protein	PR105439	10899	ENSG000001	ITB	2							0	1.384	0.109578199	24.3	282.7	204.6	17.98	0.27	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc P10606	Cytocrom	0	36.615	36	8	29	8	129	13.7	8.81	38.43	8	metabolic; cytoplasm; catalytic	PR101215	1329	ENSG000001	COSX8	1	Alzheimer	Electron Tr	TP53 Regu			17	1.382	0.495628222	4.9	10819.2	8120.4	24.08	8.74	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q5810-5	Transmem	0.006	2.484	7	1	1	1	291	32.5	9.58	0	1	membrane	PR09935	440026	ENSG000001	TMEM418	11						0	1.382	0.594948837	20.65	61.8	44.7	3.35	97.15	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9H33-1	39S riboso	0	10.491	12	3	4	1	250	29.4	10.37	8.36	3	cell organi; membrane structural	PR06984	57129	ENSG000001	MRPL47	1						6	1.38	0.007423246	6.36	1722.4	1196.6	6.65	12.17	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9Y97	Probable A	0.009	2.104	3	1	1	1	483	54.2	9.06	1.69	1	cell organi; cytoplasm; catalytic	PR00270	54555	ENSG000001	DDK49	19						5	1.378	0.130363327	28.76	346.7	203.1	26.94	18.9	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q98X5-1	AP-1 compo	0	11.059	10	3	3	3	423	48.6	7.3	9.9	3	cell organi; cytosol; Gol	PR00028	8907	ENSG000001	AP1M1	19						19	1.377	0.133160052	20.73	1018	761	10.06	14.75	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9Y508-1	general tra	0	11.096	8	3	4	3	519	59.5	6.9	2.55	3	cell differe; nucleus	PR09734	9328	ENSG000001	GTF3C5	9						6	1.374	0.152867601	16.12	1021.3	743.1	16.98	18.13	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q00622	Protein Cy	0	8.624	9	3	4	3	381	42	8.21	9.46	3	cell comm; extracellular	PR00077	3491	ENSG000001	CYR61	1						6	1.374	0.33045209	38.99	1636.9	1201.3	16.08	22.26	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q60287	nucleolar r	0	5.731	1	1	1	1	2271	254.2	6.47	2.28	1	nucleus	PR11707	9875	ENSG000001	URB1	21						0	1.372	0.22880731	4.51	291.4	294.3	33.26	25.05	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q92620	Ple-mRNA	0	6.689	2	2	2	2	1227	140.4	6.54	3.67	2	metabolic; cytoplasm; catalytic	PR00270	9785	ENSG000001	DHX38	16	Spliceosom	mRNA Pro	Cleavage o			13	1.362	0.384859129	58.38	346.8	257.1	40.16	10.42	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q00566	U3 small n	0	16.48	7	5	5	5	681	78.8	4.86	7.72	5	metabolic; chromoso	PR04006	10199	ENSG000001	MPHOSPH	2						6	1.362	0.454227873	4.62	733.8	539.5	16.88	12.41	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9BUWA8	Taukushin	0	5.182	4	1	1	1	353	37.8	6.87	4.27	1	cell organi; extracellular	PR12799	25987	ENSG000001	TSKU	11						1	1.361	0.189551725	10.98	151	120.3	11.62	12.04	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9BW86-1	N-terminal	0	12.604	17	3	3	3	223	25.4	5.52	7.07	3	cell organi; cytoplasm; catalytic	PR00891	28989	ENSG000001	NTMT1	9						0	1.359	0.081026857	23.1	293.4	214.8	2.49	22.11	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9BWK5	dnaI homo	0	7.82	15	2	2	2	260	29.9	5.73	4.89	2	regulation; cytoplasm; protein	PR00226	23234	ENSG000001	DNAJC9	10						0	1.359	0.411702812	60.61	219.6	167.3	63.62	18.46	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q96AY3	Peptidyl-pi	0	51.991	25	14	27	14	582	64.2	5.62	27.03	14	cell organi; cytoplasm; catalytic	PR00254	60681	ENSG000001	KBP10	17						0	1.354	0.022031765	7.24	7682.7	5347.5	5.65	6.43	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9Y639-1	isoform 1	0	6.815	5	1	1	1	282	31.3	6.87	3.65	1	cellular ho; cell surface	PR00047	27020	ENSG000001	NPTN	10						0	1.347	0.155524325	14.52	190.6	147.7	8.31	14.07	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q6NUK1	Calcium-bi	0	25.626	13	7	13	7	477	53.3	6.33	9.94	7	regulation; membrane	PR00036	29957	ENSG000001	SLC25A24	1	CHR_HS					1	1.347	0.246982633	32.93	2884	2563.5	24.58	13.31	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q75208-1	Ubiquitin	0	11.052	17	3	3	3	318	35.5	5.94	5.79	3	metabolic; membrane	PR08511	57017	ENSG000001	CQO9	9						4	1.343	0.302592448	43.05	111.3	82.9	27	16.3	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9NPF2-2	Neurin (C	0	10.475	14	4	5	4	291	32.4	9.1	7.5	4	cell differe; extracellular	PR05413	51335	ENSG000001	NGRN	15						0	1.34	0.16857734	30.53	577.9	443.2	15.6	15.16	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q8T872-1	pumilio ho	0	17.221	3	3	6	1	1066	114.1	7.08	15.32	3	cell organi; cytoplasm; protein	PR00806	23369	ENSG000001	PUM2	2						3	1.339	0.479344956	74.1	250.3	194.8	62.64	18.94	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc P06733-2	Syntenin-1	0	8.448	10	2	3	2	298	32.4	7.53	11.8	2	cell comm; cytoplasm; protein	PR05095	61386	ENSG000001	SDCBP	8						10	1.337	0.07186507	15.94	1841.7	1377.1	8.76	6.96	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q6ZNB6-1	nf-x1-type	0	9.317	4	3	3	3	911	101.3	8.41	5.93	3	metabolic; membrane	PR00086	152518	ENSG000001	NFXL1	4						0	1.336	0.416898312	61.1	750.3	561.6	61.92	14.67	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc P06733-2	isoform M	0	415.27	82	26	277	1	341	36.9	6.28	683.61	26	metabolic; cell surface	PR00113	2023	ENSG000001	ENO1	1						1	1.334	0.539956584	115.67	1292.8	969	127.84	87.97	High	High	High	High	High	High	High	High	1	[5277]100	
FALSE	High	Master Prc Q43768	alpha-end	0	18.07	42	5	10	4	121	13.4	7.24	15.24	5	cell divisio; cytoplasm	PR04667	2029	ENSG000001	ENSA	1						5	1.333	0.300820861	13.4	348.7	268.7	9.58	16.46	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc P10696	Alkaline ph	0	19.87	55	25	69	8	532	57.3	6.34	169.87	25	metabolic; extracellular	PR00245	251	ENSG000001	ALPLP2	2	Metabolic					6	1.333	0.694842324	67.13	4995.7	3749.1	33.39	26.54	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9XN40	OCA domain	0	24.164	18	5	8	5	245	27.6	47.9	12.55	5	regulation; endosome	PR07051	54940	ENSG000001	OCA1D	1						0	1.33	0.041034524	12.11	769	585.5	10.07	14.49	High	High	High	High	High	High	High	High	1		
FALSE	Medium	Master Prc Q9NR81-1	isoform 2	0.047	1.227	2	1	1	1	558	63.7	6.92	20.8	1	regulation; cytosol	PR00621	50650	ENSG000001	ARHGFE3	3						0	1.33	0.440653387	18.27	108.5	97.6	23.87	16.2	High	High	High	High	High	High	High	High	1	[Q27]	
FALSE	High	Master Prc P63316	Tropomycin	0	6.614	9	1	1	1	161	18.4	4.18	4.47	1	cellular co; cytosol	PR00336	7134	ENSG000001	TNNC1	3	Cardiac m;	MFAPS-me	Striated M			9	1.329	0.416774009	28.39	850.3	756	20.8	22.22	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9X188	Succinate c	0	8.012	19	3	3	3	166	19.6	6.88	3.84	3	cell organi; cytosol; protein	PR03937	54949	ENSG000001	SDHA2	11						0	1.325	0.871555006	8.6	185.2	140.9	19.62	25.02	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9BT25	HAUS augr	0	10.431	11	3	4	3	410	44.8	7.06	39.1	3	cell divisio; cytoplasm; protein	PR09323	55858	ENSG000001	HAUS5	19						16	1.322	0.282447448	5.24	69.9	67.8	18.43	15.19	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9HC07	Transmem	0	18.534	17	3	3	3	324	34.9	7.02	11.33	3	cellular ho; endosome	PR01169	11654	ENSG000001	TMEM165	4						0	1.321	0.409094362	53.78	1210.4	1114.2	69.51	18.4	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc P07919	Cytocrom	0	19.647	38	3	10	3	91	10.7	4.44	22.44	3	metabolic; membrane	PR02320	7388	ENSG000001	UCFH	1	Metabolic	Electron Tr	Respirator			12	1.319	0.005849896	2.4	3680.5	2918.5	9.32	9.97	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q15056-1	isoform Sh	0	39.096	61	11	22	11	228	25.2	8.09	25.86	11	cell organi; cytosol; catalytic	PR00766	7458	ENSG000001	IQI4H	1						1	1.317	0.074371568	2.32	2896.8	2199	3.43	15.61	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9NR80	Putative E	0	10.455	8	3	3	3	425	48	4.81	6.87	3	metabolic; cytoplasm; catalytic	PR02207	55148	ENSG000001	UBR7	1	CHR_H				0	1.317	0.398657535	54.96	369.4	280.4	56.45	13.01	High	High	High	High	High	High	High	High	1			
FALSE	Medium	Master Prc Q6ANN6	Nuclear p	0.029	1.434	2	1	1	1	443	51.2	10.49	0	1	extracellular	PR06409	440348	ENSG000001	NPPB15	1	16				0	1.316	0.061865382	15.41	287.7	201.2	13.6	6.32	High	High	High	High	High	High	High	High	1			
FALSE	High																																											

FALSE	High	Master Prq PQ9651-2	Isoform A1	0	268.742	86	31	111	1	320	34.2	9.23	302.05	31	cell comm	cytoplasm; DNA bindi	P00076, F 3178	ENSG000001HNRNP1	12		mRNA Pro		1	1.266	0.048347735	11.55	695.8	522	3.37	11.49	High	High	High	High	High	High	High	1	[R31];	
FALSE	High	Master Prq P14209	CD99 anti	0.002	4.112	5	1	2	1	185	18.8	4.75	4.97	1	regulation	cytoplasm; protein bi	P12301, 4267	ENSG000001C099	X1Y, X	Leukocyte	Immunore		7	1.266	0.315921247	34.75	1261.7	839.3	41.56	66.03	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q98PW8	Protein Nq	0	4.818	12	3	3	3	284	33.3	9.31	2.72	3	membrane	cytoplasm; protein bi	P07978, 8508	ENSG000001NBPNA1	22				0	1.265	0.304905301	5.59	841.7	665.5	3.87	22.07	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q98526	Endoplasm	0	19.362	19	7	7	7	406	46.9	5.26	17.85	7	cellular ho	cell surface catalytic ac	P00085, 23071	ENSG000001ERP44	9		Neutrophil		3	1.264	0.006168475	1.38	2532.1	1918	3.51	3.55	High	High	High	High	High	High	1			
FALSE	High	Master Prq P05026	Sodium/pc	0	57.002	25	6	16	6	303	35	8.53	46.8	6	cell comm	membrane catalytic ac	P000287, 481	ENSG000001PTB181	1		Thyroid ho	Calcium Re ion homeo	27	1.264	0.111493368	16.5	6137.3	4597.7	9.98	10.42	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q45782	E3 ubiquit	0	19.1	7	7	8	5	975	113.6	5.94	8.48	7	cell organ	nucleus catalytic ac	P00097, 56254	ENSG000001NFN30			ATM Signa	E3 ubiquit	5	1.264	0.506938701	67.53	459.6	376.4	52.36	13.01	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q14657	EKC/CEPP	0	5.447	16	1	2	1	143	14.8	8.63	0	1	metabolic	nucleus protein bi	P09341, 8710	ENSG000001LAGE3	X		tRNA modi		3	1.263	0.168312547	25.34	32.8	23.4	26.03	18.61	High	High	High	High	High	High	1			
FALSE	High	Master Prq P61254	60S riboso	0	33.623	46	10	19	2	145	17.2	10.55	44.09	10	cell organ	cytoplasm; protein bi	P00467, 6154	ENSG000001KPL16	17		Ribosome	Cytoplasm	34	1.263	0.285917517	9.39	2645.9	2349.9	14.48	9.08	High	High	High	High	High	High	1			
FALSE	High	Master Prq P13051	uracil-DNA	0	13.07	8	1	4	1	313	34.6	9.32	14.96	1	metabolic	mitochond catalytic ac	P03167, 7374	ENSG000001UNG	12		Base excisi	Recogntio	10	1.263	0.489503091	59.73	64.6	51.2	38.88	16.61	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q9NS69	Mitochond	0	8.706	25	2	3	2	142	15.5	4.34	7.77	2	cell comm	membrane protein bi	56993	ENSG000001TOMM22	22		Mitochond		4	1.263	0.703708066	55.95	1315.6	1041.4	35.44	18.19	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q9BN59-1	Thioredox	0	35.627	29	12	18	12	432	47.6	5.97	30.04	12	cellular ho	endoplasm catalytic ac	P00085, F 81567	ENSG000001TND05	6		Protein pro	Neutrophil	10	1.262	0.32601289	4.86	4835.3	3830.1	16.19	2.42	High	High	High	High	High	High	1			
FALSE	High	Master Prq P08574	Cytochrom	0	17.319	16	5	10	5	325	35.4	9	25.27	5	metabolic	membrane metal ion	P02167, 1537	ENSG000001CYC1	8		Parkinson?	Respirator	13	1.261	0.056598113	10.97	3271	2481.1	10.91	7.39	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q9H9B4	Sideroflex	0	68.356	46	9	23	8	322	35.6	9.07	59.92	9	cell differe	membrane transporte	P03820, 94081	ENSG000001SFXN1	X				0	1.261	0.153453186	19.69	9066.4	6864	13.99	12.51	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q00625	Pinin [OS=	0	37.862	33	7	12	7	290	32.1	6.92	28.99	7	cell differe	cytoplasm; catalytic ac	P02678, F 8544	ENSG000001PIR	5		Digestion		2	1.26	0.076207807	8.82	4390.1	3484.5	9.78	3.53	High	High	High	High	High	High	1			
FALSE	Medium	Master Prq Q9NP4-1	Double zinc	0.029	1.433	2	1	1	1	752	82.1	8.06	0	1		metal ion	P03174, F 55184	ENSG000001OZANK1	20				0	1.26	0.128848204	17	729.9	577.4	8.09	12.12	High	High	High	High	High	High	1	[R690];		
FALSE	High	Master Prq Q9H9E3-1	Conserved	0	7.208	4	3	3	3	785	89	5.19	7.48	3	cell organ	endoplasm protein bi	P08818, 25839	COG4	16			COP1-medi	11	1.26	0.228784483	15.18	319.6	259.6	12.4	6.66	High	High	High	High	High	High	1			
FALSE	High	Master Prq P28331-1	NADH-ubiq	0	99.821	34	17	24	17	727	79.4	6.23	59.73	17	cell organ	membrane catalytic ac	P00111, F 4719	ENSG000001NDFU51	2		CHR_HS	Oxidative E	Electron Tr	Complex 1	13	1.26	0.286956931	0.61	6820.2	5641.7	13.4	3.84	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q07581	Paralelmi	0	6.523	7	3	3	3	387	42.1	5	3.61	3	cell organ	cytoplasm; protein bi	P03285, 5064	ENSG000001PALM	19				0	1.259	0.333235716	4.05	645.4	552.2	9.4	11.4	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q9A0B-1	mitochond	0	8.636	10	3	3	3	359	39.7	6.63	4.98	3	cellular ho	membrane protein bi	P07798, 63933	ENSG000001CCDC0A	9				0	1.258	0.166713919	11.78	2413.4	1925.1	5.48	11.08	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q9BWB6	Chromoso	0	7.686	2	1	2	1	975	107.3	7.21	4.04	1	metabolic	cytosol; me catalytic ac	P00004, F 63922	ENSG000001CHT18	16			Gastric car	1	1.258	0.405062351	33.19	791	709.5	32.78	8.78	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q14699	rafflin [OS=	0	19.432	11	3	3	3	578	63.1	5.67	10.43	3	cell organ	cytoplasm; RNA bindi	P15250, 23180	ENSG000001RTN1	3				0	1.258	0.491808201	61.93	21.8	17.3	33.84	16.62	High	High	High	High	High	High	1			
FALSE	High	Master Prq P06576	ATP synth	0	394.452	74	26	148	26	529	56.5	5.4	491.8	26	cell differe	cell surface catalytic ac	P00006, F 506	ENSG000001ATP5B	12		Huntingtin	Electron Tr	Transcripti	17	1.256	0.367175758	19.01	47140.5	38033.4	17.4	6.78	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q5VTL8	Pre-mRNA	0	5.258	5	2	2	2	546	64.4	10.54	3	2	metabolic	nucleus; sp	P03371, 55119	ENSG000001PRF388	1		Spliceosom		1	1.256	0.44444627	64.74	466.3	331	51.74	25.63	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q96DV4	39S riboso	0	11.286	11	4	6	4	380	44.6	7.53	10.71	4	cell organ	membrane	P001161, 64978	ENSG000001MRPL38	17			Mitochond	6	1.255	0.221746262	25.68	1141.3	915.7	19.59	15.18	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q96H7	ERO1-like	0	25.81	22	8	9	8	468	54.4	5.68	16.9	8	cell death	endoplasm catalytic ac	P04317, 30001	ENSG000001ERL1; ERI	14		Vibrio chol	Insulin pro	8	1.254	0.11774576	4.21	2766.6	2205.9	6.96	4.39	High	High	High	High	High	High	1			
FALSE	High	Master Prq P35659-1	Protein Dc	0	8.199	6	2	3	2	375	42.6	8.56	5.64	2	cell organ	nucleus DNA bindi	P02037, F 7913	ENSG000001DEK	6			Transcripti	7	1.253	0.264994074	31.37	96.6	77.1	15.39	14.49	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q43148-1	mRNA cap	0	7.881	4	2	3	2	476	54.8	6.61	6.07	2	metabolic	nucleus catalytic ac	P03291, 8731	ENSG000001RNMT	18		mRNA surv	mRNA Pro	RNA Pol II	14	1.252	0.466895094	65.78	359.6	317	84.87	24.98	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q69YH5-1	cell divisio	0	5.75	2	1	2	1	1023	112.6	8.4	2.15	1	cell divisi	chromosom	P15276, 157313	ENSG000001CDA2	8				0	1.252	0.472972635	52.1	372.7	334.3	32.83	18.24	High	High	High	High	High	High	1			
FALSE	High	Master Prq P60033	CD81 anti	0	7.663	10	1	1	1	236	25.8	5.29	5.81	1	cell profil	membrane protein bi	P03035, 975	ENSG000001CDB1	11		Hepatitis C	B Cell Rec	Regulation	10	1.252	0.636793288	2.91	180.8	152.2	18.91	8.55	High	High	High	High	High	High	1		
FALSE	High	Master Prq P09669	Cytochrom	0	4.551	37	3	4	3	75	8.8	10.39	3.66	3	metabolic	membrane catalytic ac	P02937, 1345	ENSG000001CX6C	8		Non-alcohol	Electron Tr	TP53 Regul	17	1.252	0.820793249	5.57	457.5	374.2	12.27	20.93	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q98R6-1	ADP-deper	0	25.848	8	3	6	3	497	54.1	6.2	20.19	3	metabolic	endoplasm catalytic ac	P04587, 83440	ADPGK	15		Carbon me	Glycolysis	7	1.251	0.159374092	16.73	1458	1244.9	19.06	7.37	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q9747-1	ATP synth	0	79.292	80	11	32	11	161	18.5	5.3	81.3	11	cell organ	cytosol; me catalytic ac	P05073, 10476	ENSG000001ATP5B	17		Oxidative E	Electron Tr	Citrate cyc	14	1.251	0.386623686	14	7765.7	6490.8	18.98	4.82	High	High	High	High	High	High	1		
FALSE	High	Master Prq P27284	Catechin [C	0	226.769	46	31	117	31	592	67.5	4.6	312.17	31	metabolic	cytoplasm; metal ion	P02062, 821	ENSG000001CANX	5		CHR_H	HTLV-1 infe	Assembly c	25	1.25	0.147896253	2.48	41926.3	35527.4	6.43	7.54	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q9UHV9	Prefoldin s	0	27.377	51	7	10	7	154	16.6	6.58	10.41	7	metabolic	cytoplasm; protein bi	P01920, 5202	ENSG000001PFDM2	1			Prefoldin r	5	1.25	0.403072471	2.55	2148.4	1689.9	24.68	6.65	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q9NR84-1	Ribonucle	0.003	3.018	2	2	2	2	1374	159.2	7.87	0	2	defense re	membrane catalytic ac	P00035, F 29102	ENSG000001DROSHA	5		Proteoglyc	mRNA Bio	MicroRNA	8	1.25	0.548620571	70.55	1012.6	904.9	58.85	28.02	High	High	High	High	High	High	1	[Q1096];	
FALSE	High	Master Prq P42694	Probable h	0.009	2.147	1	2	3	1	1942	218.8	7.42	5.02	1		membrane catalytic ac	P05080, F 9931	ENSG000001HEL5	17				0	1.25	0.578359685	97.13	1069.8	1100	96.35	34.48	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q9Y679-1	Ancient ub	0	9.905	6	2	4	2	476	53	8.09	4.69	2	metabolic	endoplasm enzyme re	P02845, 550	AUP1	2				0	1.249	0.190599262	18.36	800.9	587.2	17.9	13.52	High	High	High	High	High	High	1			
FALSE	Medium	Master Prq Q9BXK7	voltage-de	0.048	1.223	3	1	1	1	260	28.1	9.17	0	1	regulation	membrane transporte	P13303, 59285	ENSG000001CACGG6	19		Cardiac me	Arrhythmic	Phase 0 - r	12	1.246	0.013438827	2.67	1151.6	940.8	13.26	11.81	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q7																																						

FALSE	High	Master Prq P13473-1	Lysosome-	0	4.909	4	2	2	2	410	44.9	5.63	0	2	cell comm	endosome	protein br	P101299	3920	ENSG000001	LAMP2	X	Tuberculosis	Sensencsc	Platelet de	11	1.225	0.109807086	13.67	528.6	431.7	5.29	6.59	High	High	High	High	High	High	High	1
FALSE	High	Master Prq C000468	Agrin [DS-	0	22.991	4	4	5	4	2067	217.1	6.39	16.62	4	cell differ	cytosol;ext	metal ion	P00050, F 375790		ENSG000001	AGRN	1	ECM-recep	Primary FG	Integrin ce	32	1.225	0.281539752	24.44	998.4	882	29.99	7.84	High	High	High	High	High	High	High	1
FALSE	High	Master Prq C000914	Striatin-4	0	10.347	4	1	1	1	753	80.5	5.4	6.2	1	metabolic	cytoplasm;	protein br	P00090, F 29888	19	ENSG000001	STRN13	1				0	1.225	0.515231367	67.37	677	610.1	61.72	12.96	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9Y389	RRP15-like	0	23.445	18	5	11	5	282	31.5	5.52	19.98	5	metabolic	cytoplasm;	protein br	P007890	55108	ENSG000001	RRP15	1				0	1.224	0.29526736	21.55	1559.1	1369.2	18.89	4.7	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q06Q24	Spermatog	0	22.653	12	5	6	5	545	59.5	8.9	15.27	5	cytoplasm;	protein br	P007139	65244	ENSG000001	SPR25	12				0	1.224	0.486635425	78.12	528.4	447.7	101.78	29.72	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P14406	Cytochrom	0	16.912	30	3	4	3	83	9.4	9.76	10.01	3	metabolic	membrane	catalytic a	P002338	1347	ENSG000001	CYOXA2	6	Alzheimer'	Electron Tr		7	1.223	0.038164733	6.25	1497.9	1224.7	11.17	5.65	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P16445	NADPH-cy	0	68.275	23	14	31	14	677	76.6	5.58	52.29	14	metabolic	endoplasm	catalytic a	P000175, F 5447		ENSG000001	POR	7			Cytochrom	4	1.223	0.217762614	7.1	11873.6	10033.9	14.96	3.61	High	High	High	High	High	High	High	1
FALSE	Medium	Master Prq C14936	peripheral	0.048	1.219	1	1	1	1	926	105.1	6.43	1.62	1	metabolic	cytoplasm;	catalytic a	P000018, F 8573		ENSG000001	CASK	X	Tight junct	Parlin-Ub	Neuprin fu	13	1.222	0.30887399	32.87	303.4	248.3	16.45	11.64	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P31150	Rab GGP d	0	49.195	24	9	18	4	447	50.6	5.14	53.14	9	metabolic	cytoplasm;	catalytic a	P000996	2664	ENSG000001	GDI1	X	Integrated	RAB GEFs c		8	1.221	0.189726675	14.71	306.5	251	34.31	18.44	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P31930	Cytochrom	0	102.173	36	11	34	10	480	52.6	6.37	109.14	11	metabolic	cytosol;me	catalytic a	P000675, F 7384		ENSG000001	UCRC1	3	Huntingtor	Electron Tr	Respirator	12	1.221	0.336162383	20.99	12526	10262.5	15.9	4.86	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9UPN7	Serine/thr	0	5.173	1	1	1	1	881	96.7	4.55	0	1	cell organ;	cytoplasm;	protein br	P001354, F 22870		ENSG000001	PPP6R1	19			COPII (Coa	8	1.221	0.888957898	3.77	269.1	247.1	17.81	25.93	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q43493-1	Trans-Gol	0	10.798	11	5	5	5	480	51.1	5.73	2.6	5	cell organ;	cytosol;eni	protein br	10618		ENSG000001	TGOLN2	2			Post-transl	13	1.219	0.159847245	1.16	1224.1	1012	22.94	1.11	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q8TBF4	Zinc finger	0.004	2.71	4	1	2	1	217	24.6	8.53	1.8	1	metabolic	nucleus;sp	metal ion	P000076, F 85437		ENSG000001	ZC8R1	12			mRNA Spli	4	1.219	0.255557225	16	969.6	773.8	30.19	11.94	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q92734-1	Protein TF	0	41.605	34	9	11	9	400	43.4	5.1	19.33	9	cell organ;	cytoplasm;	protein br	P00564, F 10342		ENSG000001	TFG	3	Thyroid cas	COPII (Coa		10	1.218	0.016427817	5.56	1239.2	1017.2	4.22	10.47	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q96EC8-1	Protein YIF	0	9.738	9	3	3	3	236	26.2	5.64	2.54	3	endoplasm	protein br	P04893	286451	ENSG000001	YIPF6	X			Golgi Assoc	5	1.218	0.044596018	0.76	236.9	195.8	4.79	1.34	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q13586	stromal int	0	7.051	4	2	2	2	685	77.4	6.67	4.62	2	cellular ho	cytoplasm;	metal ion	P00430, F 6786		ENSG000001	STIM1	11	Calcium sig	Ion homeo		13	1.217	0.192380738	17.03	390.9	321.3	13.06	10.59	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P62987	Ubiquitin	0	38.408	50	7	30	2	128	147	9.83	64.1	7	cell comm	cytoplasm;	protein br	P00240, F 7311		ENSG000001	UBA52	19	Ribosome	DNA Repli	NOTCH1 tr	361	1.217	0.396469027	22.09	1397.9	1148.8	20.13	2.64	High	High	High	High	High	High	High	1
FALSE	High	Master Prq C13KM03	heterogen	0	110.014	30	19	30	19	747	85.1	4.91	63.77	19	membrane	protein br	P000622, F 221092		ENSG000001	HNRNPUL	11				0	1.216	0.13216932	9.37	5810.8	4634.8	14.55	6.55	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q95182	NADH deH	0	18.845	33	3	5	3	113	12.5	10.18	8.98	3	cell organ;	membrane	catalytic a	P007347	4701	ENSG000001	NADUFA7	19	Parkinson'	Electron Tr	Complex i	13	1.216	0.336983374	15.82	1636	1345.6	11.43	8.29	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q5UC64-1	ER membr	0	10.321	9	2	2	2	262	27.3	6.13	4.04	2	extracellul			284361		ENSG000001	EMC10	19				0	1.216	0.900895736	10.14	500.4	421.2	35.23	14.29	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q16822-1	Phosphoiso	0	32.372	17	7	9	7	640	70.7	8.62	21.35	7	cellular ho	mitochond	catalytic a	P00821	5106	ENSG000001	PCK2	14	Pyruvate re	Adipogene	Glucoseox	21	1.215	0.2629629	16.76	1743.3	1435.1	48.94	26.7	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q50552	Vasodilator	0	53.817	34	10	16	10	380	39.8	7.94	30.52	10	cell organ;	cytoplasm;	protein br	P00568	7408	ENSG000001	VASP	19	Leukocyte	Integrin m	Cell-extrac	18	1.215	0.277038955	13.71	3882.3	3194.7	8.67	8.29	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P10809	60 kDa he	0	682.116	82	53	471	53	573	61	5.87	1230.33	53	cell organ;	cell surface	catalytic a	P00118	3329	ENSG000001	HSP01	2	RNA degra	Apoptosis-	TFAP2A ac	13	1.215	0.489983504	20.7	131000.8	10781.7	11.66	11.46	High	High	High	High	High	High	High	1 [567(99.2)
FALSE	High	Master Prq Q7269	E3 ubiquiti	0	6.897	2	2	2	2	1792	201.4	9.64	7.24	2	metabolic	chromoso	catalytic a	P00097, F 5930		ENSG000001	RBBP6	16				4	1.214	0.169457888	16.96	761.5	628.5	14.35	1.05	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q51729	alanine-IR	0	39.212	15	9	11	9	985	107.3	6.27	28.42	9	cell organ;	cytoplasm;	catalytic a	P001411, F 57505		ENSG000001	AARS2	5	Aminoacyl-		Mitochond	5	1.214	0.391168678	38.3	4269.9	3723.9	22.21	14.3	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9HD15	Steroid rec	0	7.528	13	2	2	2	236	25.7	7.03	1.1	2	cell death;	cytoplasm;	protein br	P007304	10011	ENSG000001	SRA1	1				0	1.214	0.452493169	53.78	380.1	336	78.82	24.99	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9GZP4	PITF dom	0.003	3.482	6	1	1	1	211	24.2	5.74	3.24	1	response i	nucleus		P06201	57095	ENSG000001	PITFD1	1				0	1.213	0.031592243	9	805.8	692	11.8	12.39	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P23219	Prostaglan	0	16.36	13	6	8	6	599	68.6	7.23	17.53	6	defense re	cytoplasm;	antioxidan	P00008, F 5742		ENSG000001	PTGS1	5	Serotonerg	Selenium H	COX reacti	17	1.213	0.208955379	18.6	2660.4	2177.9	17.16	8.37	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P55809	Succinyl-Co	0	205.374	52	24	91	24	520	56.1	7.46	256.83	24	metabolic	mitochond	catalytic a	P001144	5019	ENSG000001	OXCT1	5	Synthesis a	Synthesis a	Utilization	8	1.213	0.414029092	21.21	31394.2	25871.3	12.45	10.71	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q960X5	Ankyrin re	0	10.192	13	2	2	2	294	31.8	6.98	5.06	2	metabolic	cytosol;mi	protein br	P00678, F 140462		ENSG000001	ASB9	8			Antigen pr	7	1.213	0.476912221	50.34	463.4	456	41.45	12.18	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9NDU8	UPF0600 p	0	6.934	12	2	2	2	294	33.6	5.26	2.2	2	cytosol			285636		ENSG000001	Csorf51	5				0	1.213	0.91961512	0.88	27.2	25.1	18.99	20.59	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q43678	NADH deH	0	15.75	46	4	9	4	99	109	9.57	15.82	4	cell organ;	membrane	catalytic a	P005047	4695	ENSG000001	NADUFA2	5	Huntingtor	Electron Tr	Complex i	13	1.212	0.01419373	8.54	2862.3	2566.9	8.94	8.97	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P42166	Lamina-as	0	49.28	19	8	17	4	694	75.4	7.66	41.07	8	regulation	chromoso	DNA bindi	P003020, F 7112		ENSG000001	TMP3	12				0	1.212	0.1963158	21.64	2353.3	1941.8	12.95	5.84	High	High	High	High	High	High	High	1 [T74(100)
FALSE	High	Master Prq Q518A6-1	Transport-	0	26.148	4	8	9	8	1907	213.6	4.84	15.53	8	cell organ;	endoplasm	protein br	P002463, F 375056		ENSG000001	MIA3	10			Post-transl	10	1.212	0.176643117	13.73	719.9	643	7.63	10.33	High	High	High	High	High	High	High	1
FALSE	High	Master Prq C13151	Heterogen	0	89.759	40	13	39	12	305	30.8	9.29	90.87	13	defense re	nucleus	protein br	P00076, F 10949		ENSG000001	HNRNPAD	5			mRNA Spli	4	1.211	0.21982356	0.34	8562.3	7408.7	9.13	3.93	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q00784	Target of h	0	7.786	4	1	1	1	492	53.8	4.7	4.97	1	transport	cytoplasm;	protein br	P00790, F 10043		ENSG000001	TMPO	22	Neutrophil			3	1.211	0.551536087	41.07	148.6	160.2	37.79	14.74	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q335M5	inactive hy	0	11.984	17	3	3	3	330	37	8.72	9.84	3	mit																										

FALSE	High	Master Prq Q94776	Metastasi	0	33.57	15	10	11	10	668	75	9.66	21.41	10	cell organ	membrane catalytic a	P100429, F 9219	ENSG000001	MTA2	11		ERCC5 (CS	20	1.19	0.280974215	24.58	4239.2	3622.8	20.05	6.66	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q7L86	FAST kinas	0	6.145	1	1	2	1	764	86.5	8.13	4.61	1	cell organ	mitochond catalytic a	P06743, F 60493	ENSG000001	FASTK205	20			0	1.19	0.609700196	45.85	477.8	485.2	32.9	15.74	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq P40926	Malate de	0	232.562	66	19	105	19	338	35.5	8.68	266.39	19	metabolic	membrane catalytic a	P00456, F 4191	ENSG000001	MDH2	7	Metabolic	Amino Acid	Glucosam	16	1.189	0.042947945	7.43	40239.9	34798.2	6.72	4.11	High	High	High	High	High	High	High	1	
FALSE	Medium	Master Prq Q14524-1	Nuclear en	0.015	1.552	2	1	1	1	444	50.6	6.93	2.2	1	membrane		P10225	23306	ENSG000001	TMEM194	12			0	1.189	0.136219596	12.94	208.6	175.4	5.6	9.96	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P52306-1	Rap1 GTPa	0	9.795	2	1	1	1	607	66.3	5.31	3.6	1	cell organ	cytosol/eni enzyme re	P00514	5910	ENSG000001	RAP1G0S1	4			0	1.188	0.609987004	65.63	747.6	565.2	49.83	43.35	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q75439	mitochond	0	81.579	41	15	21	14	489	54.3	6.83	54.57	15	metabolic	membrane catalytic a	P00875, F 9512	ENSG000001	PMPC8	7			5	1.187	0.038079303	1.04	6509.9	5516.3	4.93	1.54	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq P13937	UDP-gluc	0	11.674	8	1	2	1	396	41.3	9.96	9.85	1	metabolic	endoplasm protein br	P04142	7355	ENSG000001	SLC35A2	X	Defective s		8	1.187	0.597271694	96	225.4	194.8	99.79	55.27	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9BTX1	Nucleopor	0	12.165	4	2	4	2	674	76.3	9.09	12.27	2	cell organ	cytoplasm; structural	P09931	55706	ENSG000001	NDCL1	TM1	RNA trans	Rev-media	64	1.186	0.265072021	17.9	136.8	126.4	27.83	5.26	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q8NE22	Vacuolar p	0	14.15	9	2	2	2	397	44.3	5.57	7.65	2	cell comm	cytosol/eni protein br	P07200	137492	ENSG000001	VP537A	8	Endocytosi	Budding a	13	1.186	0.407256743	35.84	649.9	559.8	37.78	15.96	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9UNH7-1	Sorting ne	0	19.319	14	5	5	5	406	46.6	6.16	6.25	5	cell organ	cytoplasm; protein br	P00787, F 58533		ENSG000001	SNKE	14	Endocytosi		1	1.186	0.445397038	44.48	381.7	321.7	39.58	7.34	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9BUR4	Telomeras	0	6.158	7	3	3	3	548	59.3	4.58	4.03	3	cell organ	cytoplasm; protein br	P04040	55135	ENSG000001	WRAP53	17	Association		9	1.186	0.82324302	8.37	838.4	669.3	7.46	43.86	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P31937	3-hydroxy	0	64.808	35	8	16	8	336	35.3	8.13	56.49	8	metabolic	mitochond catalytic a	P02254, F 11112	ENSG000001	HIBADH	X	Valine, leu	Amino Acid	Branched-<	6	1.185	0.362711507	19.08	4115.3	3562.9	16.35	3.61	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q75381-1	Peroxisom	0	8.464	6	2	4	2	377	41.2	4.94	7.42	2	cell organ	membrane protein br	P04695	5195	ENSG000001	PEX14	1	Peroxisom		1	1.185	0.413094208	37.23	878.9	837.4	36.03	10.72	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9HCC0-1	Methylcro	0	54.168	22	9	11	9	563	61.3	7.68	36.23	9	cell organ	cytosol;mi catalytic a	P101039	64087	ENSG000001	MCCC2	5	Metabolic	Branched-<	13	1.184	0.201282518	12.82	4329.9	4004.6	23.55	7.31	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9BW71-1	HIRA-inter	0	14.478	4	2	4	2	556	61.9	8.54	4.15	2	cell organ	nucleus protein br	P09649	8479	ENSG000001	HIRAP3	16			0	1.183	0.356038996	31.25	174.9	152.7	14.71	12.56	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9S155	Ubiquitin	0	20.347	8	8	11	8	1302	146.1	6.55	22.44	8	cell organ	cytoplasm; catalytic a	P104564, F 10277	ENSG000001	UBE48	1	Protein prc		2	1.183	0.476338362	48.18	837.5	707.9	40.51	11.66	High	High	High	High	High	High	High	[R654];		
FALSE	Medium	Master Prq Q14814-1	Myocyte-s	0.012	1.997	2	1	1	1	521	55.9	7.88	2.27	1	cell death	cytoplasm; DNA bindi	P03015, F 4209	ENSG000001	MEF2D	1	cGMP-PKG	Energy Me	Transcripti	16	1.182	0.16652818	7.15	477.5	391.4	10.1	12.43	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9H788	SH2 domai	0	5.079	3	1	2	1	454	52.7	8.06	8.27	1	regulation	cytoplasm; protein br	P00017	63898	ENSG000001	SH2D4A	8			0	1.182	0.346017245	30.25	470.9	405.9	23.38	6.28	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q42765	3-ketocya	0	177.396	89	25	51	25	397	41.9	8.09	133.13	25	cell organ	membrane catalytic a	P100308, F 10449	ENSG000001	ACAA2	18	Fatty acid	Fatty Acid	Mitochond	10	1.182	0.628661412	26.75	16446.2	13911.3	17.74	11.47	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P136352	alpha-int	0	45.887	27	12	16	10	499	55.4	5.4	32.06	12	cell differe	cytoskelet structural	P100338, F 9118	ENSG000001	INA	10			0	1.181	0.437933629	18.68	2160.9	1988.8	12.76	14.97	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q75607	Nucleoplai	0	9.095	16	2	2	2	178	19.3	4.63	3.71	2	metabolic	cytoskelet protein br	P102087, F 10360	ENSG000001	NPM3	10			0	1.18	0.255822915	4.98	228.3	195.5	6.72	5.85	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq P62745	Rho-relate	0	5.769	18	2	2	2	196	22.1	5.24	2.85	2	cell death	cytosol/eni catalytic a	P100255, F 388	ENSG000001	RHO28	X	Androgen	G alpha (L	24	1.18	0.283683833	3.68	619.2	507.1	36.97	9.47	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q97978	Acetate	0	90.659	31	15	26	15	780	85.4	7.61	69.5	15	metabolic	mitochond catalytic a	P100330, F 50	ENSG000001	AC02	22	Citrate cyc	Amino Acid	Mitochond	14	1.178	0.382638178	27.78	4258.8	3256.9	45.61	19.86	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P10101	Protein dis	0	271.594	72	36	124	36	505	56.7	6.35	327.68	36	cellular ho	cell surface catalytic a	P100085, F 2923	ENSG000001	PD1A3	15	Antigen pr	ER-Phagoc	13	1.179	0.137046007	5.25	42728.8	36236.4	6.92	2.2	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq P08648	Integrin al	0	15.142	3	2	4	2	1049	114.5	5.77	9.45	2	cell differe	cell surface metal ion	P101839, F 3678	ENSG000001	ITGA5	12	Dilated car	Integrin-m	RUNX2 reg	33	1.179	0.275852897	16.47	922.3	766	26.98	11.23	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P06748	Nucleopho	0	243.63	55	23	206	6	294	32.6	4.78	513.44	23	cell growth	cytoplasm; DNA bindi	P03066	4869	ENSG000001	NPM1	5	Nuclear in		18	1.178	0.410790968	17.77	11892.8	10407.1	5.33	8.85	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q92779-1	Symplekin	0	8.315	3	2	2	2	1274	141.1	6.19	33.1	2	metabolic	cytoplasm; protein br	PF11935, F 8189	ENSG000001	SYMPK	19	Tight junct		16	1.178	0.361419141	30.19	366.9	311.5	26.1	9.21	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q75348	V-type pro	0	16.06	21	3	5	3	118	13.7	8.79	12.51	3	cellular ho	cytosol;me catalytic a	P101179	9550	ENSG000001	ATPEV1G1	9	Vibrio chol	Osteoclast	Transferr	21	1.178	0.468139235	45.03	1067.9	970.7	40.28	8.71	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P20962	Parathym	0	16.079	28	4	6	4	102	11.5	4.16	9	4	metabolic	nucleus	5763		ENSG000001	PTMS	12			0	1.177	0.011368586	2.17	1377.1	1169.6	4.71	8.34	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P20962	Parathym	0	16.079	28	4	6	4	102	11.5	4.16	9	4	metabolic	nucleus	5763		ENSG000001	PTMS	12			0	1.177	0.011368586	2.17	1377.1	1169.6	4.71	8.34	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9H788	SH2 domai	0	5.079	3	1	2	1	454	52.7	8.06	8.27	1	regulation	cytoplasm; protein br	P00017	63898	ENSG000001	SH2D4A	8	Complexe	Regulation	17	1.177	0.066409941	9.47	4635.2	3639.8	9.14	5.12	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q16629	serine/argi	0	46.799	33	8	21	8	238	27.7	11.82	38.72	8	metabolic	cytoplasm; metal ion	P10076, F 6432	ENSG000001	SRSF7	2	Spliceosom	mRNA Pro	Cleavage o	15	1.177	0.16231505	0.71	6086.3	5910.7	8.57	7.75	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9N263	Telomere i	0	6.031	8	2	2	2	289	33.4	4.74	3.3	2	cytosol	protein br	P107052	51759	ENSG000001	C1orf78	9			0	1.177	0.31728763	27.83	629	546	15.35	8.92	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P28482	mitogen-a	0	13.447	9	2	3	2	360	41.4	6.98	5.7	2	cell comm	cytoplasm; catalytic a	P100669, F 5594	ENSG000001	MAPK1	32	MicroRNA	IL-5 Signa	phospho-p	290	1.177	0.3500778	32.65	219.3	179.4	16.29	13.23	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q15234	Protein CA	0	10.677	5	2	2	2	703	76.2	6.48	4.17	2	metabolic	cytoplasm; protein br	P109405	22794	ENSG000001	MDM2	17	RNA trans	mRNA 3'-e	19	1.176	0.425864793	37.99	393.7	329.6	57.05	19.03	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9NF37	Lysophosp	0	22.828	12	5	13	5	534	59.1	6.02	29.12	5	metabolic	endoplasm catalytic a	P101553, F 79888	ENSG000001	LCPIA1	1	Ether lipid	Synthesis c	14	1.175	0.091045611	0.04	1349.3	1171.7	6.21	1.28	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q9UPQ0-1	LM and ca	0	5.754	3	3	3	3	1083	121.8	6.47	2.67	3	cellular ho	metal ion	P100307, F 22998	ENSG000001	UPC11	4			0	1.175	0.307418539	27.09	645.7	549.4	10.97	11.12	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq P30084	Enoyl-CoA	0	150.1	62	17	56	17	290	31.4	8.																												

FALSE	High	Master Prq	P48729-3	Isomorf 3	0	12.887	14	3	6	1	325	37.5	9.48	18.83	3	cell division	cytosol;mel	catalytic	ac	P00069, F 1452	ENSG000001	CNCK1A1	5			T-Cell Recd	4	1.162	0.461629863	37.01	187.7	161.6	18.99	19.52	High	High	High	High	High	High	1
FALSE	Medium	Master Prq	Q60313	Dynamilin-1	0.031	1.427	1	1	1	1	960	111.6	7.87	0	1	cell death	cytosol;mel	catalytic	ac	P00350, F 4976	ENSG000001	OPA1	3			Regulation	3	1.162	0.475078141	18.04	575.2	555.5	14.54	14.23	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q10713	Mitochondr	0	50.616	27	10	16	10	525	58.2	6.92	40.71	10	metabolic	membrane	catalytic	ac	P00075, F 23203	ENSG000001	PMPCA	9			Processing	5	1.161	0.038850818	1.06	3226.6	2758.5	2.52	7.16	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q95302	Peptidyl-pi	0	19.021	10	5	10	5	570	63	5.08	17.32	1	metabolic	cytoplasm;	catalytic	ac	P00054, F 11328	ENSG000001	KFBP9	9			Associatio	4	1.16	0.069373663	2.74	3739.5	3417.8	5.27	3.6	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q9NVT1	Protein SD	0	8.826	1	1	2	1	687	79.8	9.25	4.91	1	cell organ	nucleus			P05825, F 55153	ENSG000001	SOD01	4				0	1.16	0.184495811	15.35	786.5	678	6.55	11.42	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q16543	Hsp90 co-c	0	49.103	36	11	15	11	378	44.4	5.25	31.27	11	cell division	cytoplasm;	catalytic	ac	P00334, F 11140	ENSG000001	CD37	19			P3K-Akt si	17	1.16	0.364580773	25.37	2422.3	2363.6	14.86	9.99	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q05155	BET1 norm	0	11.537	25	2	4	2	118	13.3	9.06	18.03	2	cell organ	endoplasm	protein bi	re	P05739, F 10282	ENSG000001	BET1	10			SNARE int	10	1.159	0.108007812	2.14	2596.3	2197.7	9.75	3.02	High	High	High	High	High	High	1
FALSE	High	Master Prq	P09110-1	3-ketocacyl	0	9.757	8	2	2	2	424	44.3	8.44	3.95	2	metabolic	extracellular	catalytic	ac	P00108, F 30	ENSG000001	ACA1	3			Metabolic	21	1.159	0.185599584	16.36	268.3	259.3	16.6	8.47	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q16778	Histone H2	0	108.838	75	15	93	3	126	13.9	10.32	246.61	15	cell organ	chromoso	DNA bindi	re	P00125, F 8349	ENSG000001	HIST2H2B	1			Systemic li	75	1.159	0.273730141	23.34	4805.4	3988.7	28.33	13.54	High	High	High	High	High	High	1
FALSE	High	Master Prq	P19013	Keratin, ty	0	22.171	9	5	21	1	534	57.3	6.61	36.48	5	cell death	cell surface	protein bi	re	P00038, F 3851	ENSG000001	KRT4	12			Formation	3	1.159	0.611263343	19.51	780.3	673.4	12.75	10.73	High	High	High	High	High	High	1
FALSE	High	Master Prq	P00414	Cytochrome	0	5.001	5	1	2	1	261	29.9	7.31	6.4	1	cell organ	membrane	catalytic	ac	P00510, F 4514	ENSG000001	CDX3	MT			Non-alcohol	17	1.157	0.142181138	9.03	1218.4	965.9	12.85	18.46	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q95854	Homocyste	0.001	4.535	2	1	2	1	406	45.1	5.06	4.26	1	response i	membrane	protein bi	re	P00240, F 64224	ENSG000001	HERPUD2	7				0	1.157	0.257911233	20.52	1165.2	1041.4	13.06	7.62	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q56199	Integrin al	0	21.449	5	5	7	5	1179	130.8	6.29	12.64	5	cell organ	cell surface	metal ion	re	P00092, F 3672	ENSG000001	ITGA1	5			P3K-Akt si	27	1.157	0.652271323	6.25	1038.3	997.2	9.19	15.78	High	High	High	High	High	High	1
FALSE	High	Master Prq	P11310-1	medium-cl	0	64.513	37	12	17	12	421	46.6	8.37	34.14	12	metabolic	membrane	catalytic	ac	P00441, F 34	ENSG000001	ACADM	1			PPAR sign	24	1.156	0.038815144	5.35	2816.9	2496.1	5.69	5.39	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q96ER9	Coiled-coil	0	12.151	8	2	3	2	411	45.8	8.19	7.49	2	membrane				79714	ENSG000001	CCDC51	3				0	1.156	0.264174948	5.53	784.4	672.3	2.63	11.17	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q9UGI8	Testin [OS	0	10.424	10	4	5	4	421	48	7.68	6.1	4	regulation	cytoplasm;	metal ion	re	P00412, F 26136	ENSG000001	TES	7				0	1.156	0.369090955	27.14	769.5	665.5	20.16	19.88	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q43304	Glycerol-3	0	5.373	4	3	5	3	727	80.8	7.69	3.97	3	metabolic	membrane	catalytic	ac	P00036, F 2820	ENSG000001	GPD2	2			Glyceroph	9	1.156	0.38985886	25.38	800.8	732.7	33.02	15.12	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q95391	Pre-mRNA	0	20.105	11	6	8	6	586	68.3	7.14	9.78	6	cell organ	cytoplasm;	catalytic	ac	P11708, F 10569	ENSG000001	SU17	5			Spliceosom	12	1.156	0.485375652	37.91	300.6	286.6	24.37	12.1	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q43674-1	NADH dehyd	0	9.736	15	2	2	2	189	21.7	9.63	8.17	2	cell organ	membrane	catalytic	ac	P00971, F 4711	ENSG000001	NDUFBS	3			Huntington	13	1.156	0.77756523	19.55	1070.7	926.3	14.43	13.21	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q9U42-1	Carboxype	0	16.626	5	1	3	1	421	47.3	6.7	14.1	1	cell organ	extracellular	catalytic	ac	P00246, F 51200	ENSG000001	CPA4	7				0	1.155	0.558853845	25.93	830.2	795.4	21.7	8.21	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q96G46	tRNA-dihy	0	4.687	3	1	1	1	650	72.5	8.05	4.05	1	metabolic		catalytic	ac	P01207, F 56931	ENSG000001	DUSL3	9				0	1.155	0.596346582	52.08	143.2	138.2	35.72	16.17	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q9YSY2	Cytosolic f	0	14.984	19	2	3	2	271	28.8	5.83	12.41	2	cell organ	cytoplasm;	metal ion	re	P00142, F 10101	ENSG000001	NUPB2	16			Cytosolic li	2	1.155	0.71815539	42.41	282	36.4	57.96	36.6	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q9Y2W1	Thyroid hor	0	102.986	23	20	45	20	955	108.6	10.15	96.79	20	metabolic	nucleus	DNA bindi	re	P15440, F 9967	ENSG000001	THRAP3	3			Interactor	7	1.154	0.059774675	6.82	18923.1	16393.4	9.82	4.74	High	High	High	High	High	High	1
FALSE	High	Master Prq	P54725-1	UV excision	0	14.618	13	3	6	2	363	39.6	4.58	10.99	3	metabolic	cytoplasm;	DNA bindi	re	P00240, F 5886	ENSG000001	NDAI3A	19			Nucleotide	11	1.154	0.255127776	18.26	588.8	498.3	8.78	13.89	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q15230	Laminin su	0	29.047	3	7	9	7	3695	399.5	7.02	16.17	7	cell differe	extracellular	catalytic	ac	P00052, F 3911	ENSG000001	LAMAS	20			Toxoplasma	27	1.154	0.367820838	28.56	2358.9	2255.9	24.84	6.7	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q9NFQ8	Torsin-1A	0	9.216	6	3	3	3	470	51.2	4.66	6.7	3	cell organ	endoplasm	enzyme re	re	P05069, F 163590	ENSG000001	TOR1AIP2	1				0	1.154	0.43123173	32.08	642.6	492.8	21.75	22.66	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q9UM00	Calcium ion	0	25.733	21	4	9	4	188	21.2	9.74	27.44	4	cellular hor	endoplasm	transporte	re	P01956, F 54499	ENSG000001	TMC01	1				0	1.154	0.483998648	35.51	2537.7	2318.1	17.43	12.67	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q92905	COP9 sign	0	7.085	6	1	1	1	334	37.6	6.54	4.92	1	cell organ	chromoso	catalytic	ac	P01398, F 10987	ENSG000001	COP9	8			TGF-beta S	14	1.154	0.683149423	27.82	369.3	317.3	25.67	4.89	High	High	High	High	High	High	1
FALSE	Low	Master Prq	Q9BGQ2	Olfactory r	0.057	1.136	2	1	1	1	313	35.4	7.97	0	1	regulation	membrane	receptor r	re	P00001, F 26686	ENSG000001	OR4E2	14			Olfactory s	4	1.154	0.758196393	28.53	84.6	73.3	12.24	20.05	High	High	High	High	High	High	1
FALSE	High	Master Prq	P99687	Acidic leuc	0	42.35	29	8	17	6	249	28.6	4.09	37.53	8	cell organ	cytoplasm;	protein bi	re	P11279, F 8125	ENSG000001	ANP32A	15			HuR [ELAV	3	1.153	0.041936887	3.07	1512.3	1285.1	2.55	6.37	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q9BTL3	RNMT-acti	0	9.465	19	1	2	1	118	14.4	8.94	9.02	1	cell organ	nucleus	catalytic	ac	P15320, F 83640	ENSG000001	FAM103A	15				0	1.153	0.065575055	3.65	111.5	94	13.24	8.84	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q968N8	Ubiquitin t	0	25.845	24	5	5	5	352	40.2	4.57	12.79	5	defense re	cytoplasm;	catalytic	ac	P101275, F 90268	ENSG000001	FAM105B	5			Regulation	8	1.153	0.158752307	11.54	1637.8	1538.9	10.62	4.69	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q75380	NADH dehyd	0	31.079	48	4	8	4	124	13.7	8.28	29.53	4	cell organ	membrane	catalytic	ac	P10276, F 4726	ENSG000001	NDUF56	5			Metabolic	13	1.153	0.458883992	3.12	1069	934.6	13.63	0.53	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q86B11	Elongator	0.002	3.818	2	1	1	1	424	46.6	8.51	2.91	1	cell organ	cytoplasm;	catalytic	ac	P005425, F 26610	ENSG000001	ELP4	11			Mesoderm	4	1.153	0.480092937	41.56	462.2	477.7	42.46	12.84	High	High	High	High	High	High	1
FALSE	Low	Master Prq	Q9UWPR	Suprabasin	0.069	1.052	4	1	1	1	590	60.5	7.01	0	1	extracellular				374897	ENSG000001	SBSN	9				0	1.153	0.863093962	65.08	280.4	243.1	27.38	22.76	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q9BNP9-1	Sulfatase-r	0	28.325	23	5	10	5	301	33.8	8	29.6	5	metabolic	endoplasm	metal ion	re	P013871, F 25870	ENSG000001	SUMF2	17			The activat	8	1.152	0.01088111	4.3	2163.9	1878.9	1.29	4.17	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q13322	Nucleoside	0	7.209	17	2	2	2	169	19	7.84	7.73	2	cell death	cytosol;mel	catalytic	ac	P00334, F 4832	ENSG000001	NME3	16			Intercom	6	1.152</													



FALSE	High	Master Prq C9JUX7	Nuclear pc	0	28.637	26	6	6	6	468	50.1	7.06	16.9	6	cell organ	membrane protein br	P00638, F 10762	ENSG000001NUP50	22	RNA trans		Rev-media	64	1.144	0.010513968	3.21	1377.7	1204	1.12	3.79	High	High	High	High	High	High	1
FALSE	Medium	Master Prq C75368	SH3 domain	0.011	2.039	6	1	2	1	114	12.8	5.25	2.41	1	cellular ho	cytoplasm; catalytic ac	P04602, F 6451	ENSG000001SH3BGR_L	X				0	1.144	0.221077805	11.39	1251.7	1087.2	2.63	9.61	High	High	High	High	High	High	1
FALSE	High	Master Prq C9B107	methylethio	0	24.053	6	6	9	6	369	39.1	6.3	15.22	6	metabolic	cytoplasm; catalytic ac	P04708, F 84245	ENSG000001MBR11	19	Cysteine ac	Methionin		0	1.144	0.476248931	6.99	2102.8	1891.3	7.32	8.36	High	High	High	High	High	High	1
FALSE	High	Master Prq P0DM98	Cancer/Inte	0	5.189	14	2	2	2	189	21.1	9.55	4.63	2			P15300, 10272363	ENSG000001LOC10272	X				0	1.144	0.479371861	67.09	308.3	269.6	100.01	26	High	High	High	High	High	High	1
FALSE	High	Master Prq C9Y9V8	SEC23-inter	0	13.186	5	4	4	4	1000	111	5.54	8.02	4	cell organ	cytoplasm; catalytic ac	P00536, F 11196	ENSG000001SEC23IP	10				8	1.144	0.575400976	13.76	55.7	53.2	13.43	9.96	High	High	High	High	High	High	1
FALSE	High	Master Prq C94UQ4	Transmem	0	9.655	5	3	4	3	689	77.1	9.14	7.12	3	cell death	cytosol; en	P10151, 54867	ENSG000001TMEM214	2				0	1.144	0.5989603	35.54	110.1	86.8	34.67	9.96	High	High	High	High	High	High	1
FALSE	High	Master Prq C99T47	Gamma-se	0	7.688	6	2	2	2	312	34.7	5.41	2.9	2	cell organ	membrane protein br	P14938, 8774	ENSG000001NAPG	18				14	1.143	0.317982199	21.51	1001.8	771.3	8.8	21.77	High	High	High	High	High	High	1
FALSE	High	Master Prq P46937	Transcripti	0	83.022	51	12	20	12	504	54.4	5.17	75.18	12	cell organ	cytoplasm; DNA bindi	P00397, 10413	ENSG000001YAP1	11	Hippo sign	Mesoderm RUNX2 reg		26	1.143	0.365434927	24.15	3041.1	2719.7	32.52	4.45	High	High	High	High	High	High	1
FALSE	High	Master Prq P50895	Basal cell c	0	14.239	5	2	3	2	628	67.4	5.81	9.04	2	regulation	cell surface protein br	P00047, F 4059	ENSG000001SCAM	19				0	1.142	0.164897132	0.78	416.5	396.5	9.46	7.05	High	High	High	High	High	High	1
FALSE	High	Master Prq C9BUU7	MAPK reg	0	12.237	23	2	2	2	160	17.8	9.41	6.76	2	cytoplasm;	protein br	P14799, 84331	ENSG000001FAM159A	16				0	1.142	0.196153811	14.63	992.9	863.8	8.72	6.48	High	High	High	High	High	High	1
FALSE	High	Master Prq C12849	G-rich seq	0	25.285	14	5	7	5	480	53.1	6.19	17.01	5	metabolic	cytoplasm; RNA bindi	P00076, F 2926	ENSG000001GRSF1	4				6	1.142	0.387704203	21.47	521.2	488.4	57.57	8.1	High	High	High	High	High	High	1
FALSE	High	Master Prq C9P015	39S riboso	0	7.911	9	2	3	2	296	33.4	10.01	7.14	2	cell organ	membrane protein br	P00828, 29088	ENSG000001MRPL15	8				7	1.142	0.392877577	23.99	2602.8	2189	4.92	21.57	High	High	High	High	High	High	1
FALSE	High	Master Prq C9JUL25	Ras-relate	0	46.623	33	8	13	8	225	24.3	7.94	35.42	8	cellular co	cytosol; en; catalytic ac	P00025, F 23011	ENSG000001RAB21	12				7	1.142	0.445730895	1.97	4684.7	4100.5	8.94	3.54	High	High	High	High	High	High	1
FALSE	High	Master Prq P47985	cytochrom	0	26.831	40	6	7	6	274	29.6	8.32	24.34	6	metabolic	membrane catalytic ac	P00355, F 7386	ENSG000001UQCRF51	19	Non-alcoh	Electron Tr Respirator		12	1.141	0.028130735	4.16	712.8	643	5.77	3.64	High	High	High	High	High	High	1
FALSE	High	Master Prq C96MU7	YTH domai	0	6.842	2	1	2	1	727	84.6	6.23	2.16	1	cell organ	membrane protein br	P04146, 91746	ENSG000001YTHDC1	4, CHR_HS				0	1.141	0.305111629	20.38	283.5	248.4	18.1	5.26	High	High	High	High	High	High	1
FALSE	High	Master Prq C96MU7	NADH deH	0	14.645	21	3	8	3	179	21.8	8.38	25.8	4	cell organ	membrane catalytic ac	P05347, F 4715	ENSG000001NDFB9	18	Oxidative e	Electron Tr Complex I		13	1.141	0.408796928	27.53	1989.1	1746	64.07	10.44	High	High	High	High	High	High	1
FALSE	High	Master Prq P62857	40S riboso	0	20.761	52	4	10	4	69	7.8	10.7	10.52	4	cell organ	cytosol;rib	P01200, 6234	ENSG000001RPS28	19	Ribosome	Cytoplasm; Peptide ch		38	1.141	0.696075754	57.69	684.6	599.8	21.66	25.81	High	High	High	High	High	High	1
FALSE	High	Master Prq C91005	Signal pep	0	14.348	22	3	5	3	226	25	8.47	10.1	3	metabolic	endoplasm catalytic ac	P06703, 9789	ENSG000001SPCS2	11	Protein ex	Synthesis		9	1.14	0.011858845	2.32	872.5	786.5	5.69	5.39	High	High	High	High	High	High	1
FALSE	High	Master Prq C9BD01	EH domain	0.001	4.474	1	2	3	1	1231	139.9	5.35	0	2	transport	cytoplasm; protein br	P00307, F 23301	ENSG000001EHPA1	10				0	1.14	0.266034145	3.04	1129.1	1018.4	3.56	7.22	High	High	High	High	High	High	1
FALSE	High	Master Prq C94A7-1	Sideroflexi	0.006	2.35	4	1	1	1	337	38	9.19	0	1	transport	membrane transporte	P03820, 119559	ENSG000001SFXNA	2				0	1.14	0.334483186	22.73	265.1	215.8	13.21	17	High	High	High	High	High	High	1
FALSE	High	Master Prq C9288-1	Rho ganci	0.007	2.235	1	1	1	1	912	102.4	5.66	3.02	1	cell profile	cytoplasm; enzyme re	P00621, F 9138	ENSG000001ARHGFE1	6	Proteoglyc	G Protein G alpha (12)		20	1.14	0.616433299	26.51	199.9	175.4	7.42	16.36	High	High	High	High	High	High	1
FALSE	High	Master Prq C9P5197	Reticulari	0.003	3.137	1	1	1	1	1032	112.5	4.96	4.21	1	cell death;	endoplasm protein br	P02453, F 10313	ENSG000001RTN3	11	Alzheimer'	Synaptic ac		4	1.139	0.05932131	0.89	468.6	430.6	4.36	6.61	High	High	High	High	High	High	1
FALSE	High	Master Prq P84074	Neuron-sp	0	6.431	15	3	4	3	193	22.4	4.97	4.89	3	regulation	cytoplasm; metal ion	P00036, F 3208	ENSG000001HPCA	1				0	1.139	0.131780002	2.85	54.1	45.9	13.34	5.93	High	High	High	High	High	High	1
FALSE	High	Master Prq C9BW92	Threonine-	0	10.747	4	2	3	2	718	8.1	7.3	12.3	2	metabolic	cytoplasm; catalytic ac	P00587, F 80222	ENSG000001TARS2	1	Aminoacyl	Mitochond		5	1.139	0.213956923	13.23	933.2	825.9	7.09	9.02	High	High	High	High	High	High	1
FALSE	High	Master Prq C014732-1	inositol m	0	13.831	7	2	4	2	288	31.3	6.61	9.92	2	metabolic	cytoplasm; catalytic ac	P00459, 3613	ENSG000001IMPA2	18	Inositol ph	Synthesis c		6	1.139	0.367458181	24.22	1503.1	1295.4	20.33	14.1	High	High	High	High	High	High	1
FALSE	High	Master Prq C9BNC0	Carbohydr	0	7.246	6	2	2	2	376	43	9.48	3.95	2	metabolic	Golgi;mem	P03567, 113189	ENSG000001CHST14	15	Glycosami	Metathapsin Defective c		11	1.139	0.417459372	28.89	1161.5	1006.2	17.01	13.98	High	High	High	High	High	High	1
FALSE	High	Master Prq P13928	Annexin A1	0	66.385	36	12	26	1	327	36.9	7.78	64.73	12	cell organ	cytosol;me	P01091, 653145; 7	ENSG000001ANXA8; AN	10				0	1.139	0.517064524	40.42	754.4	673.2	28.96	17.05	High	High	High	High	High	High	1
FALSE	High	Master Prq P13995	Bifunction	0	47.119	42	9	13	9	350	37.9	8.73	33.98	9	metabolic	metal catalytic ac	P00763, F 10797	ENSG000001MTHFD2	2	Metabolic	Folate Met Metabolis		10	1.138	0.033767724	0.22	4164.3	3664.4	8.81	5.31	High	High	High	High	High	High	1
FALSE	High	Master Prq C9P6P5	E3 ubiquiti	0	38.947	21	5	13	5	407	43.4	5.86	36.58	5	cell differ	cytoplasm; protein br	P00076, F 26528	ENSG000001DAZAP1	19	mRNA sur			1	1.138	0.042687576	3.52	2767.4	2492.9	6.44	7.15	High	High	High	High	High	High	1
FALSE	High	Master Prq C95071	D3-abso	0	20.001	3	5	5	5	2799	309.2	8.55	8.73	5	cell profile	cytosol;me	P00632, F 51366	ENSG000001UBR5	8	Ubiquitin	in Mesoderm		3	1.138	0.078493755	0.13	216.2	190.9	0.93	4.36	High	High	High	High	High	High	1
FALSE	High	Master Prq C9H307	Plinin (OS)	0	41.365	18	10	13	10	717	81.6	7.14	33.32	10	metabolic	membrane DNA bindi	P04696, F 5411	ENSG000001PNN	14	RNA trans			2	1.138	0.085374729	2.95	864.8	779.1	1.7	5.12	High	High	High	High	High	High	1
FALSE	High	Master Prq C9B7C07-1	TBC1 domi	0	6.054	1	1	2	1	691	79.4	5.67	4.03	1	regulation	cytoplasm; enzyme re	P00566, F 64786	ENSG000001TBC1D15	12		TBC/RABG		4	1.138	0.341863428	21.49	565.4	473.9	17.31	14.81	High	High	High	High	High	High	1
FALSE	High	Master Prq P05187	alkaline ph	0	229.369	58	26	83	9	535	57.9	6.29	208.04	26	metabolic	cell surface catalytic ac	P00345, 2150	ENSG000001ALPP	2	Metabolic	Intra-Golgi		7	1.138	0.961203318	38.13	10939.4	9612.8	18.5	23.02	High	High	High	High	High	High	1
FALSE	High	Master Prq P18754-1	Regulator	0	12.272	12	4	5	4	421	44.9	7.52	6.88	4	cell divisi	chromosor DNA bindi	P00415, F 1104	ENSG000001RCC1	1	Rev-media			9	1.137	0.031922243	1.3	665	580.4	5.01	2.26	High	High	High	High	High	High	1
FALSE	High	Master Prq C9BIV8	Phospholip	0	11.307	10	3	4	3	490	54.7	6.47	5.18	3	metabolic	endoplasm catalytic ac	P00614, F 23646	ENSG000001PLD3	19	Ether lipid	Synthesis c		12	1.137	0.102616291	4.35	753.3	662.2	2.02	8.72	High	High	High	High	High	High	1
FALSE	High	Master Prq C9NKR29	Lymphoid-	0.002	3.761	3	2	2	2	838	97	7.93	2.59	2	cell divisi	membrane catalytic ac	P00176, F 3070	ENSG000001HELLS	10	Apoptosis;			2	1.137	0.133148954	2.06	617.1	574.6	5.75	7.61	High	High	High	High	High	High	1
FALSE	High	Master Prq C9H414	Serine-sp	0	5.318	3	1	2	1	574	65	8.56	4.09	1	metabolic	cytoplasm; catalytic ac	P02902, 26168	ENSG000001SENP3	17	Major pat			4	1.137	0.433018223	13.3	167.4	147.3	20.34	5.13	High	High	High	High	High	High	1
FALSE	High	Master Prq C9TAC12-1	ATP synth	0	5.843	7	2	3	2	328	36.4	7.96	6.94	2	cell organ	mitochond protein br	P06644, 64756	ENSG000001ATP1A1	10				0	1.137	0.592607885	3.87	608.8	574.3	9.05	8.16	High	High	High	High	High	High	1
FALSE	High	Master Prq C104949	Cytochrom	0	17.975	38	4	9	4	82	9.9	10.08	16.55	4	metabolic	membrane catalytic ac	P02939, F 27089	ENSG000001UQC9C	5	Non-alcoh	Electron Tr Respirator		12	1.136	0.0741671	8.49	3340.1	3150.8	5.77	7							

FALSE	High	Master	QC39YN0	slifredize	0	26.37	39	4	4	4	137	14.3	8.19	16.35	4	metabolic	cytoplasm	antioxidant	PI02195	140809	ENSG000001SRXN1	20	Photodyna	1	1.129	0.755807259	27.47	1096	996	12	42.25	High	High	High	High	High	High	1	[R16]		
FALSE	High	Master	QC314320	Protein FA	0	28.145	15	5	7	5	339	40.2	6.83	13.45	5	nucleus	RNA bindi	PI04921	91330	ENSG000001FMSA2	4		0	1.128	0.066785417	25.9	1286.4	1145.9	3.23	3.38	High	High	High	High	High	High	1				
FALSE	High	Master	QC313271	Carbamoyl	0	646.64	59	85	301	81	1500	164.8	6.74	761.59	85	cell differe	cytoplasm	catalytic a	PI00117	19130	ENSG000001CPSA2	2	Nitrogen m	Amino Acid	Urea cycle	12	1.128	0.0384604039	71.3	101584.8	91422.2	11.35	6.44	High	High	High	High	High	High	1	
FALSE	High	Master	QC309NE7-1	E3 ubiquiti	0	17.496	19	6	9	6	303	34.8	5.87	19.27	6	metabolic	cytoplasm	catalytic a	PI00515	F_10273	ENSG000001STUB1	16	Protein prc	Androgen r	Regulation	25	1.128	0.698268752	1.57	2657	2465	22.34	10.77	High	High	High	High	High	High	1	
FALSE	High	Master	QC316298	serine/threo	0	4.831	6	2	2	2	524	5.9	5.91	20.8	2	cell differe	cytosol	catalytic a	PI00149	5532	ENSG000001PP3CB	10	Natural kill	Physiology	Signaling b	52	1.128	0.77686454	3.39	467	50.9	20.18	19.58	High	High	High	High	High	High	1	
FALSE	High	Master	QC343399	Tumor pro	0	45.228	62	9	20	9	206	22.2	5.36	42.98	9	regulation	cytoplasm	protein bin	PI04201	7165	ENSG000001PDS212	20		0	1.127	0.0935050267	3.82	3846.6	3426.8	8.39	3.79	High	High	High	High	High	High	1			
FALSE	High	Master	QC3GNW6-4	Pr-r-mRNA	0	9.896	9	4	4	4	420	46.9	8.54	7.86	4	cell organi	cytoplasm	metal ion	PI00076	F_55696	ENSG000001RBM22	5	Spliceosom	mRNA Spli	5	1.127	0.193588202	9.28	930.3	820.2	9.42	4.78	High	High	High	High	High	High	1		
FALSE	High	Master	QC313895	Bystin [iso	0	6.143	7	3	3	3	437	49.6	8.12	2.81	3	cell differe	cytoplasm	protein bin	PI05291	705	ENSG000001BVL6	6	Major patt		4	1.127	0.35059317	22.85	535.2	474.8	3.74	15.85	High	High	High	High	High	High	1		
FALSE	High	Master	QC3GNK20	395 riboso	0	6.624	8	2	2	2	251	28.4	10.13	2.7	2	cell organi	membrane	RNA bindi	PI00252	5498	ENSG000001MRPL16	11	Ribosome	Mitochond	7	1.127	0.352533482	8.37	107.8	105.8	11.26	6.09	High	High	High	High	High	High	1		
FALSE	Medium	Master	QC3G6972	THO comp	0.01	2.068	6	1	1	1	204	23.7	5.67	0	1	metabolic	cytoplasm	protein bin	PI05615	80145	ENSG000001THOC7	3	RNA trans		10	1.127	0.546875364	12.04	592.6	529.8	7.36	9.86	High	High	High	High	High	High	1		
FALSE	High	Master	QC3T2725-1	TRMT1-like	0	21.535	6	3	4	3	733	81.7	18.8	16.02	3	metabolic		catalytic a	PI02005	F_81627	ENSG000001TRMT1	1		0	1.127	0.68567728	4.46	1011.3	897.2	6.54	9.42	High	High	High	High	High	High	1			
FALSE	High	Master	QC3P0519	Heme oxy	0	60.835	43	10	19	10	316	36	54.1	57.2	10	cellular ho	endoplasm	catalytic a	PI01126	3163	ENSG000001HMOX2	16	CHR_H	Mineral ab		0	1.126	0.197927332	11.1	2271.1	2179.6	17.3	7.3	High	High	High	High	High	High	1	
FALSE	High	Master	QC3Q5621	Beta-actin	0	118.41	21	10	137	2	376	42	5.59	3																											

FALSE	High	Master Pcr Q8BW56	Poly(ADP-ribose) synthase	0	5.466	2	1	1	1	976	111	6.43	4.97	1	metabolic	cytoplasm; catalytic a	P105028	8505, 670	ENG50000 PARG; BPG	10; 6		POLB-Dep	5	1.116	0.709091717	2.13	431.3	417.3	11.6	5.3	High	High	High	High	High	High	1		
FALSE	High	Master Pcr Q14671.3	Isomorph 3	0	39.221	8	7	10	5	1188	126.6	6.84	27.19	7	cell differe	cytosol; protein b	PD0806	9698	ENG50000 PUM1	1			0	1.115	0.238121748	2	572.1	518.5	5.72	2.12	High	High	High	High	High	High	1		
FALSE	High	Master Pcr Q36M20	Protein LSF	0.004	2.655	4	1	2	1	195	21.7	6.74	4.76	1			PI09793	128401.6	ENG50000 LSM12; LSI	17; 8			0	1.115	0.283713314	13.54	345.7	310.1	9.89	12.3	High	High	High	High	High	High	1		
FALSE	High	Master Pcr P50750	Cyclin-dep	0	4.598	7	2	2	2	372	42.8	8.79	2.39	1	cell profile	chromosome	PD00669	1025	ENG50000 CDK9	9	Transcripti	MicroRNA	RNA polyd	35	1.115	0.378192393	21.78	134.9	120.9	21.56	16.7	High	High	High	High	High	High	1	
FALSE	High	Master Pcr Q96136	Cytochrome	0.006	2.349	12	1	1	1	57	6.6	9.55	1.73	1	cell organi	metabolic	PT14880	84987	ENG50000 CXD14	12			9	1.115	0.457598663	8.15	1345	1149.7	3.85	14.3	High	High	High	High	High	High	1		
FALSE	High	Master Pcr P78310.1	Cosackevir	0	11.232	7	2	3	2	365	40	7.56	2.29	2	cell commu	cytoplasm; protein b	PD7679, F	1525	ENG50000 CXADR	21	Viral myoc			6	1.115	0.78726208	16.35	667.5	613.3	24.55	4.79	High	High	High	High	High	High	1	
FALSE	High	Master Pcr Q980Q3	Goli ergo	0	16.455	8	2	2	1	440	46.5	4.5	8.91	2	cell organi	Goli; mem	PD4495, F	64689	ENG50000 CXOPR1	3			COPII (Coal	14	1.115	0.283000244	33.72	229.7	206	23.65	8.11	High	High	High	High	High	High	1	
FALSE	High	Master Pcr Q9HD34	LYR motif	0	4.839	15	1	2	1	91	10.8	10.73	8.07	1	metabolic	mitochond	PD5347, F	57128	ENG50000 LYRM4	6			MT	2	1.114	0.060398077	7.12	1224.4	1095.3	1.62	6.61	High	High	High	High	High	High	1	
FALSE	High	Master Pcr P16070	CDA4 anti	0	47.821	13	9	26	9	742	81.5	5.33	47.47	9	cell organi	cell surface	PD00193	960	ENG50000 CD4	11	ECM-recep	Hepatitis B	Integri	25	1.114	0.14092143	9.18	3159.7	2835.2	11.06	4.55	High	High	High	High	High	High	1	
FALSE	High	Master Pcr Q15007	Pre-mRNA	0	7.68	7	2	2	2	396	44.2	5.19	6.84	2	metabolic	membrane		9589	ENG50000 WTP4	6			Processing	2	1.114	0.332763738	9.4	1022.3	975.1	3.87	9.88	High	High	High	High	High	High	1	
FALSE	High	Master Pcr Q9E435	395 riboso	0	8.634	16	3	4	3	216	24.9	9.29	1.7	3	cell organi	membrane	PD00467	79590	ENG50000 MRPL24	1			Ribosome	2	1.114	0.474960706	32.58	292.3	279.8	30.78	7.33	High	High	High	High	High	High	1	
FALSE	High	Master Pcr P04062	glycosylce	0	19.11	11	4	7	4	536	59.7	7.61	18.76	4	cell comm	membrane	catalytic a	PD2055	2629	ENG50000 GGA4	19	Other glyci		Glycosph	12	1.113	0.36450278	5.31	3126.3	2735.5	5.56	9.17	High	High	High	High	High	High	1
FALSE	High	Master Pcr Q03252	Lamin-B2	0	43.251	21	15	21	10	620	69.9	5.59	30.18	15	membrane	catalytic a	PD00038, F	84823	ENG50000 LMNB2	8	Apoptosis	Gastric car		3	1.113	0.187667217	6.46	4420.1	4080.8	5.86	4.3	High	High	High</					

FALSE	High	Master Prq P26885	Peptidyl-pi	0	14.49	19	2	4	2	142	15.6	9.13	10.43	2	metabolic; endoplasm; catalytic	ai P00254	2286	ENSG00000 FKBP2	11								0	1.102	0.139168773	8.96	2066.1	1874.6	2.18	4.75	High	High	High	High	High	High	1
FALSE	High	Master Prq P43034	Platelet-ac	0	13.449	9	3	5	3	410	46.6	7.37	19.14	3	cell comm; chromosor; catalytic	ai P04000; F5048	ENSG00000 PAFAH1B1	17	Ether lipid	Wnt Signa	COP1-inde					37	1.102	0.22388281	10.81	2190.1	1956.8	7.69	6.42	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q14980.1	nuclear mi	0	109.812	14	25	29	25	2115	238.1	5.78	84.14	25	cell differe; chromosor; protein bi	P04111; F4926	ENSG00000 NUNMA1	11		Ecotomer i	Mitotic Pr					7	1.102	0.393172828	20.61	8684.5	8047.4	25.63	6.74	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q064E4.2	isoform 2	0	177.517	49	28	74	2	653	68.6	7.31	134.95	28	metabolic; nucleus	DNA bindi	P00738; F8880	ENSG00000 UBP1	1							0	1.102	0.406631627	21.48	214.1	221.2	37.24	8.91	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q096K25	Uridine-cyt	0.002	3.641	2	1	1	1	548	61.1	7.36	3.8	1	metabolic; cytoplasm; catalytic	ai P00045; F54963	ENSG00000 UCKN1	20	Metabolic		Pyrimidine				7	1.102	0.419819872	23.52	447.6	406.3	17.06	7.11	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q096H8	Alpha-1,2-	0.002	4.098	2	1	1	1	611	69.8	8.68	3.52	1	metabolic; endoplasm; catalytic	ai P03091	79796	ENSG00000 ALG9	11	N-Glycan	Biosynthe				10	1.102	0.88322171	27.24	274.9	330.4	40.33	18.57	High	High	High	High	High	High	1		
FALSE	High	Master Prq P01802	HLA class I	0	131.685	34	12	41	1	365	40.9	6.99	117.88	12	cell comm; cell surface; protein bi	P00129; F3105; 1009	ENSG00000 HLA-A; LOC	6	CHR_H5	Proteasom	Interferon				25	1.101	0.129646718	7.38	2407.2	2134.7	1.82	9.08	High	High	High	High	High	High	1		
FALSE	High	Master Prq P11166	Solute can	0	16.327	10	3	4	3	492	54	8.72	16.14	3	cell comm; cytoplasm; protein bi	P00083; F6513	ENSG00000 SLC2A1	2	Pathways	Cori Cycle	Lactose sy				33	1.101	0.313095554	15.32	764.5	694.5	26.28	10.38	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q13057	Bifunction	0	52.327	23	9	14	9	564	62.3	6.99	41.15	9	metabolic; cytoplasm; catalytic	ai P01121; F80347	ENSG00000 COASY	17	Metabolic		Coenzyme				7	1.101	0.357443371	8.9	3116.9	2829.9	43.83	0.52	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q10540	Syntaxin-7	0	16.585	20	4	5	4	261	29.8	5.55	9.16	4	cell organ; endosome; protein bi	P005739; F8417	ENSG00000 STX7	6	SNARE int					2	1.101	0.447185317	25.82	452.5	406.4	16.62	3.68	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q32M24.2	isoform 2	0	35.316	11	6	8	6	784	86.4	4.65	26.43	6	metabolic; cytoplasm; DNA bindi	P00738	9208	ENSG00000 URRP1	1					0	1.101	0.489662617	38.91	2204.1	2002.6	5.11	16.98	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q098Q6	MICOS cor	0	9.759	7	1	2	1	235	26.4	8.85	9.13	1	cell organ; cytosol; me	protein bi	P005300	84303	ENSG00000 CHCHD6	2			Cristae for			3	1.101	0.545439489	36.75	251.8	228.8	21.93	15.08	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q098X8-1	Redox-reg	0	31.366	28	5	11	5	229	25.7	8.84	23.92	5	metabolic; cytoplasm; antioxidant	P13911	84293	ENSG00000 FAM213A	10						0	1.101	0.911365255	12.01	1402.4	1273.7	12	9.25	High	High	High	High	High	High	1		
FALSE	High	Master Prq P51114-1	Fragile X r	0	28.978	12	5	10	3	621	69.7	6.15	30.29	5	cell death; cytoplasm; protein bi	P00013; F8087	ENSG00000 FXR1	3	RNA trans		Signalling b				5	1.1	0.211569327	6.95	1927.7	1752.6	1.06	6.41	High	High	High	High	High	High	1		
FALSE	High	Master Prq A4D1E9-1	GTP-bindir	0.001	4.286	4	2	2	2	387	42.9	9.03	3.93	2	metabolic; chromosor; catalytic	ai P00005; F85865	ENSG00000 GTPBP10	10						0	1.1	0.283740223	1.54	279.9	271.1	9.6	5.93	High	High	High	High	High	High	1			
FALSE	High	Master Prq QASPL7	transmeml	0.007	2.307	6	2	2	2	270	31.1	6.83	2	2	metabolic; cytoplasm; catalytic	ai P010520	387521; 38	ENSG00000 TMEM189	20						0	1.1	0.339986624	17.95	259.9	231.7	1.41	15.12	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q00139	Kinesin-iii	0	17.611	4	3	5	2	706	79.9	6.68	8.52	3	cell differe; cytoplasm; catalytic	ai P00225	3796	ENSG00000 KIF2A	5						27	1.1	0.354839761	14.17	1412.5	1283.9	34.2	3.35	High	High	High	High	High	High	1		
FALSE	High	Master Prq P84047	ATP synth	0	47.204	56	9	18	9	213	23.3	9.96	45.34	9	cell organ; membrane; catalytic	ai P00213	539	ENSG00000 ATP5O	21	Oxidative e	Electron Tr	Cristae for			14	1.1	0.390905052	6.04	3341.9	3132.1	2.12	8.69	High	High	High	High	High	High	1		
FALSE	High	Master Prq P31153	S-adenosyl	0	74.201	34	14	33	10	395	43.6	6.48	84.52	14	cell organ; cytosol; catalytic	ai P00438; F4144	ENSG00000 MAT2A	2	Cysteine ar	Trans-sulfi	Methylation			10	1.1	0.490887108	16.58	16459	14967.8	5.68	10.12	High	High	High	High	High	High	1			
FALSE	High	Master Prq P62873	Guanine bi	0	105.523	52	11	30	7	340	37.4	6	106.55	11	cell death; cytosol; me	catalytic	P00400	2782	ENSG00000 GNB1	1	Dopamine	Nicotinic A	G alpha (z)			84	1.1	0.679814108	23.07	5301	4819.2	16.62	5.93	High	High	High	High	High	High	1	
FALSE	High	Master Prq A3KMh1	von Willeb	0.001	4.193	0	1	2	1	1905	214.7	7.4	7.37	1	mitochondr	catalytic	P23078	ENSG00000 VWA8	13						0	1.099	0.010607778	0.91	401.7	365.4	4.02	5.82	High	High	High	High	High	High	1		
FALSE	High	Master Prq P27797	Calreticul	0	241.664	62	24	101	24	417	48.1	4.44	301.23	24	cell differe; cell surface; DNA bindi	P00262	811	ENSG00000 CALR	19	Antigen pri	Androgen	Scavenging			32	1.099	0.018978121	2.14	36738.9	33443.1	1.73	4.03	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q0BTW9	Tubulin-sr	0	26.359	7	6	6	6	1192	132.5	6.19	13.57	6	cell organ; cytoplasm; enzyme re	P121612	6904	ENSG00000 TBCD	17			Post-charge			3	1.099	0.036687604	1.81	741.4	687.2	2.26	2.82	High	High	High	High	High	High	1		
FALSE	High	Master Prq P62241	40S riboso	0	49.004	39	8	27	8	208	24.2	10.32	79.43	8	cell organ; cytoplasm; protein bi	P010201	6202	ENSG00000 RPS18	1	Ribosome	Cytoplasm	Peptide ch			38	1.099	0.153840536	9.49	11654.7	10590.4	2.37	6.08	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q00839	Heterogen	0	350.09	52	49	172	6	825	90.5	6	403.53	49	cell differe; cell surface; DNA bindi	P00622; F3192	ENSG00000 HNRNP1	1	Spliceosom	mRNA Pro	mRNA Spli			6	1.099	0.184558897	1.69	5214.7	4370.4	13.69	5.98	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q0N490-2	isoform 2	0	6.117	12	1	2	1	142	15.4	10.58	6.21	1	metabolic; membrane; catalytic	ai	25953	ENSG00000 PNKD	2						0	1.099	0.199318808	6.13	890.2	737.1	9.93	8	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q0NQR4	Omega-arr	0	41.122	35	9	12	9	276	30.6	7.21	23.49	9	metabolic; cytoplasm; catalytic	ai P00795	56954	ENSG00000 NIT2	3	Alanine, as		Neurotroph			4	1.099	0.199702795	4.34	2983.5	2766.5	3.4	5.84	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q14137	Ribosome	0	51.051	25	11	12	11	746	83.6	6.19	32.11	11	cell organ; nucleus	protein bi	P00400; F23246	ENSG00000 BOP1	8			Major path			4	1.099	0.209250095	3.19	1660.8	1511.3	1.67	8.24	High	High	High	High	High	High	1		
FALSE	High	Master Prq P49790	Nuclear pc	0	55.226	10	11	16	11	1475	153.8	8.73	39.4	11	cell organ; cytosol; me	DNA bindi	P00641; F9972	ENSG00000 NUP153	6	RNA trans	TGF-beta 5	Rev-media			65	1.099	0.245769294	5.05	2689.6	2449.3	4.55	3.16	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q0BT03	Uncharact	0	8.024	4	1	2	1	319	36.6	6.3	3.08	1		P15112	159013	ENSG00000 Cxorf38	X					0	1.099	0.526176967	12.59	243.8	236	13.68	3.6	High	High	High	High	High	High	1			
FALSE	High	Master Prq P62328	Thymosin i	0	97.455	57	11	64	8	44	5.1	5.06	157.51	11	cell differe; cytoplasm; catalytic	ai P01290	7114	ENSG00000 TMS48X	X	Regulation	Barbasase	Platelet de			7	1.099	0.575312003	32.11	11692	11872.1	21.04	12.85	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q72777	39S riboso	0	8.35	19	2	2	2	128	15.1	7.27	3.22	2	cell organ; membrane; structural	P009776	128308	ENSG00000 MRP155	1			Mitochond			6	1.098	0.001302564	0.69	711.1	643.8	1.01	0.81	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q09H96	L2-hydrox	0	17.659	10	4	5	4	463	50.3	8.15	13.04	4	metabolic; membrane; catalytic	ai P01266	79944	ENSG00000 L2HGD3	14	Butanone		Interconve			5	1.098	0.462028336	26.65	1610.8	1693.5	29.48	8.96	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q105031	Probable L	0	15.534	6	4	4	4	903	101.9	8.22	10.63	4	cell organ; mitochondr	catalytic	P00133; F23395	ENSG00000 LARS2	3	Aminoacyl	Amino Acid	Mitochond			6	1.098	0.480523352	1.65	763.2	719.2	6.5	3.55	High	High	High	High	High	High	1		
FALSE	High	Master Prq P31942	Heterogen	0	137.57	64	13	44	12	346	36.9	6.87	118.89	13	cell differe; nucleus; sp	protein bi	P00196; F3189	ENSG00000 HNRNP17	11						0	1.098	0.531095513	25.34	8332.3	7474.2	17.87	1.52	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q0NKR2	39S riboso	0	11.831	21	3	6	3	175	20	10.11	11.41	3	cell organ; membrane; protein bi	P01196	63875	ENSG00000 MRP17	11	Ribosome		Mitochond			7	1.098	0.732746797	44.85	909.5	930.6	25.19	17.87	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q00401	Neural Wn	0	6.538	3	1	1	1	505	54.8	7.93	4.98	1	cell division; cytoplasm; catalytic	ai P00568; F8976; 1429	ENSG00000 WASL	ASB	Regulation	Pathogen	Nephrin fx			37	1.098	0.931024647	13.7	333.1	395.9	23.96	15.12	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q16718	NADH deH	0	32.124	53	6	11	6	116	13.5	5.99	32.01	6	cell organ; membrane; catalytic	ai P004716	4698	ENSG00																							

FALSE	High	Master Prq Q8TE01	Probable g	0	12.012	16	3	5	3	209	23.9	9.35	12.58	3	metabolic; membrane	antioxidan	PD0555, F 493869	ENSG00000 GPX8	5	Thyroid ho	Detoxifica	6	1.092	0.169914909	9.3	463.3	420.1	0.59	8.53	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q60568	Procollagen	0	44.709	22	12	16	12	738	84.7	6.05	37.19	12	cell organ; endoplasm	catalytic ac	P03171, 8985	ENSG00000 PLOC3	7	Other type	Collagen	5	1.092	0.277085227	8.89	3275	2895.9	2.47	8.61	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q0B7A6	Beta-caten	0	31.174	14	9	11	9	563	65.1	5.05	19.7	4	cell death; cytoplasm;	protein bi	P08216, 56259	ENSG00000 CTNNB1	20	Spliceos	NLRN Spli	5	1.092	0.394996548	19.19	2035.2	1933.7	18.61	7.29	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q9H045	Transmem	0.0003	3.343	2	1	1	1	589	67.8	7.21	1.92	1	membrane		P02990, 56889	ENSG00000 TM9SF3	10			0	1.092	0.428807747	22.22	673.4	595.6	21.63	13.62	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q9B7A0	vesicle-ass	0	0.012	8	1	2	1	100	11.4	7.34	4.98	1	cell organ; cytoplasm;	protein bi	P00957, 8673	ENSG00000 RMP68	2	SNARE inte		17	1.092	0.432579459	3.22	1176.8	1148.1	7.84	3.83	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q07960	rho GTPase	0	22.371	17	5	9	5	439	50.4	6.29	21.28	5	regulation; cytoplasm;	enzyme re	P00620, 392	ENSG00000 ARHGAP1	11		Rho GTPase	3	1.092	0.487746847	4.79	4828.9	4424	2.2	8.22	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q60568	delta-1-gly	0	181.652	44	25	61	25	795	87.2	7.12	159.6	25	metabolic; cytoplasm;	catalytic ac	P00017, 15832	ENSG00000 ALDH1B1	10	Metabolic	Amino Acid	8	1.092	0.669746878	5.41	18357	17520.9	6.73	7.39	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q9N294	EH domain	0	15.698	10	5	8	4	543	61.1	6.46	15.28	5	cell organ; cytoplasm;	catalytic ac	P00050, 30846	ENSG00000 HDO2	19	Endocytosi	Insulin Sign Factors inv	4	1.092	0.986358352	0.92	1913.3	1867.5	11.41	6.41	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q04941-1	proteolipid	0	0.5378	9	1	4	1	152	16.7	7.24	14.22	1	regulation; endoplasm	protein bi	P01284, 5355	ENSG00000 PLP2	X			0	1.091	0.150479644	4.82	1874.7	1675.4	4	9.27	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q95168-1	NADH deH	0	10.996	36	4	5	3	129	15.2	9.85	0	4	cell organ; membrane	catalytic ac	P07225, 4710	ENSG00000 NDUF8	1	Oxidative E	Electron Tr Complex I	13	1.091	0.156999555	6.21	236	225.7	7.89	16.07	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq P09622	Dihydrolip	0	107.396	40	14	45	14	509	54.1	7.85	119.85	14	cellular ho	mitochond	catalytic ac	P00070, F 1738	ENSG00000 DLD	7	Metabolic	Fatty Acid	29	1.091	0.164889044	7.16	16885.1	15928.5	5.32	2.5	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q08945	FACT comp	0	58.913	19	13	22	13	709	81	6.87	51.85	13	metabolic; chromosom	DNA bindi	P00505, F 6749	ENSG00000 SRP1	11	Longevity	HIV elonga	24	1.091	0.397501766	3.74	6778.6	6383.4	2.23	6.98	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q9Y4C2-1	TRPM8 ch	0.007	2.239	1	1	1	1	921	102.1	6.54	2.28	1	regulation; membrane	protein bi	P13402, 9747	ENSG00000 FAMP115A	7			0	1.091	0.403189646	20.03	612.5	561.2	17.48	7.94	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq P82932	28S riboso	0	12.525	44	4	5	4	125	14.2	9.26	6.78	4	cell organ; membrane	protein bi	P01250, 64968	ENSG00000 MRP56	21	Ribosome	Mitochond	7	1.091	0.407752718	19.23	961	925.7	35.59	9.43	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q0UVK1	Chondroit	0	37.488	5	8	11	8	2322	250.4	5.47	22.94	8	cell differe; cell surface	protein bi	P00054, F 1464	ENSG00000 CSPG4	15		Spinal Cord A tetrasac	19	1.091	0.462431606	26.86	1098.9	1007	28.54	8.53	High	High	High	High	High	High	High	High	High	1	
FALSE	Medium	Master Prq Q9NKG0-1	Centelin C	0.02	1.612	1	1	2	1	1405	161.5	8.15	4.98	1	cell organ; cytoplasm;	protein bi	P02463, F 54875	ENSG00000 CNTLN	9			0	1.091	0.579005653	28.65	601.6	588.2	4.05	23.28	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q15125	3-beta-hyd	0	12.501	5	1	3	1	230	26.3	7.9	9.8	1	metabolic; endoplasm	catalytic ac	P05241, 10682	ENSG00000 EBP	X	Metabolic	Cholesterol	8	1.091	0.899630786	0.78	703	656.4	9.01	17.65	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q09168-1	HLA class I	0	117.398	36	11	38	2	365	40.9	6.7	104.9	11	regulation; cell surface	protein bi	P00129, F 3105	ENSG00000 HLA-A	6	Proteasom	Interferon	14	1.09	0.399528745	22.06	235.1	212.9	27.58	11.23	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q105027-1	Protein tra	0	41.564	6	9	16	9	2179	233.4	5.63	32.09	9	cell organ; cytosol;eni	protein bi	P112931, F 9919	ENSG00000 SEC16A	9		COPII (Coa	8	1.09	0.465866703	23.26	995.4	913.2	12.77	7.96	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P55789	FAD-linked	0	9.977	18	2	2	2	205	23.4	7.62	4.38	2	metabolic; cytoplasm;	catalytic ac	P04777, 2671	ENSG00000 GFER	16		Mitochond	2	1.09	0.497940898	29.67	420	399.8	28.21	9.48	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q99729-3	Isomorf 3	0	131.442	54	19	68	17	285	30.6	7.91	195.79	19	cell organ; cytoplasm;	DNA bindi	P00076, F 3182	ENSG00000 HNRNPAB	5			2	1.09	0.629921276	3.87	17330.7	16503.3	6.89	5.29	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P17813	Endoglin li	0	31.263	11	6	10	6	658	70.5	6.61	25.66	6	cell differe; cell surface	catalytic ac	P00100, 2022	ENSG00000 ENG	9		Hydrolysis	2	1.09	0.9547117	5.78	2006.7	1886.7	9.15	8.61	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q02218	2-oxogluta	0	171.861	31	26	44	26	1023	115.9	6.86	125.15	26	cellular org cytosol;me	catalytic ac	P00076, F 4967	ENSG00000 OGDH	7	Protophyal	TCA Cycle Lysine cata	17	1.089	0.287797457	14.2	11835.7	10724.7	5	7	High	High	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9NRR5-1	Ubiquitin-L	0	16.642	9	4	8	2	601	63.8	5.22	15.16	4	metabolic; cytoplasm;	protein bi	P00040, F 56893	ENSG00000 UBQLIN4	1	Protein prc		1	1.089	0.30156471	0.48	428.5	396.1	6.84	1.4	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q06737-1	Putative Ri	0	41.759	14	8	10	8	977	107.1	10.08	23.28	8	metabolic; membrane	protein bi	P00076, F 64783	ENSG00000 RBM15	1			0	1.089	0.443203481	24.85	1581.2	1452.3	32.26	9.31	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q09H50	Probable A	0	9.418	2	2	2	2	1430	160.1	8.4	2.98	2	metabolic; cytoplasm;	catalytic ac	P00071, F 64848	ENSG00000 YTHOC2	5			0	1.089	0.462205236	32.36	164.4	151	49.19	8.21	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9BX56	Nucleolar	0.003	3.443	2	1	1	1	441	49.4	9.91	3.33	1	cell division; chromosom	DNA bindi	51203	ENSG00000 NUSAP1	15			0	1.089	0.480739719	28.81	865.4	794.6	28.38	8.75	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q8UI81	Interferon	0	16.305	11	5	5	5	584	61.6	8.18	9.93	5	metabolic; nucleus	catalytic ac	P00097, F 26145	ENSG00000 IRF2B1	19			0	1.089	0.551743078	41.76	313.1	287.5	39.06	13.38	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q0UI70	N-acetyl-D	0	11.12	11	3	3	3	344	37.4	6.24	4.21	3	metabolic; cytosol	catalytic ac	P01869, 55577	ENSG00000 NAGK	2	Metabolic	Synthesis of	8	1.089	0.553853194	42.14	366.4	339.7	40.73	13.13	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q09571	Persulfide	0	31.882	46	6	9	6	254	27.9	6.83	30.22	6	metabolic; cytoplasm;	catalytic ac	P00753, F 23474	ENSG00000 ETHE1	19	Sulfur met	Sulfide oxi	6	1.088	0.024181867	0.23	1167.1	1074.7	4.13	2.12	High	High	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q06A9-1	Isomorf 1	0.006	2.352	11	1	1	1	203	23.4	6.15	2.21	1	cell organ; cytosol;eni	protein bi	P05008, F 143187	ENSG00000 VT1IA	10			0	1.088	0.070010688	0.71	239.6	221.2	6.93	12.29	High	High	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P36776	Lon protea	0	52.412	18	13	18	13	959	106.4	6.39	30.37	13	cell organ; cytosol;me	catalytic ac	P00004, F 30606	ENSG00000 LONP1	19			0	1.088	0.071490928	0.58	2888.1	2653.4	4.97	8.06	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9NYU2-1	UDP-pluco	0	67.337	12	16	22	16	1555	177.1	5.63	49.57	16	metabolic; endoplasm	catalytic ac	P06427, 56886	ENSG00000 UGGT1	2	Protein prc	ER Quality	7	1.088	0.113428869	6.15	3508.7	3357.6	5.5	2.65	High	High	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P14116	Interleukin	0	13.649	13	3	6	3	193	22.3	4.67	58.7	3	cell comm; cytosol;ext	protein bi	P00340, 3606	ENSG00000 IL18	11	Influenza A	Nucleotide Interleukin	25	1.088	0.233064464	11.25	920.4	806.4	5.18	7.86	High	High	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q0G273-1	SRA stem	0	40.632	67	6	19	6	109	12.3	10.24	54.5	6	cell organ; cytoplasm;	protein bi	P00076, F 81892	ENSG00000 SURP	14			0	1.088	0.245371137	1.96	9182.5	8836.3	4.32	3.71	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9H488-1	GDP-fucos	0.003	3.251	3	1	1	1	388	43.9	8.53	3.23	1	metabolic; endoplasm	catalytic ac	P01250, 23509	ENSG00000 POFU1	20	Other type	Pre-NOTO	5	1.088	0.366380073	14.47	501.9	466.7	25.1	6.94	High	High	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9NQC3-1	Isomorf 2	0	48.57	21	6	17	6	373	40.3	4.78	49.47	6	cell death; endoplasm	protein bi	P02453, 57142	ENSG00000 RTN4	2		Spinal Cord	1	1.088	0.567349654	10.87	6394.7	5891.3	2.1	10.49	High	High	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P07866	Beta-hexo	0	13.601	8	4	4	4	556	63.1																													

FALSE	High	Master Prq Q9H4K7	Mitochondr	0	7.182	5	2	3	2	406	43.9	9.45	4.24	2	metabolic; membrane catalytic a	P00025, P 26164	ENSG000001	GTPBP5; N 20						0	1.082	0.524699683	24.15	1009.5	933.2	9.56	7.85	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P00040-1	Endoplasm	0	86.356	53	14	42	14	261	29	7.31	90.79	14	metabolic; cell surface catalytic a	P070479, F 10961	ENSG000001	ERP29	12	Protein prc				1	1.082	0.568462363	18.33	11963.5	11055.6	12.35	2.78	High	High	High	High	High	High	1	
FALSE	High	Master Prq P12004	Neural cell	0	68.627	15	16	23	16	1257	139.9	6.24	45.28	16	cell differe cell surface protein br	P000041, F 3897	ENSG000001	LCAM	1	Cell adhesi	Basigin int		11	1.082	0.13976742	2.54	7220	6677.4	5.88	1.62	High	High	High	High	High	High	1		
FALSE	High	Master Prq P98008	Mucin-SAC	0	10.99	1	4	4	4	5654	585.2	7.02	6.26	4	metabolic; cytoplasm; protein br	P000094, F 4586	ENSG000001	MUC5AC	11; CHR_H	Defective c		15	1.081	0.306660037	9.57	267	247	23.21	6.14	High	High	High	High	High	High	1			
FALSE	High	Master Prq P00390	Glutathion	0	24.439	13	4	7	4	522	562	8.5	12.94	4	cellular ho cytoplasm; antioxidant	P000070, F 2936	ENSG000001	GSR	8	Glutathion	Glutathion	Detoxificat	13	1.081	0.479690747	28.01	1283.1	1246.4	34.86	8.6	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q5V752	Regulation	0	12.441	4	3	4	3	1461	155.9	7.42	7.25	3	metabolic; cytoplasm; catalytic a	P04018, F 23248	ENSG000001	PPR02	1		RNA polye		3	1.081	0.495808069	40.5	935.2	935.2	60.63	9.43	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q60318	Germinall	0.004	2.793	1	1	1	1	1980	218.8	6.39	3.38	1	transport; cytoplasm; catalytic a	P03999, F 8888	ENSG000001	MCN3AP	21				0	1.081	0.949066538	6.76	333.3	340.7	17.23	6.52	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q9V935	Acyl-coen	0	24.639	16	7	15	7	439	49.9	8.6	35.25	7	metabolic; mitochondr catalytic a	P03061, F 23597	ENSG000001	ACOT9	X		Mitochondr		4	1.081	0.971356255	13.33	4981.3	4744.3	22	1.92	High	High	High	High	High	High	1		
FALSE	High	Master Prq P06730	Eukaryotic	0	8.341	10	2	4	2	217	25.1	6.15	8.48	2	defense re cytoplasm; protein br	P01652, F 1977	ENSG000001	EIF4E	4	HIF-1 signa	Translatior	SG15 anti	45	1.08	0.056426775	3.5	718.2	680.9	4.49	7.22	High	High	High	High	High	High	1		
FALSE	High	Master Prq P06831	PRA1 fami	0	13.542	16	2	3	2	178	19.2	9.19	7.58	2	transport; endosome	P01308, F 11230	ENSG000001	GRAM7	X				0	1.08	0.579153542	9.33	2118.1	1970.7	5.17	6.66	High	High	High	High	High	High	1		
FALSE	High	Master Prq P63172	Dynein lig	0	6.319	16	1	1	1	113	12.4	5.08	6.12	1	cell divisio cytoplasm; catalytic a	P03645, F 6993	ENSG000001	DYNL1T	6		Neutrophil		3	1.08	0.715833522	42.66	107	98	23.48	7.76	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q04724	Transducir	0	27.025	7	3	4	1	770	83.1	7.24	11.7	3	developm cytosol;nu protein br	P00400, F 7088	ENSG000001	TLE1	9		Notch Sign	NOTCH1 ir	11	1.08	0.872209052	25.26	430.6	398.7	28.74	8.24	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q99638	cell cycle c	0	5.924	6	1	1	1	391	42.5	5.66	3.01	1	metabolic; cytoplasm; catalytic a	P04139, F 5883	ENSG000001	RAD9A	11		Androgen	G2/M DNA	26	1.08	0.940377755	24.39	123.3	119.2	22.44	11.78	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q96IR7	4-hydroxy	0	16.292	11	3	4	3	371	39.4	7.03	13.71	3	metabolic; cytoplasm; catalytic a	P112681, F 84842	ENSG000001	HPDL	0				0	1.079	0.035367946	2.02	2727.1	2516.4	2.88	5.37	High	High	High	High	High	High	1		
FALSE	High	Master Prq P62140	Serine/thr	0	76.16	53	14	27	4	327	37.2	6.19	91.2	14	cell divisio cytoplasm; catalytic a	P00149, F 5500	ENSG000001	PP1CB	2	Insulin sig	Common P	Triglycerid	43	1.079	0.337822024	6.43	2127	2082.3	5.76	5.76	High	High	High	High	High	High	1		
FALSE	High	Master Prq P13984	General tr	0	4.839	13	2	2	2	249	28.4	9.23	2.81	2	metabolic; cytoskelet catalytic a	P002270, F 2963	ENSG000001	GTZF2F	13	Basal trans	Eukaryotic	Signaling b	56	1.079	0.358892973	15.27	530.8	496.7	2.35	15.5	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q15631-1	Translin [c	0	29.58	33	8	12	8	228	26.2	6.44	31.18	8	metabolic; cytoplasm; catalytic a	P01997, F 7247	ENSG000001	TSN	2		Small inter		3	1.079	0.47067636	2.07	5340.5	5270.7	5.31	5.13	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q00169	Phosphati	0	9.289	16	3	4	2	270	31.8	6.55	4.2	3	cell organi cytoplasm; transport	P002121, F 5306	ENSG000001	PITPNA	17		Gene and		9	1.079	0.555172261	50.5	168.2	171.1	59.67	15.98	High	High	High	High	High	High	1		
FALSE	High	Master Prq P12004	proliferati	0	101.689	50	11	39	11	261	28.8	4.69	116.79	11	cell differe nucleus catalytic a	P00705, F 5111	ENSG000001	PCNA	20	HTLV-1 infe	Cell Cycle	Translatio	80	1.079	0.604705403	1.05	13122.4	12077.4	9.13	0.87	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q15526	Surfeit lo	0	10.139	9	1	1	1	300	33.3	9.6	5.18	1	cell organi membrane catalytic a	P002104, F 6834	ENSG000001	SURF1	9; CHR_H	Electron Tr	TP53 Regu	11	1.079	0.975866396	26	146.8	136	17.36	10.67	High	High	High	High	High	High	1			
FALSE	High	Master Prq P09493-3	Isomorf 3	0	59.065	38	16	32	3	284	32.9	4.78	49.22	16	cell organi cytoplasm; protein br	P00261, F 7168	ENSG000001	TPM1	15		Striated M		1	1.078	0.09159197	1.26	2415.9	2256.4	1.79	4.54	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q13310-3	Isomorf 3	0	133.138	30	22	54	11	660	72.3	9.35	148.45	22	coagulation cytoplasm; protein br	P00076, F 8761	ENSG000001	PABPC4	0				0	1.078	0.210507686	9.09	3947.7	3533.8	2.34	9.15	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q8WT72	Nucleoel	0	16.355	7	4	6	4	800	92.5	9.17	16.23	4	cell differe mitochondr RNA bindi	P00314, F 64138	ENSG000001	NOC1L	10				0	1.078	0.237691348	6.38	1395.3	1252.9	11.01	2.69	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q14802	DNA-direc	0	8.817	4	3	3	3	1390	155.5	8.48	5.97	3	3 defense re cytosol;nu catalytic a	P00623, F 11128	ENSG000001	POLR3A	10		Purine met	RNA Poly	18	1.078	0.239629794	7.58	307.3	285.1	26.17	10.22	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q08170	Serine/arg	0	26.787	15	8	12	4	494	56.6	11.52	17.97	8	metabolic; nucleus protein br	P00076, F 6429	ENSG000001	SRSF4	1		Spliceosom	mRNA Pro	Cleavage o	14	1.078	0.169136139	10.21	1546.4	1367.4	32.1	9.04	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q92974	Rho guanin	0	10.821	4	4	6	4	986	111.5	7.27	6.76	4	cell divisio cytoplasm; metal ion	P000130, F 9181	ENSG000001	ARHGGEF	1		Pathogeni	Pathogeni	G alpha 1	13	1.078	0.405826868	16.93	1125.9	1003.3	4.34	12.48	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q8BKT5	RNA-bindi	0	4.904	2	2	2	2	1001	118	6.81	2.22	2	protein br	P00076, F 389677	ENSG000001	RAM12B	8				0	1.078	0.530609728	38.22	608.4	657.3	47.49	9.83	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q9Y4E1	WASH cor	0	16.882	4	3	3	3	1318	144.6	4.79	6.88	3	3 regulation cytosol;eni protein br	P115255, F 253725	ENSG000001	FAM121C, V	10	Endocytos			1	1.078	0.570655979	39.88	776.4	793.2	39.92	8.04	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q92879	CUGBP El	0	46.189	11	5	11	5	486	52	8.46	32.89	5	cell organi cytoplasm; protein br	P00076, F 10658	ENSG000001	CLF1	11		Adipogene		2	1.078	0.643962249	21.97	4654.2	4317.8	15.96	1.98	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q96H79	Zinc finger	0	17.579	14	3	3	3	300	32.9	8.13	10.41	3	3 cytosol metal ion	92092	ENSG000001	ZC3HAV1	7				0	1.078	0.718410508	25.06	1685.9	1373.3	15.17	27.51	High	High	High	High	High	High	1		
FALSE	High	Master Prq P49406	39S riboso	0	15.081	20	4	4	4	292	33.5	9.5	8.25	4	cell organi membrane structural	P01245, F 9801	ENSG000001	MRPL19	2		Ribosome	Cytoplasm	Mitochondr	8	1.078	0.790402254	6.09	286.2	264.2	5.01	13.39	High	High	High	High	High	High	1	
FALSE	High	Master Prq P47914	60S riboso	0	37.403	30	6	19	6	159	17.7	11.66	39.77	6	cell organi cytosol;nu protein br	P017179, F 6159	ENSG000001	RP129	3		Ribosome	Cytoplasm	Peptide ch	34	1.077	0.16217416	5.42	6448.9	5974	3.06	11.13	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9Y265	RuvB-like 1	0	78.962	35	11	22	11	456	50.2	6.42	7.6	11	cell divisio cytoplasm; catalytic a	P00004, F 8607	ENSG000001	XR82	3		Wnt signal	Gastric Car	Ub-specific	25	1.077	0.199305713	2.69	8400.9	8001.8	4.09	1.93	High	High	High	High	High	High	1	
FALSE	High	Master Prq P51116	Fragile X n	0	30.91	12	7	10	5	673	74.2	6.32	27.01	7	7 regulation cytoplasm; protein br	P00013, F 9513	ENSG000001	FMR1	17		RNA trans		1	1.077	0.23915268	7.57	2052.6	1906.2	15.2	4.81	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q6PU02	Neutral ch	0	7.373	6	2	3	2	408	45.8	7.23	10.85	2	metabolic; endoplasm catalytic a	P00135, F 57552	ENSG000001	NCEH1	1		Bile secret		5	1.077	0.253186644	8.87	575.7	523.1	10.67	1.52	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q43395	U4/U6 sm	0	21.863	12	8	10	8	683	77.5	9.5	17.34	8	cell organi cytosol;nu protein br	P010480, F 9129	ENSG000001	PRPF3	1		Spliceosom	mRNA Pro	mRNA Spli	6	1.077	0.476334717	26.68	2397.2	2226.1	27.57	6.04	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q92597	Protein NC	0	27.729	14	3	4	3	394	42.8	5.82	12.67	3	cell organi cytoplasm; protein br	P00561, F 10397	ENSG000001	NRDGL1	6		VEGA-VEE	TP53 regul	7	1.077	0.510525998	10.75	959.6	1028.4	14.37	10.13	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q8N3U4-1	Cohesin su	0	20.086	5	4	5	4	1231	141.2	5.43	12.28	4	cell divisio chromosor protein br	P000670, F 10735	ENSG000001	STAG2	X	Cell cycle	Meiotic sy		21	1.077	0.515497112	45.57	406.8	377.7	61.3	16.59	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q105504	nucleosori	0.003	3.2	3	1	1	1																														

FALSE	High	Master Prq	P36542-1	ATP synth	0	62.529	37	11	33	11	298	33	9.22	51.43	11	cell organ	membrane catalytic	at	P00231	509	ENSG000001	ATP5CL	10	Huntington Electron Tr	Cristate for	13	1.072	0.963544739	10.14	10410.1	10036.9	17.8	1.98	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q94874-1	E3 UFM1- c	0	15.299	10	7	9	7	794	89.5	6.79	13.6	7	cell differe	cytoplasm; catalytic	at	P09743	23376	ENSG000001	UFL1	6	Antigen pr		4	1.071	0.038765397	1.09	2344.4	2204.7	4.3	2.15	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q09446	Golgi phos	0	30.413	23	6	7	6	298	33.8	6.44	23.94	6	cell organ	cytosol;eni	protein bi	P05719	64083	ENSG000001	GOLPH3	5	Transcripti		1	1.071	0.139664771	2.92	3143.6	2993.5	8.11	2.79	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	P05556-1	Integrin be	0	115.766	27	18	47	18	798	88.4	5.39	132.34	18	cell differe	cell surface enzyme re	at	P00084	3688	ENSG000001	TG61	10	Arrhythm	Integrin-m	Integrin ce	74	1.071	0.155914848	6.29	19419.5	18014.9	1.42	5.34	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	P15529-2	Isolform B	0	42.207	18	9	20	9	399	44.2	6.39	43.35	9	defence re	cell surface catalytic	at	P00084	4179	ENSG000001	CD46	1	Complexe		1	1.071	0.229795741	0.28	7306.5	6961.5	1.75	4.67	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q08709	Protein cal	0	4.732	6	2	2	2	278	30.7	5.49	4.83	2	defence re	endoplasm	protein bi	P11938	10695	ENSG000001	CNPY3	6	Trafficking		4	1.071	0.420009664	17.58	626.8	585.3	39.17	12.54	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q60115-1	Pre-mRNA	0	10.566	7	3	3	3	594	66.5	5.59	5.9	3	metabolic	nucleus	protein bi	P05182	81608	ENSG000001	PP1L1	6	mRNA sur	mRNA 3'-e	15	1.071	0.469835818	55.8	195.3	182.4	111.21	30.32	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q08C22-1	Temin-3 [C	0	40.832	7	6	8	6	1445	155.2	6.81	26.56	6	cellular co	cytosol	protein bi	P00017	64759	ENSG000001	TNE3	7	MET inter		5	1.071	0.528279968	23.54	2168.3	1935.7	13.01	14.47	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q15564-1	thyroid re	0	30.978	18	5	7	5	476	50.3	7.37	24.19	5	cell organ	cytoplasm; metal ion	at	P00412	7205	ENSG000001	TRIP6	7	NOD-like r		1	1.071	0.637856161	17.84	1341.1	1251.7	21.05	5.43	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q14318-2	Isolform 2	0	14.025	10	4	5	4	413	44.6	4.84	8.9	4	cell death;	cytoplasm; catalytic	at	P00254	23770	ENSG000001	KFBP8	19	Senescenc		1	1.071	0.728458886	7.81	418.1	390.4	4.22	7.58	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q9H299	Sodium-co	0	7.971	6	3	4	3	487	54	7.02	5.15	3	transport	membrane	protein bi	P01490	81539	ENSG000001	SLC38A1	12	GABAergic	Synaptic V	Amino acid	11	1.07	0.06087674	3.17	377.3	349.5	10.02	7.86	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q13421	mesotheli	0	12.529	9	5	6	5	630	68.9	6.38	8.95	5	metabolic	cell surface	protein bi	P06060	10232	ENSG000001	MSLN	16	Post-transl		0	1.07	0.064573416	3.93	838.5	791.8	4.72	3.94	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q13283	Ras GTPas	0	61.753	32	9	18	9	466	52.1	5.52	61.9	9	metabolic	cytoplasm; catalytic	at	P00076	10146	ENSG000001	G3BP1	5			0	1.07	0.088346638	3.21	4775.7	4662.1	3.13	4.02	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	P51659-1	peroxisom	0	113.656	32	18	28	18	736	79.6	8.84	85.75	18	cell differe	membrane catalytic	at	P00106	73295	ENSG000001	HSD17B4	5	Peroxisom	Steroid Bi	Beta-oxida	16	1.07	0.195164069	6.89	7928.3	7864.9	12.03	8.05	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q9BTV4	Transmem	0	18.541	14	5	9	5	400	44.8	8.13	18.31	5	cell organ	endoplasm	protein bi	P07787	79188	ENSG000001	TMEM43	1			0	1.07	0.211864586	1.16	1195.3	1117	8.75	4.58	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q9247-1	Glutaryl-Co	0	42.199	8	11	13	11	1726	198.9	4.91	30.39	11	cell organ	nucleus	DNA bindi	P00017	76830	ENSG000001	SUPT6H	17		Formation		5	1.07	0.27894746	5.33	2326.5	2215.2	18.53	3.49	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q92947-1	GRAP1- assoc	0	17.408	9	2	3	2	438	48.1	8.06	15.68	2	metabolic;	mitochondr	catalytic	at	P00441	7639	ENSG000001	GCDH	19	Lysine deg	Fatty Acid	Lysine cata	10	1.07	0.328236682	9.04	1236.1	1230.5	20.6	5.29	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	P41328	GRIP1- assoc	0	5.799	2	2	2	2	841	95.9	5.11	4.2	2	transport	cytosol;eni	protein bi	Q9V3P1	X					0	1.07	0.483484762	18.88	858.2	770	8.59	10.58	High	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq	P15130-3	Isolform 3	0	59.295	25	14	20	14	637	68.7	5.33	49.15	14	cell organ	cytosol	catalytic	at	P00009	2935	ENSG000001	GSP1	16			0	1.07	0.519305276	24.59	7644.4	7462.5	20.8	6.18	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q15213	WD repeat	0	6.163	2	1	1	1	610	68	9.67	3.32	1	metabolic	nucleus	protein bi	P00400	9277	ENSG000001	WDR46	4			5	1.07	0.78477032	30.64	277.8	265.4	15.61	10.08	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	P12270	Nucleopor	0	292.356	32	62	94	62	2363	267.1	5.02	226.58	62	cell divisi	chromosom	catalytic	at	P00038	71175	ENSG000001	TPR	1	RNA trans		69	1.069	0.036550045	0.97	25602.1	24105.2	4.57	2.86	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	P62834	ras-related	0	63.548	61	10	24	3	184	21	6.67	6.39	10	cell organ	cytoplasm; catalytic	at	P00009	5906	ENSG000001	RAP1A	1	Renal cell	Integrin-m	Signaling b	67	1.069	0.28896404	0.13	1460.6	1378.1	6.5	2.94	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q04206	Transcript	0	21.81	9	4	6	4	551	60.2	5.68	14.75	4	defence re	cytoplasm; DNA bindi	P00554	5970	ENSG000001	RELA	11	Epstein-Ba	Androgen	C/EBTA/Int	153	1.069	0.445595042	16.82	1048.9	981.5	6.27	5.82	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q095721	Synaptosom	0	10.549	12	2	2	2	258	29	5.81	6.73	2	cell organ	cytoplasm; protein bi	P00835	9342	ENSG000001	SNAP29	22	SNARE int	Intra-Golgi		8	1.069	0.494228433	37.79	47.7	44.6	57.66	13.37	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q095372	acyl-prote	0	24.111	31	5	6	5	231	24.7	7.23	19.15	5	cellular co	cytoplasm; catalytic	at	P00561	71133	ENSG000001	LYPLA2	4	Glyceroph		4	1.069	0.536931188	23.48	704.6	648.7	12.13	12.62	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q093N1	Thioredoxin	0	21.915	19	5	6	5	280	31.8	4.98	10.55	5	cellular ho	endoplasm catalytic	at	P00805	81542	ENSG000001	TMX1	14			0	1.069	0.554053068	15.97	2268.9	2225.2	12.69	2.96	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	P78406	mRNA exp	0	78.589	38	10	19	10	368	40.9	7.83	65.09	10	cell divisi	cytoplasm; protein bi	P00400	8480	ENSG000001	RAE1	20	RNA trans		65	1.069	0.897820512	2.26	4135.5	3960.1	9.5	2.43	High	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq	Q946A6	Synapse-ai	0	21.159	17	4	5	4	352	39.9	4.53	15.63	4	cytosol;Go	protein bi	P03099	94056	ENSG000001	SYAP1	X			0	1.068	0.73610847	3.65	1704.4	1581.6	1.53	26.33	High	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq	Q9NR92	COX assem	0.001	4.236	20	2	6	2	79	9.5	7.87	10.2	2	mitochond		P08583	56942	ENSG000001	CSMC2	16			2	1.068	0.077940422	1.51	1657.7	1466.8	4.22	4.54	High	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq	Q09Y49	U6 snRNA	0	9.01	32	2	3	2	91	9.9	4.54	8.18	2	metabolic	cytosol;nu	protein bi	P01423	23658	ENSG000001	LSM2	7	RNA degra	mRNA Spli		8	1.068	0.995843928	2.19	3346.3	3134.6	2.97	0.19	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q08X29	Lipolysis-st	0	10.943	6	3	3	3	649	71.4	7.97	3.34	3	regulation	membrane		P00070	51599	ENSG000001	LR8	19	VDLJ clear		5	1.068	0.237165726	5.36	501.9	436.7	5.81	9.32	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q13838-1	spliceosom	0	104.378	45	16	44	7	428	49	5.67	11.049	16	cell organ	cytoplasm; catalytic	at	P00270	7919	ENSG000001	XDR3	6	CHR_H5	mRNA sur		13	1.068	0.288878439	11.18	5577.5	4807.7	9.15	6.19	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	P49792	E3 SUMO-	0	209.055	24	53	76	37	3224	358	6.2	144.85	53	cell organ	cytoplasm; catalytic	at	P00160	5903	ENSG000001	RANBP2	2	RNA trans		77	1.068	0.292620668	10.24	9044.2	8470.2	6.42	4.47	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	P20700	Lamin-B1	0	108.579	48	29	47	24	586	66.4	5.16	80.5	29	cell organ	membrane catalytic	at	P00038	74001	ENSG000001	LMNB1	5	Apoptosis	Fas Ligand	Gene and i	34	1.068	0.300564777	11.33	6242.2	6050.8	11.92	4.26	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q00341	Lysine-spe	0	43.887	19	10	11	10	852	92.8	6.52	29.6	10	cell organ	nucleus	catalytic	at	P01366	23028	ENSG000001	KDM1A	1	Androgen	Activated f		16	1.068	0.320390009	9.01	1764.1	1613.4	4.48	7.57	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q07065	Cytoskelet	0	125.067	43	24	44	23	602	66	5.92	111.57	24	metabolic	cytoplasm; RNA bindi	P01366	10970	ENSG000001	CKAP4	12																						

FALSE	High	Master PrC P11233	Ras-relate	0	25.791	33	7	13	4	206	23.6	7.11	20.3	7	cell division	cell surface catalytic ac	P00025, F 5898	ENSG000001 RALA	7	Rap1 signal RALA down	Translocat	22	1.064	0.762175809	2.17	2421.9	2308.7	7.1	2.19	High	High	High	High	High	High	High	1	
FALSE	High	Master PrC P08559	Pyruvate d	0	54.935	41	18	31	18	390	43.3	8.06	44.74	18	metabolic	mitochondr catalytic ac	P000676, 5160	ENSG000001 PDHA1	X	Carbon me	TCA Cycle	Regulation	22	1.064	0.80963084	0.41	10093.2	9717.8	10.56	5.09	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q09287	Succinate-	0	54.036	30	12	21	12	463	50.3	7.42	45.33	12	metabolic	mitochondr catalytic ac	P000549, F 8803	ENSG000001 SUCLA2	13	Metabolic		Ub-signal	22	1.064	0.063751276	1.77	9701.5	9239.5	6.55	4.6	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q04826	Mitochond	0	111.873	43	21	38	21	608	67.4	7.12	94	21	cell comm	membrane protein br	P000515, F 9868	ENSG000001 TOMM70M	34				7	1.063	0.135096392	0.71	16490.4	15509.9	9.26	4.05	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q70199-1	Protein un	0	20.818	8	5	5	5	1090	123.2	6.65	13.01	5	defense re	cytoplasm; protein br	P000168, F 201294	ENSG000001 UNC130	17		Deregulate	Neutrophil	4	1.063	0.23455524	4.56	462.3	423.1	6.41	5.82	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q09180-1	SUMO-acti	0	57.941	55	14	17	14	346	38.4	5.3	43.54	14	metabolic	cytoplasm; catalytic ac	P000899	ENSG000001 SAE1	19	Ubiquitin r	SUMO is ci		7	1.063	0.282946594	9.2	3770.6	3561.3	7.82	2.24	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q07AE8	Growth an	0	10.499	14	2	3	2	222	25.4	10.02	3.97	2	cell organ	mitochondr protein br	P101147	ENSG000001 GAD60A5G	19				6	1.063	0.342371191	12.04	1350.5	1276.2	5.92	3.23	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q062U8	Protein FA	0	10.932	10	3	3	3	254	28.9	5.45	2.84	3	nucleus	protein br	P101887	ENSG000001 FAM193A	16				0	1.063	0.441514124	16.85	482.4	453.8	8.58	11.31	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q15343	NEDD8 [O	0	10.512	43	4	9	4	81	9.1	8.43	6.78	4	cellular ho	cytosol;nuo	P00240, F 4738	ENSG000001 NEDD8	14		EGF/EGFR	Cargo reco	16	1.063	0.57395125	29.42	2710.2	2587.7	24.69	5.53	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q09115	Transgelin	0	10.315	18	3	5	2	199	22.5	7.33	3.64	3	regulation	nucleus	P003007, F 29114	ENSG000001 TAGLN3	13				0	1.063	0.926473065	30.52	889.8	1029.5	29.88	16.08	High	High	High	High	High	High	High	1
FALSE	High	Master PrC P21281	V-type pro	0	62.02	34	10	15	10	511	56.5	5.81	58.85	10	cellular ho	cytoplasm; catalytic ac	P00006, F 526	ENSG000001 ATP6V1B2	8	Metabolic	Transferrin		20	1.063	0.944338542	2.57	2411	2403.1	5.78	8.72	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q08225-1	Isform 1	0	12.673	9	3	4	3	438	49.5	6.46	7.14	3	cell death;	cytoplasm; protein br	P005918	ENSG000001 APIS	11				0	1.063	0.966902064	13.8	271.4	257.1	12.28	6.65	High	High	High	High	High	High	High	1
FALSE	High	Master PrC P52294	Importin s	0	30.544	16	6	10	3	538	60.2	5.01	30.59	6	metabolic	cytoplasm; protein br	P005514, F 3836	ENSG000001 KPN1A	1	Influenza A	Integration		25	1.062	0.038183798	1.22	651.4	592.9	7.69	7.39	High	High	High	High	High	High	High	1
FALSE	High	Master PrC P00533-1	epidermal	0	128.756	25	22	36	22	1210	134.2	6.68	109.77	22	cell organ	cell surface catalytic ac	P000609, F 1956	ENSG000001 EGFR	7	Breast can	Androgen	EGFR inter	115	1.062	0.172477182	1.65	8881.2	8592.2	2.83	2.23	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q075438	NADH deH	0	9.049	19	1	5	1	58	7	8.92	14.77	1	cell organ	membrane catalytic ac	P008040	ENSG000001 NDUF81	14	Alzheimer'	Electron Tr	Complex I	13	1.062	0.188608988	3.63	1610.2	1604.5	9.35	7.79	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q15479	Melanoma	0.001	4.51	6	3	3	2	319	35.3	8.76	0	3	metabolic	protein br	P014454	ENSG000001 MAGEB2	X				0	1.062	0.208156731	1.59	72.6	69.1	8.89	21.73	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q06623	Ceramide	0	12.755	12	3	5	3	380	44.8	8.98	5.18	3	metabolic	endoplasm catalytic ac	P03798	ENSG000001 CER2S	2	SpHINGolip	SpHINGolip	SpHINGolip	8	1.062	0.346855746	12.11	1628.2	1476.4	8.32	4.89	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q09N24	H/ACA ribc	0	34.134	41	3	10	3	153	17.2	8.22	36.92	3	cell organ	nucleus	P012148	ENSG000001 NHP2	5	Ribosome		SpHINGolip	10	1.062	0.347481102	12.44	1326	1253.8	25.1	10.89	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q09UBT	SUMO-acti	0	44.947	22	12	15	12	640	71.2	5.29	31.72	12	metabolic	cytoplasm; catalytic ac	P000899, F 10054	ENSG000001 UBR2	19	Ubiquitin r	SUMO is ci		7	1.062	0.37894619	11.69	5308.1	4968.3	13.89	8.74	High	High	High	High	High	High	High	1
FALSE	High	Master PrC P01116-2	Isform 2B	0	27.003	52	6	7	3	188	21.4	8.21	20.74	6	cell comm	cytoplasm; catalytic ac	P000009, F 3845	ENSG000001 KRA2	12		IL-5 Signa		21	1.062	0.422925264	15.99	1453.9	1368.5	18.11	5.46	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q15067	Phosphori	0	54.591	12	11	15	11	1338	144.6	5.76	39.84	11	metabolic	cytoplasm; catalytic ac	P00586, F 5198	ENSG000001 PFAS	17	Purine met	Purine ribc		6	1.062	0.487995506	18.04	3812.4	3550	10.4	8.48	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q06P11-1	Probable 2	0	20.185	13	4	5	4	429	46.7	8.62	14.08	4	metabolic	nucleus	P011189	ENSG000001 NSUN5	5				0	1.062	0.50097537	25.4	1327.5	1269.2	29.85	5.27	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q09447-1	ethanolam	0	9.395	7	2	2	2	389	43.8	6.92	0	2	metabolic	membrane catalytic ac	P01467	ENSG000001 PCYT2	17	Metabolic	Kennedy p	Synthesis c	9	1.062	0.58833224	49.43	572.8	662.2	58.23	15.14	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q06HY6-1	DORRG do	0	25.44	18	4	6	4	314	35.6	5.12	17.24	4	regulation	cytoplasm; protein br	P097956	ENSG000001 DORRGK1	20				0	1.061	0.081122754	0.26	1896.6	1807.7	4.12	2.64	High	High	High	High	High	High	High	1
FALSE	High	Master PrC P31948	stress-indu	0	191.131	65	39	106	39	543	62.6	6.8	175.27	39	response t	cytoplasm; protein br	P005515, F 10963	ENSG000001 STP1	11	Prion disea	HSPP90 cha		4	1.061	0.418334168	4.18	27919.4	26808.6	6.81	1.6	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q08TCA-1	NEDD8-act	0	36.812	17	5	8	5	463	51.8	5.45	23.34	5	metabolic	cytoplasm; catalytic ac	P000899, F 9039	ENSG000001 UBR2	13	Ubiquitin r	NIK--nonn		15	1.061	0.515380276	24.36	2682.2	2527.8	23.44	9.34	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q09Y282-1	Endoplasm	0	10.808	7	3	3	3	383	43.2	6.06	2.21	3	transport	endoplasm	P07970, F 51614	ENSG000001 ERGIC3	20				0	1.061	0.68694813	25.3	809.5	763	8.32	9.82	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q06AC1	Fermitin fu	0	19.791	5	3	5	3	680	77.8	6.7	15.12	3	cell organ	cell surface protein br	P001609, F 10979	ENSG000001 FERMT2	14		Cell-extrac		3	1.061	0.940948028	13.95	1050.8	1003.2	12.29	6.12	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q095Y4	Coiled-coil	0	12.279	28	2	2	2	110	12.4	6.73	5.9	2	cell organ	mitochond	P06747	ENSG000001 CHCHD5	2		Mitochond		2	1.061	0.989232044	1.52	251.2	252.7	6.32	6.57	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q095456	Proteasom	0	8.498	11	3	4	3	288	32.8	7.17	9.99	3	cell organ	cytoplasm; protein br	8624	ENSG000001 PSMG1	21				0	1.06	0.094419621	4.63	1352.6	1286.9	2.91	0.92	High	High	High	High	High	High	High	1
FALSE	High	Master PrC P61421	V-type pro	0	23.658	17	5	6	5	351	40.3	5	18.12	5	cell organ	endosome; catalytic ac	P01992	ENSG000001 ATP6V0D1	16	Collecting c	Transferrin		26	1.06	0.213166531	4.36	2838	2646.6	7.73	2.91	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q09K8-1	Methionin	0	19.16	7	4	5	4	725	80.4	6.49	12.75	4	metabolic	cytoplasm; catalytic ac	P000175, F 4552	ENSG000001 MTRR	18		Vitamin B1	Defective f	18	1.06	0.288990057	9.43	2043.7	1927.2	4.79	4.59	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q09N282-1	Constitut	0	37.647	9	7	7	7	1118	121.8	8.88	23.88	7	cytoplasm;	RNA bindi	23196	ENSG000001 FAM120A	9				0	1.06	0.477914066	22.28	2998.5	2879.3	29.32	4.82	High	High	High	High	High	High	High	1
FALSE	High	Master PrC P09493-1	Isform 5	0	45.716	36	12	24	2	245	28.4	4.77	36.88	12	cell organ	cytoskelet; protein br	P002661, F 7168	ENSG000001 TPM1	15		Striated M		1	1.06	0.553313743	8.57	309.6	291.6	7.95	4.13	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q09P03-1	SH3 domai	0	5.763	2	1	1	1	963	107.4	7.71	4.53	1	regulation	cytoplasm; enzyme re	P00018, F 23677	ENSG000001 SH3BP4	2				0	1.06	0.556910494	37.39	192.5	181.5	39.35	7.74	High	High	High	High	High	High	High	1
FALSE	High	Master PrC Q06GQ7	Probable A	0	63.054	25	18	26	18	796	89.8	9.28	51.57	18	metabolic	chromoso/ catalytic ac	P00270, F 55661	ENSG000001 DDX27	20				0	1.06	0.652632562	22.43	8931.1	8869.3	13.22	6.4	High	High	High	High	High	High	High	1
FALSE	High	Master PrC P55337	Tumor pro	0	41.154	31	6	9	6	224	24.3	4.83	23.14	6	cell differ	cytoplasm; metal ion	P04001	ENSG000001 TPDS2	8				5	1.06	0.802593939	14.31	2889.3	2615.9	15.34	6.83	High	High	High	High	High	High	High	1
FALSE	High	Master PrC P30566	adenosely	0	14.16	11	3	3	3	484	54.9	7.11	10.8	3	cell organ	cytosol;met catalytic ac	P000606, F 158	ENSG000001 ADSL	22	Metabolic	Nucleotide	Purine ribc	8	1.059	0.142074713	6.56	393	388.2	6.35	9.54	High	High	High	High				



FALSE	High	Master Prc Q135642	Cdc42-inte	0	27.958	15	6	6	6	601	68.3	5.73	11.01	6	cell comm	cytoplasm; enzyme re	P00018, F 9322	ENSG000001	TRIP10	19	Insulin sign	Angiogenesis	Rho GTPase	8	1.055	0.75020682	23.28	189.2	181.3	18.92	17	High	High	High	High	High	High	High	High	1					
FALSE	High	Master Prc P427171	cyclin-depe	0	31.35	45	4	10	4	156	16.5	5.81	23.43	4	cell organ	cytoplasm; catalytic ac	P12796, F 1029	ENSG000001	CDKN2A	9	HTLV-1 infe	TP53 Netw	Cyclin D as	32	1.055	0.750726699	6.22	1859	1872.6	7.27	5.31	High	High	High	High	High	High	High	High	1					
FALSE	High	Master Prc Q8Y88	ATP-deper	0	21.691	5	3	6	3	786	87.9	7.99	15	3	cell organ	mitochondr	catalytic ac	P000271, F 6832	ENSG000001	SUPV3L1	10				0	1.055	0.876910009	17.01	708.4	671.6	10.61	12.55	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prc Q00059	Transcripti	0	18.451	28	7	10	7	246	29.1	9.72	12.08	7	cell organ	cytosol;mi	DNA bindi	P000505, F 7019	ENSG000001	TAM	10	Huntington	Energy Met	Mitochondr	10	1.054	0.01193592	0.15	1157.9	1113.4	5.86	5.61	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prc Q99459	Cell divisio	0	94.612	27	14	26	14	802	92.2	8.18	95.39	14	cell organ	cytoplasm; DNA bindi	P000409, F 9088	ENSG000001	CDCL5	6	Spliceosom		mRNA Splic	5	1.054	0.203826788	2.03	6970.5	6613.8	4.65	4.48	High	High	High	High	High	High	High	High	1					
FALSE	High	Master Prc Q43930	NADH dehyd	0	17.972	47	4	4	4	106	12.5	9.14	13.91	4	cell organ	membrane	catalytic ac	P112000	4725	ENSG000001	NDUF55	1	Oxidative x	Electron Tr	Complex I	13	1.054	0.3325506	7.8	1539	1432.4	13.68	1.15	High	High	High	High	High	High	High	High	1			
FALSE	High	Master Prc Q8N163-1	Cell cycle r	0	94.102	27	18	26	18	923	102.8	5.22	70.01	18	cell organ	cytoplasm; enzyme re	P14443, F 57805	ENSG000001	CA2, KIF	8			Regulation	4	1.054	0.376893738	11.1	4289.3	4068.2	8.28	7.28	High	High	High	High	High	High	High	High	1					
FALSE	High	Master Prc Q95573	long-chain	0	124.538	34	17	33	15	720	80.4	8.38	97.44	17	cell organ	endoplasm	catalytic ac	P000501	2181	ENSG000001	ACSL3	2	Metabolic	Fatty Acid	Synthesis c	16	1.054	0.467135307	17.38	8851.9	8581.4	19.67	4.43	High	High	High	High	High	High	High	High	1			
FALSE	High	Master Prc Q95340	bifunction	0	58.445	22	11	15	10	614	69.5	8.03	43.2	11	coagulation	cytosol	catalytic ac	P01583, F 9060	ENSG000001	PAPSS2	10	Selenocom	RANL/RNA	Transfer	20	1.054	0.497406801	22.72	3139.9	2978.7	27.38	0.82	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prc Q9K532	182 kDa ta	0	106.809	18	23	31	23	1729	181.7	4.86	67.24	23	cell organ	chromosom	protein br	P115327	85456	ENSG000001	SNB1BP1	11	TP53 regul			9	1.054	0.571774923	30.6	4171.8	3968.1	29.11	8.45	High	High	High	High	High	High	High	High	1			
FALSE	High	Master Prc Q15397-1	Importin-8	0	9.334	4	3	4	2	1037	119.9	5.16	9.3	3	regulation	cytoplasm; protein br	P03810, F 10526	ENSG000001	IP08	12			Transcripti	3	1.054	0.668364867	49.35	249.7	236.9	40.31	12.8	High	High	High	High	High	High	High	High	1					
FALSE	High	Master Prc Q15540	Fatty acid	0.006	2.5	5	1	2	1	132	14.9	5.59	4.49	1	cell differe	cytoplasm; transport	P00061, F 2173	ENSG000001	FABP7	6	PPAR sign	PPAR sign	Triglycerid	6	1.054	0.864421675	4.93	492	472.7	9.27	6.07	High	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prc Q9ULT8	E3 ubiquiti	0	21.884	3	6	7	6	2610	289.2	5.35	12.63	6	metabolic	cytoplasm	catalytic ac	P00023, F 25831	HCTD1	14			Antigen pr	4	1.054	0.888943777	27.77	876.8	896.5	22.3	5.68	High	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prc Q5T653	39S riboso	0	7.1	5	1	1	1	305	33.3	11.3	1.62	1	cell organ	membrane	catalytic ac	P00181, F 51069	ENSG000001	MRP12	6	Ribosome		Mitochondr	7	1.054	0.996113322	70.39	381.3	357.7	46.05	8.78	High	High	High	High	High	High	High	High	High	1			
FALSE	High	Master Prc Q9UBX3	Mitochondr	0	28.415	21	4	8	4	287	31.3	9.54	30.05	4	metabolic	membrane	protein br	P00153	1468	ENSG000001	SLC25A10	17	Proximal tr		Glucose	13	1.053	0.079503007	3.31	3382.9	3106.6	5.09	4.3	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9NWT8	Aurora kin	0.002	4.013	5	1	1	1	199	22.3	10.76	2.14	1	cell organ	membrane	catalytic ac	P08213	54998	ENSG000001	AURKAIP1	1	Mitochondr		Mitochondr	6	1.053	0.310105918	8.48	772.7	721.4	7.76	1.52	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q15276	Rab GTPase	0	26.174	10	6	6	6	862	99.2	5.01	14.04	6	cell death	cytoplasm; enzyme re	P01496, F 9135	ENSG000001	RABEP1	17	Endocytosi		TBC/RABG	5	1.053	0.315006706	2.33	324.7	289.2	18.22	4.44	High	High	High	High	High	High	High	High	High	High	1			
FALSE	High	Master Prc Q9H936	Mitochondr	0	22.995	22	5	7	5	323	34.4	9.29	15.55	5	transport	membrane	transport	P00153	14988	ENSG000001	SLC5A22	11			Organic ac	4	1.053	0.334790631	2.61	978	920.4	0.89	4.63	High	High	High	High	High	High	High	High	High	1		
FALSE	Low	Master Prc Q4A288-1	Probable r	0.071	1.037	3	1	1	1	527	58	8.68	0	1	metabolic	cytoplasm; catalytic ac	P115977	340152	ENSG000001	C23H120	6				0	1.053	0.499286694	22.41	825.3	806.4	28.22	7.12	High	High	High	High	High	High	High	High	High	1			
FALSE	High	Master Prc P62979	Ubiquitin	0	72.075	64	9	39	4	156	18	9.64	119.63	9	cell organ	cytoplasm; metal ion	P000240, F 6233	ENSG000001	RPS27A	2	Ribosome	Cytoplasm	NOTCH1 r	364	1.053	0.511798381	3.19	2160.1	2146.6	2.78	5.88	High	High	High	High	High	High	High	High	High	High	1			
FALSE	High	Master Prc Q43819	Protein SC	0	8.59	14	3	4	3	266	29.8	8.85	5.94	3	cell organ	membrane	antioxidan	P00578, F 9997	ENSG000001	SCD2	22	Central car	Copper hox	TP53 Regu	11	1.053	0.67893721	40.94	46.1	43.9	29.51	8.98	High	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9N985	CDKN2A-ir	0	16.343	9	4	5	4	580	61.1	9.01	12.17	4	regulation	nucleus	protein br	P115952	55602	ENSG000001	CDKN2AIP	4				0	1.053	0.736685874	20.15	407.1	386.4	1.1	15.63	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc P67870	Casein kin	0	20.349	30	3	6	3	215	24.9	5.55	20.1	3	cell comm	chromosom	catalytic ac	P01214	1460	ENSG000001	CNK2B	6, CHR_H5	Adherens j	WNT medi	47	1.053	0.798374131	11.92	1001.8	920.4	12.29	4.55	High	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q96552	GPI transac	0	15.909	8	3	3	3	555	61.6	6.49	10.85	3	metabolic	endoplasm	catalytic ac	P10510	94005	ENSG000001	PIGS	17	Metabolic		Attachme	6	1.052	0.119635372	5.07	1446.5	1375.1	3.95	7.36	High	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc Q87233	Brain acid	0	336.367	87	21	174	21	227	22.7	4.63	44.29	21	cell differe	cytoplasm; DNA bindi		10409	ENSG000001	BASP1	5				0	1.052	0.326376573	5.96	45828.9	48378.3	7.65	3.96	High	High	High	High	High	High	High	High	High	High	1		
FALSE	Low	Master Prc Q8BXQ3	Uncharacter	0.065	1.081	6	1	1	1	194	21.1	5.01	0	1				P115017	55071	ENSG000001	C1orf40	9				0	1.052	0.415825862	12.5	260.8	247.9	5.2	8.45	High	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc Q75306-1	NADH dehyd	0	46.328	19	7	16	7	463	52.5	7.55	40.83	7	cell organ	membrane	catalytic ac	P00346	4720	ENSG000001	NDUF52	1	Oxidative x	Electron Tr	Complex I	13	1.052	0.440248744	16.57	6959.3	6850.6	39.27	8.12	High	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc Q6ZRV2	Protein FA	0.008	2.214	2	1	1	1	1179	127	6.98	1.8	1	cell organ	cytoplasm; protein br	P07894, F 286077	ENSG000001	FAM83B	8, CHR_H5	0				0	1.052	0.605301138	36.01	981.4	1114.5	40.34	10.33	High	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc P27540	Aryl hydro	0	5.447	2	1	1	1	789	86.6	6.54	3.96	1	cell differe	cytoplasm; DNA bindi	P00010, F 405	ENSG000001	ARNT	1	Chemical c	Angiogene	Aryl hydro	23	1.052	0.607709979	29.53	559.7	554	25.39	5.79	High	High	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9H973	elongator	0.003	2.893	3	2	2	2	547	62.2	8.88	4.52	2	cell organ	cytoplasm; catalytic ac	P04055	55140	ENSG000001	ELP3	8	HATs acety			3	1.052	0.707813543	16.05	663.3	630.9	8.36	5.74	High	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q13557	Calcium/ci	0	12.458	9	2	2	1	499	56.3	7.25	8.11	2	metabolic	cytoplasm; catalytic ac	P00069, F 817	ENSG000001	CAMK2D	4	HIF-1 sign	Physiolog	Iron homeo	64	1.052	0.794020146	28.94	342	325	22.04	16.22	High	High	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9Y224	Tyrosine-t	0	24.04	18	6	6	6	477	53.2	7.88	9.11	6	metabolic	cytoplasm; catalytic ac	P00579	51067	ENSG000001	RYAS2	12	Aminoacyl		Mitochondr	5	1.051	0.196623195	1.33	1931.1	1837.5	5.05	1.9	High	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc P30405	Pestidipyr	0	72.4	70	12	27	10	207	22	9.38	48.63	12	cell death	membrane	catalytic ac	P00160	10105	ENSG000001	PIPF	10	Parkinson'			5	1.051	0.209677563	6.54	6879.2	6345.7	4.72	2.6	High	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc Q72384	Nucleopor	0	19.865	11	5	5	5	507	55.4	7.02	14.69	5	cell organ	membrane	protein br	P113874	53371	ENSG000001	NUP54	4	RNA trans		Rev-media	64	1.051	0.232399627	2.18	2016	1914.3	2.02	4.24	High	High	High	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prc Q9S801	Tetratricol	0	5.21	5	2	2	2	387	44.7	5.6	5.2	2				P13144, F 7268	ENSG000001	TTCA	1				0	1.051	0.416074551	12.94	712.9	632.7	11.61	4.49	High	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9N988	probable R	0	10.118	18	2	3																																					

FALSE	High	Master Prq P41091	eukaryotic	0	57.561	31	11	18	11	472	51.1	8.4	41.86	11	metabolic; cytoplasm; catalytic ai	P00009, F 1968	ENSG000001EF253	X	RNA trans	Translation	Formation	15	1.047	0.190055178	4.86	4034.3	3854.2	2.85	1.1	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q13499-1	cytoplasm	0	6.634	3	1	2	1	638	71.4	5.2	7.72	1	cell division; cytoplasm; catalytic ai	P00400, F 1781	ENSG000001DNC12	13	Phagosome	COPII index		48	1.047	0.449602097	15.19	870.2	766	13.29	11.25	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q17554	WW doma	0	7.275	3	1	1	1	376	42.5	5.57	3.97	1	metabolic; nucleus; metal ion	P00397, F 11193	ENSG000001WB94	13		mRNA Spli		4	1.047	0.547689794	22.76	192.2	190	22.44	9.09	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q17507	Dialcylgly	0.003	3.209	4	1	1	1	488	55.2	9.32	3.32	1	cell organi; endoplasm; catalytic ai	P03062, 8694	ENSG000001DGA1	14	Retinol me	Triacylgly	Triglycerid	17	1.047	0.673739591	12.16	552.5	538.4	13.88	4.02	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q17507	Dehydroge	0	13.994	12	2	2	2	313	33.9	7.83	9.06	2	metabolic; cytoplasm; catalytic ai	P00106, F 115817	ENSG000001DHS1	14				0	1.047	0.886088698	11.23	156.5	149.4	5.77	11.52	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q17532	Chromatin	0	34.542	23	5	11	5	248	26.4	12.23	32.41	5	metabolic; nucleus; DNA bindi	P13865, 26097	ENSG000001CHPC	1		Cleavage o		9	1.046	0.347563015	8.69	3927.3	3755.5	7.12	2.14	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q17532	Protein Pri	0	74.042	8	18	23	16	2896	316.7	9.13	53.97	18	cell organi; endoplasm; protein bir	P07001, 23215	ENSG000001PRKC	1				0	1.046	0.446173178	13.39	3975.8	3896.8	15.38	2.45	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q17547-1	PC4 and S	0	31.257	15	7	12	6	530	60.1	9.13	27.43	7	cell organi; cytosol;nu	P08555, F 11168	ENSG000001PSP1	19		2-LTR circ		13	1.046	0.462550154	13.8	1521.3	1546.2	15.33	4.03	High	High	High	High	High	High	1	
FALSE	Medium	Master Prq P84101-1	Small EDR	0.029	1.436	14	1	1	1	59	6.9	10.45	2.04	1	cytosol;nu	10169	ENSG000001SERF	2				0	1.046	0.516535073	34.97	457.8	437.7	52.13	8.66	High	High	High	High	High	High	1	
FALSE	High	Master Prq P07910-2	Isomorf C1	0	242.733	56	23	142	23	293	32.3	5.08	357.07	23	cell differe; cytoskelet; DNA bindi	P00076, F 3183	ENSG000001HNRNPF	14		mRNA Pro		1	1.046	0.548994035	8.72	50974	48754.9	4.4	3.73	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q17507	ATP-deper	0	24.012	10	6	8	6	859	96.3	9.06	18.79	6	metabolic; cytoplasm; catalytic ai	P00270, F 57062	ENSG000001DDX24	14	CHR_H			0	1.046	0.568324222	28.39	1706.7	1766.5	32.28	11.83	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q14776-1	Transcript	0	21.125	8	7	8	7	1098	123.8	8.65	11.03	7	metabolic; nucleus; protein bir	P00397, F 10915	ENSG000001TCERG1	5	Spliceosom			1	1.046	0.880567799	15.25	1809.7	1729.3	5.15	9.32	High	High	High	High	High	High	1	
FALSE	High	Master Prq P61527	60S riboso	0	13.411	39	6	13	6	97	11.1	11.74	14.62	6	cell organi; cytosol;rib	P101907, 6167	ENSG000001RPL37	5	Ribosome	Cytoplasm; Peptide ch		34	1.045	0.286668719	5.17	6240.5	5971	3.34	6.99	High	High	High	High	High	High	1	
FALSE	Medium	Master Prq Q13637	Ras-relate	0.024	1.511	6	1	1	1	225	25	6.54	0	1	cell organi; cytosol;en	P00025, F 10981	ENSG000001RAB32	6		RAB GEF s		7	1.045	0.357556825	3.36	295.7	282.8	22.22	5.03	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q13561-1	dynactin si	0	47.66	26	8	11	8	401	44.2	5.21	23.67	8	cell organi; chromosom; catalytic ai	P04912, 10540	ENSG000001DCTN2	12	Huntingtong	COPII-depe		35	1.045	0.408308775	11.2	2642.7	2521.1	18.17	2.08	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q13561-1	Transmem	0	32.415	17	4	12	4	235	27.3	8.02	28.81	4	cell organi; endoplasm; protein bir	P01105, 54732	ENSG000001TMED9	5		COPII-depe		11	1.045	0.472169029	9.16	1912.7	1853.3	5.03	3.18	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q13561-1	U6 snRNA	0	8.728	33	2	5	2	103	11.6	5.27	4.82	2	metabolic; cytosol;nu	P01423, 51690	ENSG000001LSM7	19	Spliceosom	mRNA Pro	mRNA Spli	9	1.045	0.489036395	14.97	1279	1178.3	10.21	5.7	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q13561-1	Midasin [C]	0	8.878	1	3	3	3	5596	63.2	5.68	5.88	3	cell organi; cytosol; catalytic ai	P00004, F 23195	ENSG000001MDN1	1	Ribosome			1	1.045	0.517325468	17.5	248.5	237.8	11.82	8.1	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q14247-1	Scr substr	0	124.288	49	28	56	28	550	61.5	5.4	110.02	28	cell organi; cytoplasm; protein bir	P00018, F 2017	ENSG000001CTTN	11	Proteoglyc	Pathogen; RHO GTPa		14	1.045	0.643301951	14.27	8365.3	8007.4	5.68	5.5	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q13527	Keratin, ty	0	432.298	76	44	273	37	483	53.7	5.59	593.32	44	cell death; cytoplasm; catalytic ai	P00038, F 3856	ENSG000001KRT8	12		Primary G	Formation	4	1.045	0.729177945	23.18	80708.4	77255.5	8.41	7.55	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q13527	ribulose-ph	0	11.922	12	2	2	2	228	24.9	5.58	9.64	2	metabolic; cytosol; catalytic ai	P00218, F 6120	ENSG000001PEP	9	Biosynthes	Pentose Ph	Pentose ph	9	1.045	0.739399193	22.78	224.4	214.8	11.2	5.49	High	High	High	High	High	High	1	
FALSE	High	Master Prq P35237	serpin B6	0	66.584	42	13	25	13	376	42.6	5.27	64.55	13	regulation; cytoplasm; enzyme re	P00079, 5269	ENSG000001SERPINEB	6	Amoebiasis	Extracellu	Enzyme re	7	1.045	0.823267022	25.52	5296.6	5506.9	18.79	5.87	High	High	High	High	High	High	1	
FALSE	High	Master Prq P63313	thymosin a	0	20.066	48	5	19	2	44	5	5.36	41.9	5	cell organi; cytoplasm; protein bir	9168	ENSG000001TMSB10	2				0	1.045	0.869406689	13.61	1983	1975.6	7.76	14.6	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q13523	deoxynuck	0	10.246	6	3	3	3	626	72.2	7.14	9.3	3	cell organi; membrane; catalytic ai	P00536, F 25939	ENSG000001SAMHD1	20		Nucleobas		7	1.045	0.903851669	20.91	1091	1026.8	4.77	14.65	High	High	High	High	High	High	1	
FALSE	High	Master Prq P12429	annexin A	0	90.598	40	15	36	15	323	36.4	5.92	67.78	15	defense re; cytoplasm; enzyme re	P00191, 306	ENSG000001ANXA3	4	Prostaglan			1	1.045	0.949248519	2.64	17796.2	17828.3	7.87	3.59	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q15424-1	Scaffold at	0	59.077	16	14	25	9	915	102.6	5.47	44.89	14	cell organi; nucleus	DNA bindi	P00006, F 6294	ENSG000001SFAH	19		Structural		1	1.044	0.726324223	6.4	3701.8	3519.3	2.72	4.36	High	High	High	High	High	High	1
FALSE	High	Master Prq Q13523	WD repeat	0	33.362	35	6	8	6	305	33.6	5.47	24.19	6	cell organi; cytoplasm; protein bir	P00400, F 80349	ENSG000001WDR61	15	RNA degra	mRNA dec		13	1.044	0.327491297	3.86	1410.3	1342.7	13.29	3.91	High	High	High	High	High	High	1	
FALSE	High	Master Prq P51648	Fatty acide	0	30.659	21	8	13	8	485	54.8	7.88	25.37	8	metabolic; endoplasm; catalytic ai	P00171, 224	ENSG000001ALDH3A2	17	Glycerolip	Tryptophan	Sphingolip	18	1.044	0.351711247	4.65	1419	1358.7	4.42	0.32	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q02388-1	Collagen a	0	8.153	2	4	4	4	2944	295	6.27	0	4	cell differe; extracellul	enzyme re	P00014, F 1294	ENSG000001COL1A1	3	Protein dig	Collagen d		20	1.044	0.414474846	10.74	70	66.9	16.62	9.47	High	High	High	High	High	High	1
FALSE	High	Master Prq Q14566	DNA replic	0	70.992	22	16	24	16	821	92.8	5.41	51.08	16	metabolic; nucleus	catalytic ai	P00043, F 4175	ENSG000001MCM6	2	Cell cycle; Cell Cycle; M/G1 Tran		26	1.044	0.459188983	13.44	9186.6	8803.2	9.7	6.2	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q13523	Masparidin	0.004	2.768	3	1	1	1	308	34.9	6.28	1.93	1	metabolic; cytoplasm; catalytic ai	P00561, F 51324	ENSG000001SPG21	2	Endocytosi			1	1.044	0.48821899	15.43	571.3	559.2	15.87	4.79	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q15431-1	Autophagy	0	7.758	6	2	3	2	517	56.5	5.12	6.55	2	cell organi; cytoplasm; protein bir	P101033, 9776	ENSG000001ATG13	11	Autophagy	P13K-AKT-r	Macroautic	6	1.044	0.52449627	39.56	539.2	516.2	57.72	18.2	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q12904-1	aminoacyl	0	41.571	30	7	12	7	312	34.3	8.43	35.39	7	cell comm; cell surface; protein bir	P01588, 9255	ENSG000001AIMP1	4	Cytosolic st			8	1.044	0.672080423	36.37	5778.9	6230.7	33.01	8.24	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q13523	Peptidyl-H	0	14.138	16	2	2	2	179	19.2	8.73	9.57	2	cell differe; cytosol; metal ion	P01381, 51651	ENSG000001PRH12	17	UP-specific			4	1.044	0.71238508	10.51	630.5	674	15.96	9.2	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q13523	heterogen	0	175.629	43	27	90	22	633	70.9	8.13	204.65	27	metabolic; cytoplasm; protein bir	P00076, F 10236	ENSG000001HNRNP1	15	CHR_HS	mRNA Pro	mRNA Spli	5	1.044	0.915283071	5.33	19230.5	18970.8	5.59	5.13	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q13523	Dnal home	0.003	3.13	7	2	2	2	304	34.7	8.53	40.9	2	metabolic; cytoplasm; RNA bindi	P00076, F 55192	ENSG000001NAUC1	15				0	1.043	0.952635701	23.42	487.9	468	26.34	7.36	High	High	High	High	High	High	1	
FALSE	High	Master Prq P51151	Ras-relate	0	43.55	50	6	10	6	201	22.8	5.47	33.95	6	regulation; cytosol;en	catalytic ai	P00025, F 9367	ENSG000001RAB8A	3	Measles	Retrograd		10	1.043	0.52624103	15.26	2289	2107.2	9.86	4.29	High	High	High	High	High	High	1
FALSE	High	Master Prq Q14562	Ubiquitin c	0	21.881	20	4	8	4	309	33.4	5.77	28.52	4	protein bir	P00400, F 56061	ENSG000001UBD1	16				0	1.043	0.662235749	3.91	746.2	777	18.84	6.72	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q13523	Isomorf 2	0	31.769	11	7	13	7	779	87.6	5.92	25.43	7	cell organi; cytoskelet; protein bir	P00373, F 2036	ENSG000001EPH411																				

FALSE	High	Master Pcr P61019-1	Ras-related	0	43.263	33	5	13	5	212	23.5	6.54	37.27	5	cell organi	cytosol/en	catalytic a	P00009, F	S862	ENSG00000	RAB2A	8	AMPK sign	Focal Adh	Golgi Cste	10	1.04	0.886546264	27.92	2865.2	2755.9	23.11	6.35	High	High	High	High	High	High	High	1
FALSE	High	Master Pcr Q99614	tetratricor	0	40.101	29	8	18	8	292	32.5	6.44	34.17	8	metabolic	cytosol/me	protein br	P00515, F	7265	ENSG00000	TTCL1	5				0	1.04	0.903384056	10.51	3200.9	3239.1	13.98	4.28	High	High	High	High	High	High	1	
FALSE	High	Master Pcr Q03169	Tumor nec	0	11.429	6	4	4	4	654	72.6	4.86	4.87	4	cell differe		protein br	P06046	7127	ENSG00000	TNFAIP2	14				0	1.04	0.917867221	40.50	1580.5	1580.5	5.49	5.5	High	High	High	High	High	High	1	
FALSE	High	Master Pcr P20340-2	Isomform 2	0	35.962	42	8	13	8	208	23.5	5.54	27.01	8	cellular co	cytosol/Go	catalytic a	P00009, F	5870	ENSG00000	RAB6A	11				0	1.039	0.213408775	2.87	3417.1	3401	8.88	8.5	High	High	High	High	High	High	1	
FALSE	High	Master Pcr Q95249-1	Glyc SNAP	0.003	2.942	4	1	1	1	250	28.6	9.42	16.9	1	cell organi	cytosol/Go	protein br	P112352	9527	ENSG00000	GOSR1	17	SNARE inte	COP1-me		11	1.039	0.363649587	8.41	7611	733.5	13.05	6.83	High	High	High	High	High	High	1	
FALSE	High	Master Pcr Q9UKA9-1	Polypyrini	0	9.908	10	3	3	3	531	57.5	6.86	6.98	3	cell organi	nucleus/s	RNA bindi	P00076, F	58155	ENSG00000	PTRB2	1	TarBasePal			2	1.039	0.451029955	21.18	895.5	839.2	79.62	13.36	High	High	High	High	High	High	1	
FALSE	High	Master Pcr Q98540	Latexin [C	0	12.261	17	3	4	3	222	25.7	5.78	9.57	3	defense re	cytoplasm	enzyme re	P06907	56925	ENSG00000	LXN	3				0	1.039	0.472559254	25.94	864.4	874.9	46.65	12.61	High	High	High	High	High	High	1	
FALSE	High	Master Pcr Q13347	Eukaryotic	0	8.974	56	12	24	32	325	36.5	6.54	67.96	12	cell organi	cytoplasm	protein br	P00400	8668	ENSG00000	EIF31	1	RNA trans	EGF/Transf	Formation	13	1.039	0.81594975	5.23	4752.8	4459.7	8.73	2.88	High	High	High	High	High	High	1	
FALSE	High	Master Pcr Q13357	Phosphatic	0	16.292	3	3	4	3	1258	138.5	6.54	6.64	3	cell organi	cytoplasm	catalytic a	P00017, F	3636	ENSG00000	INP1L1	1	Inositid ph	EGF/EGFR	Synthesis	20	1.039	0.859448883	24.49	1185.2	1212.5	16.02	6.57	Synth	High	High	High	High	High	1	
FALSE	High	Master Pcr P36871-1	Phosphogl	0	42.02	26	11	15	11	562	61.4	6.76	27.28	11	metabolic	cytoplasm	catalytic a	P00406, F	5236	ENSG00000	PGM1	1	Pentose pl	Ectoderm	Neutrophil	23	1.038	0.014204919	0.03	2839.1	2736.1	2.02	2.63	High	High	High	High	High	High	1	
FALSE	High	Master Pcr P14550	alcohol de	0	16.353	19	5	7	5	325	36.6	6.79	11.50	5	metabolic	cytosol/me	catalytic a	P00248	10327	ENSG00000	AKR1A1	1	Pentose al	Benzo[al]A	Catabolism	12	1.038	0.412093023	8.98	545.9	523.2	22.31	6.6	High	High	High	High	High	High	1	
FALSE	Medium	Master Pcr P29373	Cellular re	0.02	1.596	5	1	1	1	138	15.7	5.4	1.74	1	metabolic	cytoplasm	protein br	P00061, F	1382	ENSG00000	CRABP2	1	Vitamin A	Signaling b		4	1.038	0.45260215	11.98	517.1	400.9	16.03	21.18	High	High	High	High	High	High	1	
FALSE	High	Master Pcr P53365	Arifapin-2	0	24.516	20</																																			

FALSE	High	Master Prc Q14151	scaffold at	0	40.111	14	11	14	6	953	107.4	6.16	25.19	11	cell differe cytoplasm; DNA bindi	PI00076, P_9667	ENSG000001	SAFB2	19			0	1.032	0.628524714	21.8	817.8	835.8	20.47	3.32	High	High	High	High	High	1	[K746;	
FALSE	High	Master Prc P06756	Integrin al	0.002	3.644	2		2	2	1048	116.5	6.88	2.36	2	cell differe cell surface metal ion	(PI01839, P_3685	ENSG000001	ITGAV	2	Small cell   Osteopontin	Integrin ce	48	1.032	0.6779263	33.16	684.6	606.7	24.62	9.43	High	High	High	High	High	1		
FALSE	High	Master Prc Q3NV98	TBC1 dom	0	4.547	4	1	1	1	400	46.5	5.24	3.00	1	regulation cytoplasm; enzyme re	PI00556, P_54662	ENSG000001	TBC1D13	9		TBC/RABG	4	1.032	0.681827068	24.8	315	323.5	21.37	3.41	High	High	High	High	High	1		
FALSE	High	Master Prc Q8TBK3	SH3KBP1	0	7.917	4	2	2	2	1	707	76.3	8.28	4.12	2	cell organi; vacuole protein bin	PI00214, P_9259	ENSG000001	SHKBP1	19			0	1.032	0.716198618	34.42	717.2	720.4	27.24	6.72	High	High	High	High	High	1	
FALSE	High	Master Prc Q39956	Dual spec	0	11.244	8	2	2	2	384	41.8	6.11	6.53	2	metabolic cytoplasm; catalytic a	PI00012, P_18799	ENSG000001	DUSP9	X	MAPK sign	Negative r	12	1.032	0.781490986	25.97	437.7	420.1	8.64	11.74	High	High	High	High	High	1		
FALSE	High	Master Prc Q39493	Transducin	0	9.131	5	2	2	2	447	49.8	9.94	2.65	2	cell commi endoplasm protein bin	PI00400, P_26608	ENSG000001	TBL2	7			0	1.032	0.801246731	20.83	628.9	582.7	7.88	12.2	High	High	High	High	High	1		
FALSE	High	Master Prc Q43660	Pleiotropic	0	23.704	13	6	11	6	514	57.2	9.17	17.09	6	cell organi; membrane catalytic a	PI00400, P_5356	ENSG000001	PLRG1	4	Spliceosom	mRNA Spal	5	1.032	0.884038555	11.12	630	601.7	15.53	0.94	High	High	High	High	High	1		
FALSE	High	Master Prc Q39213	Glutathione	0	18.901	19	4	5	4	226	25.5	8.61	11.39	4	cell differe membrane antioxidant	PI01323, P_37156	ENSG000001	GSKT1	7	Chemical C Metapathic	Glutathione	10	1.032	0.906763837	15.87	222.02	2150.8	13.55	4.55	High	High	High	High	High	1		
FALSE	High	Master Prc P49419	Alpha-am	0	76.409	33	14	24	14	539	58.5	7.99	73.39	14	metabolic cytoplasm; catalytic a	PI00017, P_13051	ENSG000001	ALDH1A7	5	Beta-Alani Amino Acids	Lysine catal	21	1.032	0.90089382	0.99	11550.5	11417.3	5.36	40.1	High	High	High	High	High	1		
FALSE	High	Master Prc P52565	rho GDP-d	0	46.755	50	7	16	7	204	23.2	5.11	84.5	9	cell organi; cytoplasm; enzyme re	PI02115, P_396	ENSG000001	ARGHUA	17	Vasopressin	Signalling i	11	1.032	0.910223855	2.98	924.6	5334.9	5.3	4.03	High	High	High	High	High	1		
FALSE	High	Master Prc P07594	nuclear por	0	106.750	20	19	31	19	1391	155.1	6.16	41.94	19	cell organi; membrane protein bin	PI03177, P_9631	ENSG000001	NUP155	5	NASA trans	Rev-media	64	1.032	0.915409599	4.88	7935.9	7699.6	8.13	2.23	High	High	High	High	High	1		
FALSE	High	Master Prc Q43684	Mitotic ch	0	49.978	44	9	17	9	328	37.1	6.84	36.58	9	cell division chromosom protein bin	PI00400, P_9184	ENSG000001	BUB3	10	Cell cycle   Cell Cycle	Inactivation	29	1.032	0.97688107	12.17	1851.7	1798.4	4.84	7.85	High	High	High	High	High	1		
FALSE	High	Master Prc P07594	Reticulocal	0	17.479	20	5	5	5	317	36.9	4.4	11.89	5	endoplasm metal ion	(PI13499, P_5955	ENSG000001	RCN2	15			0	1.031	0.95126333	1.44	445	431.4	3.76	2.42	High	High	High					

FALSE	High	Master Prq Q9NVC6	mediator c	0	7.713	5	2	2	2	651	72.8	7.44	4.69	2	metabolic	membrane protein br	PT01556	9440	ENSG000001	MED17	11	Thyroid ho	Transcripti	10	1.026	0.905658437	9.6	640.5	624.4	9.67	2.56	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9H7M9	V-type imi	0	6.559	11	2	3	2	311	33.9	6.95	5.98	2	metabolic	membrane protein br	64115	ENSG000001	Clorf45A	10	0	1.026	0.934764796	9.26	1686.7	1716.8	5.06	11.58	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q06052	protein O-	0	47.342	14	9	12	9	916	102.8	4.91	33.76	9	metabolic	cytoplasm; catalytic ai	PT07555	10724	ENSG000001	MG6A5	10	1	1.026	0.970214053	6.28	1260.5	1334	6.76	5.15	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q13619-1	culin-4A	0	28.762	12	8	9	7	759	87.6	8.13	22.22	8	cell organi	cytoplasm; catalytic ai	PT00888	8451	ENSG000001	CU1A4	13	Nucleotide		17	1.025	0.278917428	0.83	1658.9	1462.1	6.85	9.51	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q04446	1,4-alpha-	0	25.179	11	7	8	7	702	80.4	6.32	15.32	7	metabolic	cytosol	PT00128	2632	ENSG000001	PEE1	3	Metabolic	Glycogen B	12	1.025	0.282520246	2.86	1462	1470.8	2.82	3.92	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q6RW13	Type-1 ang	0	9.725	14	1	1	1	159	17.4	6.14	5.27	1	regulation	cytosol;em	PT06396	57085	ENSG000001	ACTRAP	1			4	1.025	0.390269683	5.84	136.1	132	3.95	1.25	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q99755	Phosphati	0	8.521	6	2	2	2	562	62.6	8.21	4.87	2	cell differe	cytoplasm; catalytic ai	PT01504	8394	ENSG000001	PP5K1A	1	Metabolic	B Cell Rece	20	1.025	0.45351789	14.64	767.3	748.9	45.53	1.89	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q99999	cytochrom	0	49.35	63	9	18	9	105	11.7	9.57	34.68	9	cell death;	cytosol;me	PT00034	54205	ENSG000001	CYC5	7	Hepatitis B	mRNA Reg	54	1.025	0.511389668	0.1	2727.1	2755.5	15.68	6.12	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9P1A5	Ribosome	0	16.075	14	3	8	3	250	28.7	8.75	10.9	3	cell organi	cytoplasm; protein br	PD1172	F 51119	ENSG000001	SBD5	7	Ribosome		1	1.025	0.551901532	1.76	573.3	639.1	12.08	11.21	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9NNW7	thioredoxin	0	12.381	6	3	4	2	524	56.5	7.5	8.15	3	cellular ho	cytosol;mi	PT00070	10587	ENSG000001	TXNRD2	22	Pyrimidine	Selenium P	8	1.025	0.630043126	2.91	311.7	310.7	13.88	10.8	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q06064-1	Perlipin-3	0	164.074	69	22	49	22	434	47	5.44	150.63	22	transport	cytoplasm; protein br	PT03036	10226	ENSG000001	PLIN3	19	Triglycerid		8	1.025	0.631247176	10.85	16189.6	15853.8	4.56	4.67	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9UKM7	endoplasm	0.003	3.474	2	1	1	1	699	79.5	7.72	2.37	1	metabolic	endoplasm	PT01532	11253	ENSG000001	MAN1B1	9	Metabolic	ER Quality	13	1.025	0.645871451	28.77	344	380.9	27.82	20.11	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9NZ53-1	Podocalysi	0	5.623	2	1	4	1	605	65	4.34	6.71	1	metabolic	membrane protein br	PT06365	50512	ENSG000001	PODXL2	1		Cytosolic s	4	1.025	0.690835127	39.24	164.7	163.5	21.8	24.42	High	High	High	High	High	High	High	1
FALSE	Medium	Master Prq Q9H0K6	Pseudouri	0.037	1.326	1	1	1	1	701	80.6	7.56	0	1	metabolic	catalytic ai	PT01142	83448	ENSG000001	PUS7L	12			0	1.025	0.955040829	28.5	545.1	544.1	15.07	11.07	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q07021	Compleme	0	59.678	36	8	17	8	282	31.3	4.84	56.8	8	cell death;	cell surface protein br	PT02330	708	ENSG000001	CLQB8	17	Herpes sim	Mesoderm	5	1.025	0.973571473	45.29	5147.6	5024.3	17.64	15.41	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q5RKV6	Exosome c	0	16.329	28	5	5	5	272	28.2	6.28	9.93	15	metabolic	cytoplasm; catalytic ai	PD11138	118460	ENSG000001	EXOSC6	16	RNA degra	Major patf	15	1.025	0.979004286	14.9	614.7	599.6	6.83	6.87	High	High	High	High	High	High	High	1
FALSE	High	Master Prq S45652	Heat shock	0	149.277	26	18	106	2	639	70	5.74	245.86	18	cell differe	cell surface nucleotide	PT00012	F 3306	ENSG000001	HSPA2	14	Protein prc	Parkin-Like	24	1.024	0.305127756	1.39	63.9	60.8	3.61	5.75	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9N3V8	Guanine ni	0	28.035	15	7	7	7	582	65.5	8.44	17.31	7	regulation	cytosol;me	PT01266	F 54552	ENSG000001	GN3L1	X	Ribosome		1	1.024	0.411611962	5.57	1229.9	1201.1	16.91	7.12	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9H3K6-1	bola-like ep	0	13.693	49	3	5	3	86	10.1	6.52	14.48	3	cell organi	cytoplasm; protein br	PT01722	654483	5	BOLA2B	8	Gene and		5	1.024	0.458138415	7.13	731.2	713.8	7.08	1.43	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q14232	Translatio	0	12.539	20	4	5	4	305	33.7	7.33	10.21	4	metabolic	cytoplasm; protein br	PT01008	1967	ENSG000001	EIF2B1	16	RNA trans	Translator	7	1.024	0.526319495	21.67	1502.5	1535.5	37.76	5.31	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9BU21	Heterogen	0	47.077	15	11	16	11	856	95.7	6.92	33.81	11	metabolic	nucleus	PT00622	F 11100	ENSG000001	HNRNPUL1	19	Influenza A	mRNA Spli	5	1.024	0.609618347	3.5	3332	3255	4.69	8.01	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q26368	Splicing fa	0	50.712	26	9	19	9	475	53.5	0.99	44.74	9	metabolic	nucleus;spi	PT00076	F 11338	ENSG000001	U2AF2	19	Spliceosom	mRNA Pro	13	1.024	0.710016175	13.09	7156.1	6975.5	5.87	5.36	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P20339	Ras-relate	0	43.779	48	7	14	5	215	23.6	8.15	39.97	7	cell organi	cytoplasm; catalytic ai	PT00009	F 5868	ENSG000001	RAB5A	3	Amyotrophi	Amyotrophi	26	1.024	0.784636708	29.13	2160.7	2110.7	25	8.27	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q00429	Dynamini-3	0	97.538	31	15	24	15	736	81.8	6.81	79.86	15	cell death;	cytoplasm; catalytic ai	PT00350	F 10059	ENSG000001	MAN1B1	12	TNF signali	Synaptic Vi	6	1.024	0.84151373	0.33	2960.3	2890.5	7.5	4.43	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q10469	Alpha-1,6-	0	16.435	12	3	3	4	447	51.5	8.76	10.25	14	cellular ho	Golgi;mem	PT05660	4247	ENSG000001	MGAT2	14	N-Glycan b	Defective f	12	1.023	0.362834304	2.71	814.1	796	10.98	1.69	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q00592	Podocalysi	0	29.389	11	6	16	6	558	58.6	5.49	28.03	6	cellular co	cytoplasm; protein br	PT05109	F 5420	ENSG000001	PODXL	3	Primary Fo		3	1.023	0.379825113	1.69	4250.2	4153.3	4.16	6.54	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9Y6D0	Serine/thio	0	67.083	34	14	20	8	443	49.3	5.69	42.31	14	cell commu	cytoplasm; catalytic ai	PT00069	F 8428	ENSG000001	STK24	13	Apoptotic		4	1.023	0.403902121	5.33	4954.2	4768.7	1	4.08	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q21953	2-oxoisoxa	0.002	3.729	3	1	1	1	392	43.3	6.29	2.95	7	metabolic	mitochondr	PT02779	F 594	ENSG000001	BCDHB3	6	Propanoate	Branch-ed	7	1.023	0.430205136	6.76	221.7	203.5	13.17	8.5	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q04726	Transducin	0	45.613	17	9	12	7	772	83.4	7.2	25.25	9	metabolic	nucleus	PT00400	F 7090	ENSG000001	TLE3	15	White fat	Repression	8	1.023	0.479131413	46.85	478.5	455.3	103.5	25.69	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q14444-1	CAPRIN-1 C	0	92.076	24	14	46	14	709	78.3	5.25	111.75	14	cell differe	cytoplasm; protein br	PT12287	4076	ENSG000001	EIF2B1	11	0	1.023	0.538860309	12.59	14040.6	13687.6	8.86	8.88	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q75369-8	Isomform 8	0	592.965	43	89	202	83	2633	281.5	9.71	542.36	89	cell organi	cytoplasm; protein br	PT00307	F 2317	ENSG000001	FNLB	3	VEGFA-VEG		1	1.023	0.557952554	10.67	60705	59313.8	7.2	2.89	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q04607-2	Isomform 2	0	49.444	25	17	32	1	808	88.9	5.23	68.64	7	metabolic	catalytic ai	PT01189	F 4839	ENSG000001	NOP2	12	Imatinib in		1	1.023	0.619959242	14.75	3506.8	3143.5	11.39	6.99	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q92769	Histone de	0	19.746	13	3	4	2	488	55.3	5.91	12.15	3	cell differe	chromosom	PT00850	3066	ENSG000001	H2AC2	6	Thyroid ho	Cell Cycle	59	1.023	0.648405505	22.83	345.9	368	29.88	12.94	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9H3K6	RNA poly	0	42.019	18	10	14	10	665	75.7	6.84	24.7	10	cell commu	cytoplasm; catalytic ai	PT00515	F 79657	ENSG000001	RPA13	12			0	1.023	0.661705871	12.74	7581.2	7563.2	8.34	3.16	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q12599	Disks large	0	6.966	3	2	3	2	904	100.4	5.76	9.26	2	cell commu	cytoplasm; catalytic ai	PT00018	F 1739	ENSG000001	DLG1	3	T cell rece	Serine-Ric	20	1.023	0.713973868	18.56	2048.9	2064.8	13.92	2.82	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P30048	Thioredoxin	0	90.989	49	11	35	11	256	27.7	7.78	112.43	11	cell death;	cytoplasm; antioxidant	PT00578	F 10935	ENSG000001	PRDX3	10		Dele	4	1.023	0.76017904	23.75	14590	14262.9	15.77	12.82	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q75400	pre-mRNA	0	32.145	11	7	11	7	957	108.7	7.56	17.6	7	cell division	cytosol;me	PT00397	F 55660	ENSG000001	PRPF40A	2	Spliceosom	mRNA Pro	6	1.023	0.853196366	3.38	1731.6	1821.9	5.95	4.5	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q14240-1	eukaryotic	0	75.653	29	11	60	7	497	46.4	5.84	166.18	7	metabolic																								

FALSE	High	Master Prq	Q98YQ3	39S riboso	0	15.542	15	3	4	3	311	34.9	9.72	8.27	3	cell organ	membrane	protein	br	P00573	51073	ENSG00000	MRPL4	19	Ribosome	Mitochond	7	1.018	0.538440513	0.2	906	1037.4	9.16	10.35	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	P07437	tubulin bet	0	404.89	83	29	233	5	444	49.6	4.89	644.41	29	cell division	cytoplasm;	catalytic	ai	P00091, F	203068	ENSG00000	TUBB	6, CHR_	GAP juncti	Pathogene	Neutrophil	24	1.018	0.593524401	1.94	14788.6	14332.8	16.71	4.47	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	P22102-1	trifunction	0	162.107	38	28	42	28	1010	10.77	6.7	134.32	28	metabolic	cytoplasm;	catalytic	ai	P00051, F	2618	ENSG00000	GAT	21	Purine met	Folate Met	Purine ribc	10	1.018	0.68441447	1.13	8327.7	8234.5	7.55	1.01	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q96106	Mannose-6	0	7.255	6	2	2	2	420	46.3	7.21	5.78	2	metabolic	cytoplasm;	catalytic	ai	P00132, F	29926	ENSG00000	GMPFA	3	Fructose a	Synthesis c	9	1.018	0.752594599	27.33	185.8	210.1	26.85	11.45	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q15024	Exosome c	0	10.73	12	3	3	3	291	31.8	5.19	6.33	3	metabolic	cytoplasm;	catalytic	ai	P01138, F	23016	ENSG00000	EXSC7	3	RNA degra	Major pat	15	1.018	0.813260356	16.68	618	607.1	14.49	4.63	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q8TC79-1	Minor hist	0	42.292	17	6	19	6	377	41.5	6.43	46.8	6	cell organ	cell surface	catalytic	ai	P04458, F	81502	ENSG00000	HML13	20			0	1.018	0.957391581	14.89	6289.1	6180.7	9.83	2.71	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	P12181-1	Alpha-acti	0	163.39	38	27	97	14	892	10.3	5.41	226.97	27	cell organ	cytoplasm;	metal ion	l	P00036, F	871	ENSG00000	ACT1	14	Regulation	Arrhythmic	Platelet de	24	1.017	0.13126745	1.39	7121.1	6943.2	3.32	2.72	High	High	High	High	High	High	High	1	[Q747]
FALSE	High	Master Prq	P49589-1	Cysteine-t	0	31.351	11	8	10	8	748	85.4	6.76	29.94	8	metabolic	cytoplasm;	catalytic	ai	P01406, F	833	ENSG00000	CARS	11, CHR_	Aminoacyl	Cytosolic t	5	1.017	0.466014488	7.82	569.4	547.4	16	4.59	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	P46777	60S riboso	0	105.289	46	16	52	16	297	34.3	9.72	117.87	16	cell organ	cytoplasm;	protein	br	P00861, F	6125	ENSG00000	RPL5	1	Ribosome	Cytoplasm	Peptide ch	34	1.017	0.503659808	5.94	16832.2	15893.4	3.59	4.78	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q874W6-4	GRB10-inb	0	35.424	7	7	8	7	1299	15.0	5.54	21.93	7	cell differe	cytoplasm;	protein	br	P00213	26058	ENSG00000	GIGYF2	2			0	1.017	0.534881402	36.3	707.1	695.2	57.07	15.11	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	P51452	dual specif	0	23.279	24	3	7	3	185	20.5	7.8	19.8	3	metabolic	cytosol;nu	catalytic	ai	P01002, F	1845	ENSG00000	DUSP3	17	MAPK sign	ERKs are ir	32	1.017	0.56709977	16.59	988	971.5	19.95	5.95	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q9BYN8	28S riboso	0	10.652	18	3	7	3	205	24.2	10.39	4.66	3	cell organ	membrane	RNA bindi	ng	P11493	64949	ENSG00000	MRPS26	20		Mitochond	6	1.017	0.573948654	23.56	188.5	190.7	29.2	20.11	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q96C33	FAS-associ	0	32.059	19	6	9	6	445	52.6	5.62	26.63	6	cell organ	cytoplasm;	enzyme re	g	P00789, F	23197	ENSG00000	FAF2	5		Neutrophil	3	1.017	0.575318211	24.85	1056.6	1140.9	35.44	8.56	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	P50416	Carnitine c	0	48.687	17	12	18	12	773	88.3	8.65	37.16	12	cell differe	membrane	catalytic	ai	P00755	1374	ENSG00000	CTP1A	11	Insulin resi	AMP-activ	25	1.017	0.579269069	4.26	3752.8	3666.2	5.44	2.17	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	P50502	Hsc70-inte	0	73.131	30	12	31	12	369	41.3	5.27	66.46	12	cell organ	cytoplasm;	nucleotide		P00515, F	6767	ENSG00000	ST13	22		Regulation	4	1.017	0.603399819	4.3	16885.3	16267.6	16.68	1.84	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	P61326	Protein me	0	26.234	47	6	9	6	146	17.2	6.11	20.25	6	metabolic	cytoplasm;	protein	br	P002792	4116	ENSG00000	MAGOH	1	RNA trans	mRNA 3'-e	20	1.017	0.646337889	8.47	1267.4	1321.3	5	8.42	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q75792	Ribonucleo	0	12.932	12	2	3	2	299	33.4	5.25	5.3	2	metabolic	cytosol;nu	catalytic	ai	P01351	10535	ENSG00000	RNA5H2A	19	DNA replic		1	1.017	0.733408945	18.21	329.4	339.5	14.37	4.49	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q6P062	RNA poly	0	20.154	5	5	6	5	1173	133.4	6.77	10.21	5	cell differe	nucleus	protein	br	P08424, F	9646	ENSG00000	CTR9	11	Endosome	E3 ubiquiti	10	1.017	0.83493041	20.73	1377.3	1354	13.55	1.22	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q07812	Apoptosis	0	6.344	6	1	3	1	192	21.2	5.22	4.45	1	cell differe	cytoplasm;	protein	br	P04052	581	ENSG00000	BAX	19	Viral carc	MyRAN Reg	TP53 Regu	49	1.017	0.923737721	11.49	757.5	731.6	8.57	2.06	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	P52434	DNA-direct	0	8.817	22	4	4	4	150	17.1	4.68	4.42	4	metabolic	cytosol;nu	catalytic	ai	P03870	5437	ENSG00000	POLR2H	3	Purine met	Eukaryotic	Signaling b	98	1.017	0.972434759	12.65	1354.8	1334	5.44	7.69	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	P22059	Oxyesterol	0	31.33	12	6	8	6	807	89.4	7.3	17.41	6	metabolic	cytoplasm;	protein	br	P01069, F	5007	ENSG00000	OSBP	11		Synthesis c	7	1.016	0.37123808	3.29	992	963.9	2.19	2.36	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q9BNU8	Probable A	0	42.072	16	11	13	11	820	95.5	9.55	13.37	11	cell organ	cytoplasm;	catalytic	ai	P00270, F	9416	ENSG00000	DXX3	12	Spliceosom	mRNA Spli	6	1.016	0.506065449	4.87	407.4	440.8	14.86	15.67	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q7Z5K2-1	Wings apa	0	9.933	2	2	2	2	1190	132.9	5.44	5.97	2	cell division	chromoso	protein	br	P07814	23063	ENSG00000	WAPAL	W	10		Cohesin Lo	12	1.016	0.566035582	17.7	927	912	19.11	8.85	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q9RT05	Serine/thr	0	5.553	2	2	2	2	950	106.9	4.77	3.74	2	metabolic	cytoplasm;	catalytic	ai	9989		ENSG00000	PPPAR1	18			0	1.016	0.566179677	3.31	257.1	286.4	7.56	12.69	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q000291	Huntingtin	0	19.358	7	6	7	6	1037	116.1	5.3	9.76	6	cell death;	cytoplasm;	catalytic	ai	P00038, F	3092	ENSG00000	HIP1	7	Huntingtor	Clathrin-m	4	1.016	0.572369582	2.48	992.2	1046.2	10.18	5.43	High	High	High	High	High	High	High	1	[Q51]	
FALSE	High	Master Prq	Q06888-1	Protein Cu	0	8.708	18	2	3	2	179	19.1	5.5	5.87	2	response t	membrane	metal ion	l	P03091	51596	ENSG00000	CUTP4	6, CHR_	HS		0	1.016	0.583956202	5.87	874	860.4	4.8	9.13	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q75N03	E3 ubiquiti	0	5.799	4	1	1	1	491	54.5	8.29	3.54	1	metabolic	cytosol;nu	catalytic	ai	P00097, F	79872	ENSG00000	CBLL1	7		Intra-mem	4	1.016	0.591565296	10.84	423.9	423.3	11.75	1.11	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	P38435-1	vitamin K	0.003	2.999	2	1	1	1	758	87.5	8.02	2.57	1	coagulat	endoplasm	catalytic	ai	P05090	2677	ENSG00000	GGCX	2		Ubiquinol	Gamma-ca	6	1.016	0.59957749	1.29	618.5	635.1	11.46	4.83	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q15371	Eukaryotic	0	27.594	14	8	10	8	548	63.9	6.05	24.94	8	cell organ	cytoplasm;	protein	br	P05091	8664	ENSG00000	EIF3D	22	RNA trans	Translatior	Formation	13	1.016	0.652773021	1.77	1865	1871.5	2.3	7.5	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	P30825	High affini	0	14.691	7	3	6	3	629	67.6	5.43	16.82	3	transport	membrane	protein	br	P00324, F	6541	ENSG00000	SLC7A1	13	MicroRNA	Amino aci	5	1.016	0.562915797	15.8	709.3	701.9	15.88	10.17	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q57FE4	5'-nucleoti	0	37.952	27	8	8	8	455	51.8	6.35	22.21	8	metabolic	cytoplasm;	catalytic	ai	P05761	221294	ENSG00000	NTSDC1	6			0	1.016	0.661869874	8.74	887.4	911.6	12.57	5.8	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	P45880	Voltage-de	0	101.283	56	14	33	14	294	31.5	7.56	88.71	14	regulation	membrane	nucleotide		P01459	7417	ENSG00000	VDAC2	10	Calcium sig	Mitochond	12	1.016	0.7106401	3.27	5839.3	5667.2	9.3	2.17	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q153397	Pumilio ho	0	19.209	13	5	5	5	648	73.5	9.64	11.13	5	regulation	chromoso	DNA bindi	ng	P07369, F	9933	ENSG00000	KAOA020	9			0	1.016	0.801916425	4.19	815.8	802.7	0.45	6.86	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q14481-1	RNA-bindin	0	75.01	30	13	24	13	530	59.3	10.1	66.97	13	metabolic	cytoskelet	protein	br	P07676, F	9584	ENSG00000	RBM39	20		mRNA Pro	1	1.016	0.805083666	13.57	4645.9	4454.7	14.15	42.5	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	P36954	DNA-direct	0.009	2.178	18	1	1	1	125	14.5	5.14	0	1	metabolic	nucleus	catalytic	ai	P01096, F	5438	ENSG00000	POLR2I	29	Huntingtor	Eukaryotic	Signaling b	75	1.016	0.806363188	14.83	29.9	29.4	13.55	3.44	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	P48059	LM and se	0.003	3.473	4	1	1</																																			

[illegible]

FALSE	High	Master Prq	Q09U63-1	muskelin [l]	0	7.101	4	2	2	2	735	84.7	6.34	2.64	2	cell organ	cytoplasm; protein br	P00754, F 4289	ENSG000001	MXK1N	7						0	1.004	0.883501158	3.15	957.3	959.6	3.43	0.47	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q09Y16	Hydroxytol	0	33.172	17	6	11	6	418	45.4	7.99	21.78	6	metabolic	membrane catalytic ac	P00106, F 84263	ENSG000001	HSDF	10						0	1.004	0.934919741	53.35	1803	1795.9	23.07	15.48	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q09ZM1	Myoflerin	0	380.281	43	75	131	75	2061	234.6	6.18	316.03	75	cell organ	membrane protein br	P00106, F 26509	ENSG000001	MYOF	10						2	1.004	0.951361823	6.89	36905.5	36750.1	1.55	4.03	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q09061	heme oxy	0	8.632	8	1	1	1	288	32.8	8.25	5.61	1	cell comm	cytosol;eme catalytic ac	P01216	ENSG000001	HMOX1	22	MicroRNA	NRF2 path	Interleukin			19	1.003	0.467791769	7.65	213.6	237.2	24.37	20.29	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q13939-1	Beta-enola	0	84.996	29	9	76	4	434	47	7.71	182.5	9	metabolic	cytoplasm; catalytic ac	P00113, F 3012	ENSG000001	ENO3	17	Metabolic	Glycolysis	Glucconeol			12	1.003	0.498507795	5.58	605.8	602.1	24.17	0.28	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q62826	GTP-bindin	0	129.973	60	17	68	17	216	24.4	7.49	214.99	17	cell divisi	chromosor catalytic ac	P00025, F 5901	ENSG000001	RAN	12	Ribosome	Androgen	MicroRNA			30	1.003	0.508556702	1.39	22363.5	22906.9	3.3	6.69	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q61956	small ubiq	0	27.832	29	3	12	1	95	10.9	5.5	27.66	3	metabolic	nucleus catalytic ac	P00340, F 6613	ENSG000001	SUMO2	17	RNA trans	SLMOYlat			22	1.003	0.545457581	1.62	786	783.5	5.51	7.46	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q09Y676	28S riboso	0	22.08	23	4	10	4	258	29.4	9.38	31.09	4	cell organ	membrane protein br	P01084	ENSG000001	MRPS18B	6	CHR_H5	Vital cardis	Mitochond			7	1.003	0.597421105	3.21	2881.7	2972.6	5.99	2.21	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q42356	phosphatic	0	11.723	1	1	3	1	2102	236.7	7.06	8.67	1	cell organ	cytoplasm; catalytic ac	P00545, F 5297	ENSG000001	PA4A	22	Metabolic	Ecdoderm	Synthesis c			10	1.003	0.740242834	24.46	204.6	228.8	23.25	9.73	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q06043	Non-syndr	0	35.108	17	6	7	6	496	54.5	15.72	15.32	6	cell death	cytoplasm; catalytic ac	P00598, F 1687	ENSG000001	OFAS, G5	7						0	1.003	0.762199622	27.94	940.8	937.8	18.79	9.74	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q09WV3	Reticulon-	0	4.91	5	1	1	1	396	43.6	9.11	4.4	1	metabolic	membrane catalytic ac	P00107, F 84816	ENSG000001	RTN4P1	16						0	1.003	0.781934551	9.49	452.2	459.5	9.51	1.36	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q21926	CD9 anti-b	0	39.66	15	2	7	2	228	25.4	7.15	39.62	2	cell organ	cell surface protein br	P00335	ENSG000001	CD9	12	Hematopo		Platelet de			12	1.003	0.807271841	54.5	877.9	880	29.54	17.67	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q002127	Dihydroorn	0	6.604	6	1	2	1	395	42.8	9.67	9.93	1	metabolic	cytoplasm; catalytic ac	P01180	ENSG000001	DHODH	16	Metabolic		Pyrimidine			6	1.003	0.820330321	23.86	424.6	423.5	11.11	9.03	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q56211	cAMP-reg	0	14.744	17	2	6	1	112	12.3	9.09	13.35	2	cell divisi	cytoplasm enzyme re	P04667	ENSG000001	ARPP19	15						5	1.003	0.843763522	5.81	1691.7	1623.3	6.35	10.79	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q13148-1	TAR DNA-	0	75.981	34	11	19	11	414	44.7	6.19	52.58	11	cell organ	cytoplasm; DNA bindi	P00076, F 23435	ENSG000001	TARDBP	1						0	1.002	0.464686547	12.39	4298.8	4292.1	47.43	9.13	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q14789	Golgim sub	0	89.134	9	23	27	23	3259	375.8	5	56.26	23	cell organ	Golgi;mem catalytic ac	P01496, F 2804	ENSG000001	GOLG81	3						11	1.002	0.52455551	4.28	3174.3	3068.3	8.53	4.22	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q49959	Double-str	0	11.757	6	4	6	4	708	80.5	5.9	14.97	4	cell organ	chromosor catalytic ac	P00149, F 4361	ENSG000001	MOE11A, Y	11	Homologoi	miRNA Reg	G2/M DNA			47	1.002	0.591944791	6.63	2085	2081.1	3.55	7.25	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q09052-1	Zinc phos	0	19.331	7	5	6	5	826	92.2	7.9	11.27	5	cell organ	mitochond catalytic ac	P00753, F 60528	ENSG000001	ELAC2	7			tRNA proc			7	1.002	0.621080007	3.71	790.4	788.9	8.32	3.84	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q61011-1	signal reco	0	21.73	10	5	7	5	504	55.7	8.75	13.84	5	cell organ	cytoplasm; catalytic ac	P00448, F 6729	ENSG000001	SRP54	5			Protein exp	miRNA Pro	SRP-depen	5	1.002	0.65793306	8.27	1919.1	2014.7	8.28	6.02	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q43243	Matrin-3 [l]	0	214.987	48	37	91	37	847	94.6	6.25	262.98	37	defense re	membrane metal ion	P00076, F 9782	ENSG000001	MATR3	14						0	1.002	0.699477083	6.3	19867.5	20151.1	2.7	5.28	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q09VH1-1	Dnai hom	0	13.23	6	2	2	2	559	63.2	8.4	5.72	2	cell organ	membrane protein br	P00226, F 55735	ENSG000001	DNAIC1	11						3	1.002	0.718537315	8.84	502.7	491.1	2.56	11.27	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q36915-1	Guanine m	0	10.36	7	4	5	4	607	68.6	5.8	11	4	regulation	nucleus catalytic ac	P01266, F 2794	ENSG000001	GNL1	6	CHR_H5					0	1.002	0.844024226	5.61	736.4	703.7	13.04	11.92	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q14678-1	KN motif a	0	21.319	5	4	5	4	1352	147.2	5.3	18.91	4	cell organ	cytoplasm; protein br	P00203, F 23189	ENSG000001	KANK1	9						0	1.002	0.9449033	24.87	905.3	903.5	9.15	11.57	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q51665	26S protea	0	22.742	24	6	9	6	324	37	6.77	26.9	6	metabolic	cytosol;ext catalytic ac	P01398, F 5713	ENSG000001	PSM07	16						153	1.001	0.433597253	0.06	2147.4	2166.7	2.65	2.69	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q75083	WD repeat	0	84.855	30	13	23	13	606	66.2	6.65	64.14	13	cell differ	cytoplasm; protein br	P00400, F 9948	ENSG000001	WDR1	4						5	1.001	0.505502444	1.02	4087.9	4042	3.02	2.14	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q75083-1	Ubiquitin-1	0.001	4.471	51	2	2	2	85	9.1	9.31	51.61	2	metabolic	cytoplasm; protein br	P03671	ENSG000001	UFM1	13						0	1.001	0.511474522	14.63	243.7	231	35.08	7.93	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q62304	small nucle	0	10.656	17	2	8	2	92	10.8	9.44	11.75	2	cell organ	cytoplasm; protein br	P01423	ENSG000001	SNRPE	1						16	1.001	0.513110038	2.11	1467.3	1465.8	6.97	2.02	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q09H47	Probabke 2	0.006	2.431	1	1	1	1	919	10.3	6.93	0	1	cell differ	cytosol;mi catalytic ac	P00676, F 55526	ENSG000001	DHTKD1	10						4	1.001	0.52211383	2.14	499.4	464.9	7.28	6.79	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q11117	Lysosomal	0	10.927	8	3	3	3	423	48.3	6.74	9.01	3	cell organ	membrane catalytic ac	P00328	ENSG000001	ACP2	11						1	1.001	0.527728528	9.29	297	306.5	21.39	4.12	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q09UN25	Leydig cell	0.002	3.878	14	2	3	2	99	10.6	11.55	18.82	2	nucleus		P009495	ENSG000001	C19orf53	19						0	1.001	0.579839342	11.35	1368.8	1366.9	10.62	10.08	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q09H37	Golgi resid	0	29.065	16	6	9	6	528	60.6	5.06	22.46	6	metabolic	Golgi;mem protein br	P00373, F 64746	ENSG000001	ACOB	1						5	1.001	0.620782709	21.81	1852	1816.7	25.89	11.11	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q51731-1	Cytocromo	0	15.819	22	3	4	3	125	14.1	8.25	9.64	3	cell organ	membrane catalytic ac	P00297	ENSG000001	CAD3	6						2	1.001	0.64274736	14.42	363.4	340.3	14.36	6.79	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q09Y289	28S riboso	0	30.692	32	5	8	5	242	28.1	9.99	25.03	5	cell organ	membrane RNA bindi	P00177	ENSG000001	MRP57	17						7	1.001	0.723518123	5.21	2972.7	2970.9	8.5	3.36	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q42221-1	Signal tran	0	20.851	7	4	5	4	750	87.3	6.05	11.45	4	cell death	cytoplasm; DNA bindi	P00017, F 6772	ENSG000001	MRP21	2						81	1.001	0.746557351	4.09	566.8	542.3	2.68	4.32	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q09583-4	Isform 1	0	24.371	9	6	7	5	826	92.4	7.71	22.3	6	cell organ	cytoplasm; catalytic ac	P00069, F 6732	ENSG000001	SRPK1	6						1	1.001	0.810949234	22.58	2629	2626	15.66	6.2	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q05145	Actin-relat	0	6.393	14	3	4	3	178	20.5	8.99	2.25	3	cell organ	cytoplasm; protein br	P04062	ENSG000001	ARPC3	12						23	1.001	0.901123468	9.84	1958.6	1956.8	3.12	4.36	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q06744	glucose-6-	0	201.3																																				



FALSE	High	Master Prq Q9NY27	Serine/thr	0	14.647	11	4	4	4	417	46.9	4.54	10.72	4	metabolic	cytoplasm; enzyme re	P109184, F151987	ENSG000001	PP4R2	3	6	CHR_HS			Processing	5	0.997	0.4903699	3.68	768.4	771	9.88	1.28	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q95870.1	Protein Ab	0.001	4.415	2	1	1	1	558	63.2	8.13	4.04	1	metabolic	membrane catalytic ac	P00561, F7920	ENSG000001	ABHD16A	11	6					0	0.997	0.505039756	6.36	283.4	294.6	8.25	10.34	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q98R94	Proteasom	0	13.849	9	3	3	3	392	42.2	6.32	7.98	3	proteasom	protein br	P00400	ENSG000001	PAF1	11	0	0.997	0.543802588	4.21	576.7	574.8	6.59	10.95	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq P25787	Proteasom	0	61.89	52	9	23	9	234	25.9	7.43	56.72	9	metabolic	cytoplasm; catalytic ac	P00227, F5683	ENSG000001	PSMA2	7	151	Proteasom	Proteasom	Regulation	151	0.997	0.563299392	6.26	5867.4	5600.5	10.24	4	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q9Y477.1	plexin-D1	0	11.281	3	2	2	2	1925	21.9	7.15	8.27	2	cell organ	membrane protein br	P01403, F23129	ENSG000001	PLXND1	1	4	0.997	0.670102285	9.77	331.6	326.7	3.06	10.06	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq P30623.1	isoform 2	0	57.838	13	16	18	13	1427	160.9	5.39	32.65	16	cell differ	chromosom catalytic ac	P01302, F6249	ENSG000001	CLP1	12	1	0.997	0.679862751	49.94	1031.7	1046.6	39.51	4.01	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq Q95736	Synaptic ve	0	56.964	23	6	17	6	393	41.9	6.29	44.04	6	metabolic	cytoplasm; catalytic ac	P00107, F10493	ENSG000001	VPS1	17	3	0.997	0.803696272	9.91	5300.3	5314	5.25	4.05	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq Q9NV92	Histone ch	0	10.155	17	2	2	2	202	22.4	4.56	8.48	2	cell differ	chromosom protein br	P04729	ENSG000001	ASF1B	19	0	0.996	0.434531907	2.11	453.3	467.3	15.74	5.96	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq Q8N758	RNA polyn	0	11.719	7	3	3	3	531	59.9	4.63	7.93	3	cell organ	cytoplasm; protein br	P03985	ENSG000001	PAF1	19	10	0.996	0.462749607	2.84	141	153.3	10.84	4.93	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq Q14978.3	isoform 3	0	193.017	46	28	88	1	700	73.7	9.47	212.49	28	cell organ	cytoplasm; nucleotide	P05022	ENSG000001	NOLC1	10	0	0.996	0.50202858	17.73	382.4	453.7	23.39	28.45	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq Q60678	protein arg	0	10.263	7	3	4	3	531	59.8	5.35	8.84	3	cell organ	cytoplasm; catalytic ac	P06325, F10196	ENSG000001	PRMT3	11	6	0.996	0.603182314	11.33	492.5	532.5	26.3	11.24	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq Q72627	E3 ubiquit	0	253.95	14	46	73	46	4374	481.6	5.22	195.31	46	cell differ	cytoplasm; catalytic ac	P00632, F10075	ENSG000001	HUWE1	1	7	0.996	0.641888546	18.28	19554.3	19640.4	19.53	5.54	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq P17706-1	Tyrosine-p	0	10.436	6	2	2	2	415	48.4	8.29	2.12	2	cell differ	cytoplasm; catalytic ac	P00102	ENSG000001	PTPN2	18	18	Jak-STAT si	Negative r	5	0.996	0.684048247	3.52	517.4	531.9	7.06	2.6	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P46459	Vesicle-fus	0	26.414	12	6	10	6	744	82.5	6.95	24.76	6	cell organ	cytoplasm; catalytic ac	P00004, F4905	ENSG000001	NSF	17	25	0.996	0.786332292	16.01	2422.1	2415.8	6.69	9.77	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq P40616	ADP-ribos	0	9.382	23	3	3	3	181	20.4	5.72	8.8	3	cell organ	cytoplasm; catalytic ac	P00025, F400	ENSG000001	ARL1	12	4	0.996	0.795828431	19.9	678.6	718.3	10.31	11.42	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq Q9NM63	MICOS cor	0	15.349	14	3	4	3	227	26.1	8.28	10.99	3	cell organ	cytoplasm; protein br	P05300, F54927	ENSG000001	CHCHD3	7	5	0.996	0.881710878	42.85	2299.2	2308.2	24.29	7.52	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq P53004	Biliverdin r	0	33.786	26	7	10	7	296	33.4	6.44	27.87	7	metabolic	cytoplasm; catalytic ac	P01408, F644	ENSG000001	BLVR4	12	4	0.995	0.481316692	0.79	2151.2	2217.3	8.33	7.1	High	High	High	High	High	High	High	High	1				
FALSE	Low	Master Prq Q9UK24	Teneurin-1	0.059	1.124	1	1	1	1	2725	304.8	6.42	0	1	cell organ	cytoplasm; protein br	P06848, F10178	ENSG000001	TENM1	X	0	0.995	0.544291803	13.5	37.9	43.2	27.61	10.18	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq P84103	Serine/arg	0	43.825	47	8	22	8	164	19.3	11.65	31.08	8	metabolic	cytoplasm; protein br	P00076, F6428	ENSG000001	SRSF3	5	14	0.995	0.658200546	5.64	1489.5	1472.1	1	5.96	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq Q96KR1	Zinc finger	0	32.713	9	7	10	7	1074	116.9	9.04	22.01	7	developm	chromosom DNA bindi	P07528, F51663	ENSG000001	ZFR	6	1	0.995	0.630464617	8.45	1450.6	1441.6	9.84	1.84	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq P35241-1	radixin [OS	0	178.566	49	34	91	18	583	68.5	6.37	164.2	34	cell organ	cytoplasm; protein br	P00373, F5962	ENSG000001	RDX	11	8	0.995	0.689716555	8.93	6789.4	7112.2	11.84	2.45	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq P37871-1	T-complex	0	322.384	75	31	106	31	535	57.5	6.46	381.95	31	cell organ	cytoplasm; nucleotide	P00118	ENSG000001	CTC2	12	16	0.995	0.747785788	11.52	31418.7	30632.3	9.87	4.26	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq Q9Y649	Signal pep	0	6.045	17	1	2	1	102	11.8	9.31	6.62	1	metabolic	endoplasm catalytic ac	P06645	ENSG000001	SPC51	3	9	0.995	0.838818917	47.23	801.5	805.8	18.38	21.19	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq Q95782	AP-2 comp	0	59.769	16	11	14	6	977	107.5	7.03	46.59	11	cell organ	cytosol;me protein br	P01602, F160	ENSG000001	AP2A1	19	48	0.995	0.851127788	23.04	1220.2	1192.8	16.49	6.72	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq P62312	U6 snRNA	0	6.229	14	1	4	1	80	9.1	9.58	7.7	1	metabolic	cytoplasm; protein br	P01423	ENSG000001	LSM6	4	8	0.995	0.967967776	26.25	900.8	1082.7	27.03	10.85	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq P62136-1	serine/thru	0	6.58	48	13	25	3	330	37.5	6.33	79.01	3	cell divisio	cytoplasm; catalytic ac	P00149	ENSG000001	PP2CA	11	35	0.994	0.406576299	1.2	248.3	252.4	5.14	3.11	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq Q15404-1	Ras suppr	0	23.568	24	4	7	4	277	31.5	8.65	19.74	4	regulation	cytosol protein br	P08757	ENSG000001	RSU1	10	4	0.994	0.469747766	4.82	1306.1	1354.8	3.69	11.93	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq Q7265M-1	Rab9 effec	0	13.686	8	2	2	2	372	40.5	6.25	61.2	2	transport	cytoplasm; protein br	P01344, F10244	ENSG000001	RAB6P1	4	4	0.994	0.496894434	19.61	270.4	272.1	46.86	7.9	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq Q9NCAS	protein FA	0	32.106	10	4	5	3	519	55.4	9.03	19.7	4	metabolic	catalytic ac	P01239	ENSG000001	FAM98A	2	0	0.994	0.533278463	11.28	387.6	362.7	20.49	11.6	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq Q00499-2	isoform IIB	0	59.186	20	7	14	7	518	56.5	5.12	40.67	7	cell differ	cytoplasm; protein br	P00118, F274	ENSG000001	BIN1	2	1	0.994	0.563160466	17.57	2791.1	2807.5	28.58	1.49	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq Q13769	THO comp	0	10.773	5	3	4	3	683	78.5	6.87	117.1	3	cell differ	cytoplasm; protein br	P09766	ENSG000001	THOC5	22	0	0.994	0.575243274	0.19	1785.8	1785.7	1.57	1.75	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq P07951-1	Tropomyos	0	63.92	38	14	31	1	284	32.8	4.7	55.8	14	cell organ	cytoplasm; protein br	P00621, F7169	ENSG000001	PM2	5	8	0.994	0.580456113	9.77	93.4	96.9	5.85	11.96	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq Q13131	5'-AMP-ac	0	11.815	10	4	4	4	559	64	8.12	7.82	4	cell comm	cytoplasm; catalytic ac	P00609, F5562	ENSG000001	PKRAA1	5	41	0.994	0.581709297	16.34	144.2	152.9	14.45	13.89	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq Q9H464	Ketosamin	0	10.935	9	2	2	2	309	34.4	7.33	7.27	2	metabolic	cytosol catalytic ac	P01636, F79672	ENSG000001	ARGKRP	17	3	0.994	0.657203042	23.3	535.1	538.4	21.09	7.23	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq Q104907	Rax1-bind	0	21.133	33	3	3	3	124	13.7	8.48	10.58	3	regulation	cytoplasm; protein br	P00595, F30851	ENSG000001	TAXBP3	17	4	0.994	0.69549938	28.73	718.4	718.4	30.14	10.88	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq P62820	Tax-relate	0	70.477	60	13	28	6	205	22.7	6.21	65.62	13	cell organ	cytoplasm; catalytic ac	P00009, F5861	ENSG000001	RAB1A	2	21	0.994	0.780758201	7.18	2438.1	2461.1	3.42	3.06	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq P62913	60S riboso	0	45.34	43	9	27	9	178	20.2	9.6	47.25	9	cell differ	cytoplasm; protein br	P00189, F6135	ENSG000001	RLP11	1	34	0.994	0.976707852	23.74	7528.5	7573.9	8.71	8.73	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq P04083	annexin A1	0	193.652	69	24	105	24	346	38.7	7.02	305.75	24	cell organ	cell surface catalytic ac	P00191	ENSG000001	ANXA1	9	20	0.994	0.98710686	17.21	32606.8	32808.3	5.44	7.25	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq Q9UM06	Dual speci	0	11.43	10	2	2	2	340	37.7	6.84	7.78	2	metabolic	cytoplasm; catalytic ac	P00782	ENSG000001	DUSP12	1	0	0.9																			



FALSE	High	Master Prq Q3ZC08	Mitochond	0	40.836	21	7	12	7	353	39.6	8.37	23.96	7	cell organi	membrane	catalytic ac	P03301, 92609	ENSG000001	TMM50	19				Mitochond	2	0.985	0.782195605	4.01	1715.6	1778.3	6.73	3.2	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q96K17-1	transcripti	0	15.046	27	3	3	2	158	17.3	6.35	9.72	3			protein bin	P01849	91408	ENSG000001	BTFL3A	1					0	0.985	0.844742023	5.61	328.6	321.9	3.58	9.87	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q99023	60S riboso	0	177.395	62	26	78	26	403	46.1	10.18	180.81	26	cell organi	cytoplasm;	protein bin	P00297	6122	ENSG000001	P9031	22			Ribosome	Cytoplasm	Peptide ch	34	0.985	0.85114843	7.96	24640.4	27001.8	0.43	6.6	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q15437	protein tra	0	60.888	17	9	14	7	767	86.4	6.89	47.33	9	transport	cytoplasm;	metal ion	P00626, 10483	ENSG000001	SEC23B	30			Endocyt	Sterol Reg		2	0.985	0.878662115	18.57	1517.2	1565.8	14.96	1.34	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q06751	RUN and F	0	20.309	7	4	8	4	708	79.8	5.74	14.63	4	metabolic	cytoplasm;	metal ion	P01363, 80230	ENSG000001	RUF1	5	CHR, HC	Endocyt	Synthesis c		6	0.985	0.879560478	27.96	1517.8	1480.9	12.38	16.36	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q94906-1	Pre-mRNA	0	93.542	29	23	34	23	941	106.9	8.25	72.48	23	cell organi	membrane	protein bin	P06424, 72148	ENSG000001	PRPF6	20			Spliceosom	mRNA Pro	mRNA Spli	7	0.985	0.986001896	13.12	7459.9	7573.1	7.88	3.05	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q94911	elongation	0	157.948	59	22	63	22	452	49.9	7.61	150.47	22	metabolic	membrane	catalytic ac	P00400, 10607	ENSG000001	TUFM	16			Mitochond			4	0.984	0.151124607	0.89	18828	18994.1	0.91	0.46	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q98238	Heat shock	0	640.657	71	68	446	24	724	83.2	5.03	1169.1	68	cell organi	cell surface	enzyme re	P00083, 73326	ENSG000001	HP90A81	6			Prostate c	NR2F path	semalSA Pi	42	0.984	0.293796434	0.35	25587.7	25992.1	7.63	1.42	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9UHQ9	NADH-cyt c	0	11.845	10	2	2	2	305	34.1	9.88	3.14	2	metabolic	membrane	catalytic ac	P00175, 71706	ENSG000001	CYBSR1	1			Amino su	Oxidation	Platelet de	9	0.984	0.436667452	5.43	808.5	849.2	9.77	5.66	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q99023	3-oxoacyl-c	0	13.717	9	2	2	2	459	48.8	7.66	8.69	2	metabolic	cytosol;mi	catalytic ac	P00108, 74995	ENSG000001	OKSM	3			Metabolic			4	0.984	0.489672252	18.98	52.3	60.7	9.06	39.36	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q00765	Receptor e	0	16.119	15	4	8	4	189	21.5	8.1	8.82	4	metabolic	endoplasm	protein bin	P01314	7905	ENSG000001	REEP5	5			Olfactory s		4	0.984	0.490305886	5.17	1299.8	1351.3	5.82	6.18	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q12788	Transducin	0	39.67	14	6	7	6	808	89	6.9	18.67	6	metabolic	nucleus	protein bin	P00400, 10607	ENSG000001	TBL3	16			Ribosome	Major pat		6	0.984	0.55122581	10.87	1088.5	1103.2	26.05	4.46	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q86V48-1	Leucine zip	0	23.603	6	4	5	4	1076	120.2	8.5	14.86	4	metabolic	membrane		P04111	7798	ENSG000001	LUZP1	1					0	0.984	0.551903409	40.14	670.5	681.2	53.66	13.08	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q8N1P7	beta/gamr	0	9.48	4	1	1	1	616	68.6	5.1	4.68	1				P00030, 755057	ENSG000001	AIM1L; CR	1					0	0.984	0.583815295	7.65	305.9	306.6	6.67	1.09	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q16181	Septin-7 (C	0	29.298	18	8	10	8	437	50.6	8.63	23.83	8	cell differe	chromosom	nucleotide	P00735, 7989	ENSG000001	SEPT7	7			MAPK6/M		3	0.984	0.587427043	5.14	3896.1	3960.4	11.8	3.88	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q14880	Microsomi	0	26.343	16	2	3	2	152	16.5	9.38	15.73	2	metabolic	endoplasm	antioxidan	P01124	4259	ENSG000001	MGST3	1			Drug meta	NR2F path	Glutathion	12	0.984	0.689544835	7.25	260.6	228.3	9.06	13.2	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q8TA76-1	Nuclear pr	0	31.241	9	4	6	4	608	68.1	6.38	14.62	4	cell organi	cytoplasm;	metal ion	P05020, 75566	ENSG000001	NPLOC4	2			Protein prc	Translesio		5	0.984	0.711728166	16.29	1465.2	1390.8	15.39	5.03	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q890V3	Putative ri	0	6.011	6	1	1	1	343	38.3	7.85	4.95	1	metabolic	mitochond	catalytic ac	P02033, 79863	ENSG000001	RBFA	18					0	0.984	0.740954833	39.96	382.5	388.8	26.01	19	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q8BW12	PEST prote	0	59.591	53	8	17	8	178	18.9	7.49	44.86	8	metabolic	nucleus	protein bin	P115473	57092	ENSG000001	PCNP	3					0	0.984	0.762719499	20.45	5720.6	5816.3	17.96	3.38	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q94903	Pyridoxal p	0.009	2.128	3	1	1	1	275	30.3	7.5	2.55	1	cytoplasm;			P01168	11212	ENSG000001	PROSC; PU	8					0	0.984	0.836108611	18.15	397.2	403.5	13.16	1.1	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9P2N5	RNA-bindin	0	6.535	2	2	2	2	1060	118.6	9.19	1.65	2	metabolic	cytoplasm;	metal ion	P00076, 75439	ENSG000001	RBMT2	7					0	0.984	0.850867592	0.78	2186.4	2118.7	21.11	22.38	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q9P2P3	Aldheyde c	0	18.572	15	6	7	5	517	57.2	6.8	17.58	6	metabolic	mitochond	catalytic ac	P00171	219	ENSG000001	ALDH1B1	9			Tryptophan	Ethanol ox	17	0.984	0.92205273	31.43	826.2	839.6	21.93	4.28	High	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9UHD1	cysteine ar	0	78.117	48	12	24	12	332	37.5	7.87	71.94	12	metabolic		metal ion	P04068, 76293	ENSG000001	CHORDC1	11					0	0.984	0.926488378	14.07	7031.2	7147.4	7.02	3.73	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q9P2E9-1	Enhancer c	0	32.429	5	5	7	5	1401	151.6	5.86	25.06	5	metabolic	cytoplasm;	protein bin	P00400	23644	ENSG000001	EDC4	16			RNA degra	mRNA dec	4	0.984	0.965411418	12.94	1403.7	1470.1	12.25	3.28	High	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9UHQ3-1	Gamma-ta	0	16.503	13	5	6	5	528	60.5	7.52	7.84	5	metabolic	cytoplasm;	protein bin	P09728	55787	ENSG000001	TXLNK	X				0	0.983	0.340473184	3.57	398.2	405.2	2.02	4.68	High	High	High	High	High	High	High	High	High	1	
FALSE	Medium	Master Prq Q15047	Histone-ly	0.028	1.457	1	1	2	1	1291	143.1	6.02	1.96	1	cell organi	chromosom	catalytic ac	P00856, 79869	ENSG000001	SETD81	1			Lysine deg	Histone M	PKMTs me	6	0.983	0.504950508	22.19	714.4	724.4	3.67	46.01	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P17535	Transcripti	0	17.284	12	3	4	2	347	35.2	7.37	14.5	3	metabolic	chromosom	DNA bindin	P00170, 73727	ENSG000001	JUND	19			MAPK sign	Corticoste		10	0.983	0.509375766	2.54	200.6	199.1	14.29	7.45	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P06733-1	alpha-enol	0	60.886	81	40	410	14	434	47.1	7.39	1039.59	40	metabolic	cell surface	catalytic ac	P00113, 72023	ENSG000001	ENO1	1			Biosynthes	Glycolysis	Gluconeog	12	0.983	0.567317991	7.72	36285	36925.3	4.57	3.09	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P49459-1	Ubiquitin	0	0.802	18	2	2	2	152	17.3	5.15	5.14	2	cell organi	chromosom	catalytic ac	P00179, 7319	ENSG000001	UBE2A	X			Ubiquitin r	Synthesis c		10	0.983	0.571246778	9.22	134.6	134	20.79	5.09	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q8BU12-1	Kinectin (C	0	78.895	13	16	22	26	1357	156.2	5.64	55.06	16	cellular co	endoplasm	protein bin	3895	ENSG000001	SGOL20.1	14			Post-transl		8	0.983	0.574736311	15.3	5137.1	5223.7	28.07	4.48	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q9H9L3	Interferon	0.002	3.77	4	1	1	1	353	39.1	9.94	2.89	1	metabolic	nucleus	catalytic ac	P00929	81875	ENSG000001	SGOL20.1	14			Major pat		4	0.983	0.815745932	20.18	225.7	229.6	9.07	22.71	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9UJX5	Anaphase-	0	5.99	2	1	1	1	808	92.1	5.53	4.44	1	cell divisio	cytosol;nu	catalytic ac	P11284, 79945	ENSG000001	ANAPCA	4			HTLV-1 inf	APC/Cdcl	37	0.983	0.823103989	37.3	443.1	451	28.14	8.94	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq P24928	DNA-direct	0	27.798	3	3	4	3	1970	217	7.37	17.7	3	metabolic	cytoplasm;	catalytic ac	P00076, 75439	ENSG000001	POLR2A	17			Metabolic	Eukaryotic	Signaling b	77	0.983	0.848872788	1.74	730.1	705.5	3.92	4.43	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9Y2S5	28S riboso	0	35.102	52	5	6	5	130	14.5	9.85	23.95	5	cell organi	membrane	RNA bindin	P00366	51373	ENSG000001	MRPS17	7			Ribosome	Mitochond		7	0.983	0.873980675	8	1615.9	1655.6	2.43	5.46	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q06884	DNA homc	0	45.983	31	9	11	9	412	45.7	6.48	25.48	9	metabolic	cytosol;me	enzyme re	P00226, 710294	ENSG000001	DNAJ2	16			Protein prc	HSF90 cha	4	0.983	0.88415284	11.73	3304.8	3362.8	8.95	3.23	High	High	High	High	High	High	High	High	1		
FALSE	Low	Master Prq Q95490-1	Adhesion c	0.062	1.108	1	1	1	1	1459																																		

FALSE	High	Master	Prq	QBWUWJ	Protein BR	0	4.643	25	2	2	2	75	8.7	5.45	3.14	2	cell organ	cytoplasm	protein br	55845	ENSG00000	BRK1	3	Regulation	Regulation	Regulation	13	0.979	0.612726485	10.58	1525.5	1557.8	15.71	7.41	High	High	High	High	High	High	High	High	1		
FALSE	High	Master	Prq	Q9289B1	Polyubino	0	6.548	5	2	2	2	425	47.6	6.62	5.36	2	cell organ	cytosol;nu	catalytic ac	P103205, F	10978	ENSG00000	CLP1	11	mRNA sur	mRNA Pro	Cleavage o	15	0.979	0.684124027	24.96	775.1	792	12.52	15.91	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	P13798	Acylamino	0	34.015	14	7	10	7	732	81.2	5.48	26.85	7	cell organ	cytoplasm	catalytic ac	P100326, F	327	ENSG00000	APFH	6			Eukaryotic	6	0.979	0.781756995	3.03	2658.2	2771.2	12.24	8.62	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	Q00055	Importin s	0	8.054	7	3	4	1	521	57.8	4.94	12.39	3	cell organ	cytoplasm	protein br	P100514, F	3839	ENSG00000	KPN3	23			N51 Media	10	0.979	0.8380377	4.91	335.2	328.5	5.75	4.51	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	P50909	T-complex	0	233.157	64	37	90	37	548	59.6	6.56	198.88	37	cell organ	cytoplasm	catalytic ac	P100118	10694	ENSG00000	CTC8	11			BB5ome-r	16	0.978	0.23233904	2.67	27388.6	28268.9	3.61	1.11	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	Q9Y580	RNA-bind	0	15.957	19	3	3	3	266	30.5	9.57	7.84	3	regulation	nucleus	protein br	P100076, F	101979	ENSG00000	NBM7	10				0	0.978	0.384094304	5.14	477.3	484	2.18	4.07	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	P49023	Psallvin [O]	0	23.772	15	5	5	5	591	64.5	6.19	13.73	5	cell organ	cytoplasm	DNA bindi	P100412, F	5829	ENSG00000	PNY	12	Leukocyte	Integrin-m	Localizati	33	0.978	0.396832121	4.69	1100.7	1237.1	11.66	8.52	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	Q04760	lactoyglut	0	25.915	39	8	9	8	184	20.8	5.31	17.97	8	cell differ	cytoplasm	catalytic ac	P100003, F	2739	ENSG00000	GLO1	4	Pyruvate r		Pyruvate r	5	0.978	0.405106166	5.46	3359.8	3436.2	11.64	2.89	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	Q94979	Protein tra	0	97.363	19	18	28	18	1220	132.9	8.89	79.13	18	cell organ	cytoplasm	protein br	P101154, F	22872	ENSG00000	SEC1A	4	Protein prc	Sterol Reg	Antigen Pr	18	0.978	0.619401176	11.63	8529.7	8314.6	10.15	5.43	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	Q86VM9	Zinc finger	0	24.89	9	7	10	7	953	106.2	6.82	15.8	7	nucleus	metal ion	P100642	124245	ENSG00000	ZCH18	16				0	0.978	0.63488812	6.12	2964.1	3009.5	11.36	5.64	High	High	High	High	High	High	High	High	1		
FALSE	High	Master	Prq	Q13630	GDP-L-fuc	0	7.258	7	2	2	2	321	35.9	6.6	4.8	2	metabolic	cytoplasm	catalytic ac	P101073, F	7264	ENSG00000	TS1A3	8; CHR_	HS	Fructose a		GDP-fucos	9	0.978	0.687133736	19.07	1304	1336.2	25.73	11.23	High	High	High	High	High	High	High	High	1
FALSE	High	Master	Prq	Q9Y2A7-1	Nck-asso	0	13.995	4	4	4	4	1128	128.7	6.62	10.56	4	cell death	cytosol;me	protein br	P109735	10787	ENSG00000	NCKAP1	2	Regulation	Exercise-in	Regulation	14	0.978	0.712691628	2.78	537	547.6	3.54	5.3	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	Q15942	Zyxin [OS-	0	45.563	29	11	15	11	572	61.2	6.67	24.81	11	cell comm	cytoplasm	metal ion	P100412	7791	ENSG00000	ZYX	7	Focal adhe			3	0.978	0.754352627	22.37	967	1025.2	25.31	3.02	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	Q08243-1	Asparagine	0	9.657	6	3	3	3	561	64.3	6.86	5.77	3	cell comm	cytosol	catalytic ac	P100310, F	440	ENSG00000	ASN5	7	Alanine, s	Glutathion	Amino acid	11	0.978	0.754618308	3.09	1425.4	1458	1.92	6.25	High	High	High	High	High	High	High	High	High	1
FALSE	High	Master	Prq	Q075874	Isoctrate c	0	65.492	36	14	26	14	414	46.6	7.01	51.49	14	metabolic	cytoplasm	catalytic ac	P100180	3417	ENSG00000	IDH1	2	Biosynthes	Glutathion	Neutrophil	21	0.978	0.793879813	22.94	5449.5	5629.4	19.43	7.2	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	Q14181	DNA polyb	0	18.328	13	4	5	4	598	65.9	5.24	13.12	4	cell organ	cytosol;nu	catalytic ac	P104042, F	23649	ENSG00000	POLA2	11	Purine mef	G1 to S cell	Activation	31	0.977	0.39422968	5.41	976.7	1114.9	9.42	8.49	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	QGNPQ8	Synembry	0	20.496	11	3	3	3	531	59.7	5.33	11.93	3	cell organ	cytoplasm	enzyme re	P110165	60626	ENSG00000	RICB1	11				0	0.977	0.394430941	4.38	403.3	423.4	6.15	11.14	High	High	High	High	High	High	High	High	1	
FALSE	Medium	Master	Prq	Q8BVA0	Katanin p	0.028	1.462	1	1	1	1	655	72.3	7.56	1.85	1	cell divisio	cytoplasm	catalytic ac	P104000, F	10300	ENSG00000	KATNB1	16				0	0.977	0.481823174	7.46	1557	1807.7	13.37	8.92	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	Q9Y312	Protein AA	0	8.939	9	2	2	2	384	43.4	5.96	8.35	2	cell organ	splicesome		P105282	25980	ENSG00000	AAR2	20				0	0.977	0.551420013	4.33	153.5	161.8	4.42	7.02	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	Q8WZ82	Esterase O	0	16.464	22	2	3	2	227	24.4	6.89	15.42	2	response t	cytoplasm	catalytic ac	P103959	124641	ENSG00000	OVC42	17				0	0.977	0.578989409	19.4	412	427.6	12.7	13.45	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	Q13395	Probable n	0.003	2.886	1	1	1	1	1621	181.6	7.05	1.69	1	metabolic	nucleus	catalytic ac	P100588	6894	ENSG00000	TARBP1	1				0	0.977	0.655287249	45.91	317.9	350.5	46.7	7.79	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	Q14141-1	Septin-6 [C	0	14.768	7	3	3	3	434	49.7	6.67	7.32	3	cell differ	chromoso	nucleotide	P100735	23157	ENSG00000	SEPT6	1	Bacterial ir			1	0.977	0.700047861	11.53	1016.4	1014.4	9.11	11.78	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	Q8NSM9	Protein jag	0	9.09	7	1	3	1	183	21.1	9.73	12.35	1	cell differ	endoplasm	protein br	P107086	84522	ENSG00000	JAGN1	1				0	0.977	0.781054383	1.67	1655.2	1580.1	4.1	6.8	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	P33240	cleavage s	0	28.768	24	8	10	4	577	60.9	6.83	18.29	8	metabolic	nucleus	protein br	P100076, F	1478	ENSG00000	CSF72	1	mRNA sur	mRNA Pro	Cleavage o	15	0.977	0.888686705	10.43	177.8	181.9	7.54	1.37	High	High	High	High	High	High	High	High	High	1
FALSE	High	Master	Prq	Q8BVM0	Coiled-co	0.001	4.207	4	1	1	1	306	35.8	6.65	30.8	1	cytoplasm			P115295	152137	ENSG00000	CDC50C	3				0	0.977	0.921662134	3.39	320.7	316.3	6.59	5.53	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	Q06953	Zinc finger	0	23.911	12	5	7	5	477	54.2	6.15	15.57	5	regulation	cytoplasm	metal ion	P112171, F	90441	ENSG00000	ZNF622	5				0	0.976	0.391952319	5.03	799.5	921.4	10.39	9.85	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	Q15785	Mitochondr	0	5.032	5	2	3	1	309	34.5	8.98	7.1	2	transport	cytoplasm	protein br	P100515, F	10953	ENSG00000	TOMM34	20				0	0.976	0.391991859	4.41	180.6	190.1	2.05	15.23	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	Q15021	condensin	0	17.352	5	5	6	5	1401	157.1	6.61	17.92	5	cell divisio	chromoso	protein br	P112717, F	9918	ENSG00000	NCAPD2	12			Condensat	0	0.976	0.395468814	5.1	920.7	968.5	9.69	5.34	High	High	High	High	High	High	High	High	High	1
FALSE	High	Master	Prq	Q53LP3	ankyrin re	0	15.247	10	4	5	4	525	55.6	7.03	12.36	4	cell organ	cytoplasm	protein br	P100023, F	65124	ENSG00000	SOAHWC	4				0	0.976	0.463212514	7.85	1193	1270.1	20.41	9.39	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	Q8NER6	Calcium ur	0	22.598	19	4	6	5	351	39.8	8.65	17.19	5	cell organ	membrane	catalytic ac	P104678	90550	ENSG00000	MCU	10	NOD-like r		Processing	5	0.976	0.695530846	2.08	1209	1231	6.1	3.17	High	High	High	High	High	High	High	High	High	1
FALSE	High	Master	Prq	P61224-1	Ras-relate	0	71.43	61	10	26	3	184	20.8	5.78	67.64	10	cell organ	cytoplasm	catalytic ac	P100009, F	5908	ENSG00000	RAP1B	12	Pancreatic	Integrin-m	Gene and r	55	0.976	0.721079045	0.26	1007.4	1023.2	3.74	3.62	High	High	High	High	High	High	High	High	High	1
FALSE	High	Master	Prq	P13693	Translation	0	64.125	38	8	24	8	172	19.6	4.93	60.75	8	cell differ	cytoplasm	metal ion	P100838	7178	ENSG00000	TPST1	13				0	0.976	0.740458653	25.42	7951.8	8146.3	15.26	9.03	High	High	High	High	High	High	High	High	1	
FALSE	High	Master	Prq	P0DMM9	Sulfotransf	0	24.346	27	5	7	5	295	34.2	6.01	24.13	5	metabolic	cytoplasm	catalytic ac	P100685, F	445329; 6	ENSG00000	SULT1A4; 1	16	Chemical c	Sulfation B	Cytosolic s	11	0.975	0.838549463	4.94	1685.3	1813.8	9.13	6.41	High	High	High	High	High	High	High	High	High	1
FALSE	High	Master	Prq	Q8DHX1	ATP-depen	0	23.879	7	6	6	6	1008	114.7	6.68	11.75	6	metabolic	chromoso	catalytic ac	P100270, F	137056	ENSG00000	CHX36	3	RNA degra		TRAPE mef	12	0.975	0.419326042	6.6	699.7	685.7	10.09	4.85	High	High	High	High	High	High	High	High	High	1
FALSE	High	Master	Prq	P09104	Gamma-er	0	93.432	31	9	71	5	434	47.2	5.03	176.98	9	metabolic	cytoplasm	catalytic ac	P100113, F	2026	ENSG00000	ENO2	12	Biosynthes	Glycolysis		12	0.975	0.552842748	13.9														

FALSE	High	Master Prq C9GZP8-1	Immortal	0	23.381	43	4	10	4	106	10.9	9.73	22.28	4	cytosol;mel DNA bindi	64073	ENSG000001C19orf133	19						0	0.972	0.800350625	28.94	5737.5	5893.4	5.07	17.77	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q01780	exosome c	0	20.434	7	6	7	6	885	100.8	8.46	11.55	6	metabolic; cytoplasm; catalytic ac	P100570, F 5394	ENSG000001EXOSC10	4	RNA degra	Major patt				0	0.972	0.862317712	13.04	869.1	893.9	12.38	4.35	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q14152	Eukaryotic	0	152.800	30	41	76	41	1382	166.5	6.79	142.81	41	cell organ; cytoplasm; protein bi	P101399	ENSG000001EF3A	10	RNA trans	Translator	Formation			13	0.972	0.930969455	2.15	18085.7	18258.6	4.56	2.86	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9BU15	Tubulin be	0	117.222	53	18	67	7	446	49.8	8.88	156.3	18	cell organ; cytoplasm; catalytic ac	P100091, F 84617	ENSG000001TUBB8	18	Gap junc	Pathogeni	COP1-inde			65	0.971	0.055112635	1.02	2929.6	3010.8	5.21	3.66	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P49590	probable h	0	35.164	22	7	8	4	506	56.9	8.24	19.23	7	cell organ; cytoplasm; catalytic ac	P100587, F 23438	ENSG000001HARS2	5	Aminoacyl	Mitochond			5	0.971	0.266619819	2.73	1310.4	1324.8	3.21	8.77	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P11413-1	Glucose-6	0	154.021	58	25	70	25	515	59.2	6.84	177.87	25	metabolic; cytoplasm; catalytic ac	P100479, F 2539	ENSG000001G6P0	19	Carbon me	Glutathion	TP53 Regu			19	0.971	0.284257726	3.23	24502.4	26517.4	7.06	4.88	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q43765	Small glut	0	23.637	21	6	8	6	313	34	4.87	14.75	6	metabolic; cytoplasm; protein bi	P100515, F 6449	ENSG000001SGTA	19						0	0.971	0.388728043	6.18	359.2	369.9	11.54	2.24	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q96R58	pre-mRNA	0	10.209	20	2	4	2	191	20.9	4.39	3.15	2	metabolic; nucleus	P110773	ENSG000001T9R2	X						0	0.971	0.470635019	12.46	809.9	833.9	29.34	0.81	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9NWS8	Cell growt	0	9.914	7	3	5	3	379	43.6	9.54	10.67	3	nucleus	P108790	ENSG000001LVAR	4						0	0.971	0.504406457	4.14	2248.9	2268.5	26.27	8.35	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q17L23-1	Putative A	0	40.864	9	9	12	9	1194	133.9	8.78	26.19	9	cell organ; cytoplasm; catalytic ac	P100270, F 22907	ENSG000001DHX30	4						0	0.971	0.516390089	9.2	1693	1742.8	2.11	4.11	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9Y314	nitric oxid	0	16.075	13	3	4	4	301	33.2	8.82	13.07	3	developm; cytoplasm; catalytic ac	P104564, F 51070	ENSG000001NOSIP	19			NOSIP mec			4	0.971	0.522910593	10.4	1267.6	1317.8	9.18	0.52	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9Y6G9	Cytoplasm	0	11.597	10	3	6	3	523	56.5	6.42	10.69	3	cell divisi; chromosor	P100005, F 51143	ENSG000001DYNCL11	13	Salmonella	COP1-inde	snRNP Ass			38	0.971	0.56451306	28.58	490.8	580.1	20.2	24.42	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P54105	Methyloso	0	29.434	27	5	11	5	237	26.2	4.11	29.18	5	cell organ; cytoplasm; protein bi	P103517	ENSG000001GLNS1A	11	RNA trans					4	0.971	0.566359997	5.17	3188.5	3283.1	20.31	2.86	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9H0U3	Magnesiur	0	4.556	5	2	2	2	335	38	9.63	2.31	2	metabolic; endoplasm	P104756	ENSG000001MAGT1	X	Asparagin					8	0.971	0.59729033	11.51	152.9	159.1	3.58	5.44	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q96D46	60S riboso	0	23.182	14	5	6	5	503	57.6	7.14	16.05	5	regulation; cytoplasm; protein bi	P104981	ENSG000001NMD03	3	Ribosome					2	0.971	0.607725372	6.48	2295.4	2289.8	13.71	9.41	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q4692-1	DNA mism	0	6.584	3	2	2	2	756	84.5	5.72	3.48	2	cell organ; chromosor	P101119, F 4292	ENSG000001MLH1	3	Fancani an	Ovarian Int	Mismatch			25	0.971	0.610417761	28.32	393.6	405.5	20.38	16.33	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P61758	Prefoldin s	0	31.921	42	9	20	9	197	22.6	7.11	37.38	9	cell organ; cytoplasm; protein bi	P102996	ENSG000001VBP1	X	Prefoldin r					5	0.971	0.611376408	25.78	4152	4277.7	35.3	11.03	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P25205	DNA replic	0	113.502	34	24	45	24	808	90.9	5.77	90.93	24	metabolic; cytoplasm; catalytic ac	P100493, F 4172	ENSG000001MCM3	6	DNA replic	Cell Cycle;	M/G1 Tran			26	0.971	0.987371894	1.25	8865.5	9047.1	2.36	3.73	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P12081	Histidine--	0	53.214	25	11	14	8	509	57.4	5.88	32.27	11	cell organ; cytoplasm; catalytic ac	P100458, F 3035	ENSG000001HARS	5	Aminoacyl;	Allograft R	Cytosolic tr			6	0.97	0.058834274	1.23	2988.2	3071.1	9.12	10.19	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P33993-1	DNA replic	0	102.009	29	16	34	16	719	81.3	6.46	89.13	16	cell profile; chromosor	P100493, F 4176	ENSG000001MCM7	7	Cell cycle;	miRNA Reg	M/G1 Tran			27	0.97	0.158995042	1.62	6695	6870.3	4.45	1.72	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P53992	Protein tra	0	76.348	19	15	28	15	1094	118.2	7.06	78.72	15	cell organ; cytoplasm; metal ion	P100626, F 9632	ENSG000001SEC24C	10	Protein prc	Sterol Reg	Regulation			20	0.97	0.231750481	4.04	4287.1	4343.8	4.9	2.56	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9UK56	Protein kin	0	46.928	29	10	18	10	424	48.5	6.18	46.98	10	cell organ; cytoplasm; enzyme re	P100818, F 29763	ENSG000001PAC3N3	11			Clathrin-in			3	0.97	0.234003574	2.57	4405.8	4587.1	4.1	1.57	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9UNF1	Melanoma	0	128.714	44	28	53	28	606	64.9	9.32	120.97	28	transpor; cytosol;ext	P101454	ENSG000001MAGED2	X						4	0.97	0.342439647	5.13	10205.9	11036.7	7.15	3.48	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q95379	Tumor nec	0	7.484	10	1	1	1	198	23	7.93	4.93	1	cell organ; cytoplasm; enzyme re	P105527	ENSG000001TNAIP8	5						4	0.97	0.584544135	46.4	58.8	60.6	27.89	41.62	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q94925-3	Isoform 3	0	78.648	34	13	22	13	598	65.4	7.88	64.22	13	cell comm; cytosol;ml	P104960	ENSG000001GLS	2						1	0.97	0.608832622	15.05	3447.1	3553.8	8.41	5	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q96AX1	Vacuolar p	0.003	3.438	3	2	3	2	596	67.6	6.66	9.97	2	cell differe; endosome	P100995	ENSG000001VPS34	12						1	0.97	0.648076833	18.13	534.5	551.1	9.96	6.46	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9UIA9	exonin-7	0	18.217	6	5	6	5	1087	123.8	6.32	12.53	5	transpor; cytoplasm; protein bi	P103810	ENSG000001KP07	8						0	0.97	0.678633817	17.45	827.3	883.8	10.79	6.42	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P78346-1	ribonuclea	0	8.117	15	3	4	3	268	29.3	8.91	4.94	3	metabolic; nucleus	P101876	ENSG000001RPP30	10	RNA trans	Major patt			8	0.97	0.770136287	10.54	998.4	1029.4	13.05	3.71	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9P258	Protein RC	0	44.219	26	12	17	12	522	56	8.78	33.38	12	cell divisi; chromosor	P100415, F 55920	ENSG000001RCC2	1	CHR_HG	Amplificat			16	0.97	0.775862596	6.22	2386.5	2459.6	4.9	1.99	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q96G03	Phosphogl	0	21.807	14	8	9	8	612	68.2	6.73	15.77	8	metabolic; cytoplasm; catalytic ac	P100408, F 55276	ENSG000001PGM2	18	Glycolys	Glucuronid	Neutrophil			18	0.97	0.939044113	1.63	1125	1107.2	5.11	9.45	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P68371	Tubulin be	0	328.506	72	26	212	2	445	49.8	8.89	556.52	26	cell organ; cytoplasm; catalytic ac	P100091, F 10383	ENSG000001TUBB4B	49	Phagosome	Pathogeni	COP1-inde			74	0.969	0.181506921	2.61	3563	3613.7	5.11	7.71	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P07741-1	Adenine pl	0	58.039	79	9	17	9	180	19.6	6.02	61.17	9	metabolic; cytoplasm; catalytic ac	P100156	ENSG000001APRT	16	Metabolic	Neutrophil			9	0.969	0.313095961	2.38	3691.3	3809.2	5.37	6.47	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q13263	Transcript	0	137.384	42	23	50	23	835	88.5	5.77	91.04	23	cell organ; chromosor	P100628, F 10155	ENSG000001TRIM28	14	Corticost	Genetic Tr			6	0.969	0.360309381	6.82	14567.8	15348.3	2.55	7.47	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q96R81	THO comp	0	54.608	41	8	15	8	257	26.9	11.15	32.67	8	cell organ; cytoplasm; protein bi	P100767, F 10189	ENSG000001ALRF17	17	Herpes sim	mRNA 3'-e			19	0.969	0.403512614	7.46	5227.2	5519	10.75	8.12	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q14554	Protein dis	0	7.28	9	3	3	3	519	59.6	7.91	7.07	3	cellular ho; endoplasm	P100545, F 10954	ENSG000001PDAS	5			XBPA153 ac			4	0.969	0.498193556	12.6	719	742	7.7	8.77	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P20073-1	Anexin A7	0	63.481	29	13	32	13	488	52.7	5.68	63.67	13	cell differe; cytosol;mel	P100191	ENSG000001ANXA7	10						0	0.969	0.585106022	2.78	10753.6	11094.8	1.15	5.5	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9N2T8	Insulin-like	0	52.715	25	13	18	10	577	63.4	9.2	27.37	13	cell profile; cytoplasm; protein bi	P100133, F 10642	ENSG000001GF28P1	17	MicroRNA	Brain-Deri	MAPK6/M			8	0.969	0.588878454	21.42	3150.6	3202.1	24.46	5.43	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9BU138	Nucleolar	0	9.663	5	2	2	2	636	69.4	7.28	4.88	2		161424	ENSG000001NCP9	14																					

FALSE	High	Master Prq P09382	Galactin-1	0	65.417	81	10	33	10	135	14.7	5.5	80.63	10	cell death; cell surface protein	P00337	3956	ENSG000001	LGALS1	22				Post-transl	4	0.965	0.526015018	16.64	10202.4	10708	15.21	7.89	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q16531	DNA dama	0	151.814	37	34	48	34	1140	126.9	5.26	117.48	34	cell organ; cytoplasm; DNA bindi	P031278, F1642	1642	ENSG000001	DDI1	11	Viral cardir		Formation	19	0.965	0.563500061	9.64	12649.1	13963.4	9.86	4.83	High	High	High	High	High	High	1			
FALSE	High	Master Prq P0C378	POTE anky	0	44.16	7	7	58	1	1075	121.2	6.21	134.11	7	protein bir	P000022, F653269	653269	ENSG000001	POTE1	2					0	0.965	0.598682675	47.34	290.9	318.7	42.53	31.47	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q08T08	RNA bindi	0	15.459	13	3	3	3	480	50.4	9.63	11.24	3	regulation	protein bir	P000076, F79171	79171	ENSG000001	RRM42	19				0	0.965	0.681770147	26.78	563.8	568.4	19.61	9.55	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q5T19H	RRP12-like	0	42.254	9	8	11	8	1297	143.6	8.75	34.55	8	membrane	RNA bindi	P000061, 23223	23223	ENSG000001	RRP12	10				0	0.965	0.716595151	13.17	3667.3	3849.1	9.78	0.97	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q75116	Rho-asso	0	16.523	6	7	8	7	1388	160.8	6.02	4.36	7	cell organ; cytoplasm; catalytic	ai	P00069, F9475	9475	ENSG000001	ROCK2	2	Regulation	Androgen	EPHA-med	47	0.965	0.736551701	23.01	638.2	661.2	22.38	9.87	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q0891-1	Serine-1R	0	43.001	29	10	10	10	518	58.2	8.13	27.38	10	cell organ; cytoplasm; catalytic	ai	P000593, F54938	54938	ENSG000001	SARS2	19	CHR_H	Aminoacyl	Selenium	6	0.965	0.775943917	6.52	1360.8	1376.8	1.79	7.01	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q09H53	epidermal	0	47.625	21	10	13	10	715	80.6	6.84	31.77	10	regulation	cytoplasm; protein bir	P000018, F64787	64787	ENSG000001	PSR12	11				0	0.965	0.801377004	34.17	1290.7	1337.8	24.99	12.04	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q38B0V	Neuroblast	0.009	2.118	1	1	1	1	1214	139.3	4.78	1.79	1	metabolic	cytoplasm; catalytic	ai	P006758, 55672	55672	ENSG000001	NBP1	1			0	0.965	0.830020117	20.8	488	532.1	21.6	7.82	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q08910-1	Jupiter mtc	0	42.599	57	7	13	7	190	20.1	9.26	23.81	7	cytoplasm;		90861	ENSG000001	HN1L1, JPT	16				0	0.965	0.968317588	0.89	2196.1	2166.1	4.49	4.24	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q043592	Exportin-T	0	17.629	7	5	6	5	962	109.9	5.39	9.59	5	transport	cytoplasm; protein bir	P008389	11260	ENSG000001	XPOT	12	RNA trans		tRNA proc	4	0.964	0.147901697	1.38	241.8	251	6.99	3.13	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q75608	Acyl-prote	0.002	3.798	7	2	3	2	230	24.7	6.77	5.36	2	metabolic	cytoplasm; catalytic	ai	P00561, F10434	10434	ENSG000001	LYPLA1	8	Choline me		eNOS activ	6	0.964	0.243838649	1.92	685.6	716.4	10.66	4.28	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q04347	peptidyl-pi	0	33.894	52	8	17	6	177	19.2	8.07	28.47	8	cell organ;	cytoplasm; catalytic	ai	P00160	10465	ENSG000001	PPH1	1	Spliceosom		mRNA Spli	5	0.964	0.245567498	2.84	1206.4	1260.5	1.68	6.05	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q08D13	Probable a	0.005	2.564	3	1	1	1	523	55.8	6.87	0	1	metabolic	cytoplasm; catalytic	ai	P00883	79716	ENSG000001	NPEPL1	20			0	0.964	0.281542246	6.03	381	379.8	2.31	5.45	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q08D01	Metal tran	0	12.284	6	3	3	3	707	76.1	6.09	8	3	transport	membrane	protein bir	P00571	26505	ENSG000001	CNNM3	2			0	0.964	0.282956892	6.32	601.3	627.6	3.43	3.63	High	High	High	High	High	High	1		
FALSE	High	Master Prq P14678-1	Small nuck	0	67.589	23	6	30	6	240	24.6	11.19	91.37	6	cell organ;	cytoplasm; protein bir	P01423	6628	ENSG000001	SNRNP	20	Spliceosom	mRNA Pro	SLBP indeg	17	0.964	0.405740226	9.52	7968.2	8942.2	4.79	12.38	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q09848	Probable r	0	55.965	37	10	20	10	306	34.8	10.1	50.51	10	metabolic	nucleus	protein bir	P005890	10969	ENSG000001	EBNA1BP2	1			Major part	4	0.964	0.406333388	10.29	7480.8	7577.4	8.55	3.35	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q00306	Intron-bin	0	51.079	11	11	13	11	1485	171.2	6.37	33.07	11	metabolic	membrane	catalytic	ai	P04851, F9716	9716	ENSG000001	ALP	15	Spliceosom	Dual incisi	11	0.964	0.456294452	3.97	4031.1	4173.6	3.72	0.99	High	High	High	High	High	High	1	
FALSE	High	Master Prq P30044-1	Peroxi-red	0	122.876	69	14	50	14	214	22.1	8.7	139.06	14	cell death; cytoplasm; antioxidant	P00578, F25824	25824	ENSG000001	PRDX5	11	Peroxisom	Selenium	Deferoxal	5	0.964	0.468212217	12.28	10294.9	10677.5	11.69	4.8	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q043598-1	2'-deoxyr	0	14.339	44	4	5	4	174	19.1	5.05	6.37	4	cell differe	cytoplasm; catalytic	ai	P05014	10591	ENSG000001	GcGr108	6			Purine cat	5	0.964	0.515478246	20.35	77.9	100.2	14.69	24.82	High	High	High	High	High	High	1	
FALSE	High	Master Prq P26232	Catenin aii	0	16.103	6	5	8	2	953	105.2	5.71	15.63	5	cell differe	cytoplasm; protein bir	P01044	1496	ENSG000001	CNNM2	2	Bacterial ir	Arrhythm	CCO in my	13	0.964	0.524602008	124.83	678	703.2	115.29	27.81	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q08Z19	Methionin	0	74.058	40	12	21	12	334	37.5	7.36	68.26	12	metabolic	cytosol; mti	catalytic	ai	P01006, F27430	27430	ENSG000001	MAT2B	5	Metabolic	Trans-sulf	Ub-specific	15	0.964	0.592027399	10.02	9682.6	10045.9	5.16	2.76	High	High	High	High	High	High	1
FALSE	High	Master Prq Q0Q0C0-1	E3 ubiquti	0	8.881	3	1	1	1	670	74.6	7.15	6.58	1	cell death; membrane	catalytic	ai	P00097, F84231	84231	ENSG000001	TRAF7	16			Antigen pr	4	0.964	0.597744005	10.12	85.2	88.4	20.2	10.92	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q09J01	THO com	0.001	4.385	5	2	2	2	351	38.7	6.09	4.61	2	metabolic	nucleus	protein bir	P04000, F84321	84321	ENSG000001	THOC3	5	RNA trans		Cleavage o	11	0.964	0.672376651	29.62	704.5	719	32.49	13.42	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q01473	Tripeptidyl	0	30.388	17	6	8	6	563	61.2	6.48	17.37	6	cell differe	mitochondr	catalytic	ai	P09286	1200	ENSG000001	TPP1	1	Lysoosom		XBP1(S) ac	5	0.964	0.706653186	23.8	1318.6	1367.9	18.51	3.07	High	High	High	High	High	High	1
FALSE	High	Master Prq Q08620-1	Protein TB	0	23.053	10	6	7	6	631	70.7	7.42	17.93	6	metabolic	mitochondr	catalytic	ai	P06143, F9238	9238	ENSG000001	TRBG4	7				0	0.964	0.873842393	6.71	1823.3	1938.7	13.6	4.66	High	High	High	High	High	High	1
FALSE	High	Master Prq P1614-3	Isomorf Be	0	24.351	5	5	5	5	1805	200.6	6.3	9.76	5	cell comm; cell surface protein	bir	P00041, F3691	3691	ENSG000001	ITGB4	1	Integrin-m			8	0.964	0.997848824	7.51	373.9	396	15.31	5.4	High	High	High	High	High	High	1		
FALSE	High	Master Prq P16240	Valine-1R	0	138.247	28	26	42	26	1264	104.4	7.59	101.07	26	metabolic	cytoplasm; catalytic	ai	P00043, F7407; 571	7407; 571	ENSG000001	VARS, VAR	6; CHR_H	5	Aminoacyl	Amino Acid	Cytosolic ti	6	0.963	0.941688962	1.67	9776.1	10340.3	2.85	2	High	High	High	High	High	High	1
FALSE	High	Master Prq Q0UNM6	265 protea	0	43.828	25	9	12	9	376	42.9	5.81	32.05	9	cell organ; cytosol; ext	catalytic	ai	P01399	5719	ENSG000001	PSMD13	11	Epstein-Ba	Proteasom	Regulation	153	0.963	0.486750454	3.22	3198.9	3217.2	4.99	5.9	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q015160	DNA-direct	0	19.329	18	4	6	4	346	39.2	5.5	19.61	4	metabolic	cytosol; mti	catalytic	ai	P01000, F9533	9533	ENSG000001	POLR1C	6	RNA polyr		RNA Polyr	29	0.963	0.549581282	0.95	881.5	912.7	19.22	3.4	High	High	High	High	High	High	1
FALSE	High	Master Prq Q09K45-1	cleft lip an	0	11.415	5	2	3	2	538	62.2	8.56	10.23	2	cell death; membrane		P05602	81037	ENSG000001	CLPTM1L	5; CHR_H	5				0	0.963	0.550879254	13.15	576.6	598.6	5.56	4.48	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q015235	28S riboso	0	6.486	18	1	2	1	138	15.2	10.29	8.61	1	cell organ; membrane	protein bir	P01004	6183	ENSG000001	MSPS12	19; CHR_H	19	Ribosome		Ribosome	0	0.963	0.564360464	26.98	183.5	172.2	31.49	18.69	High	High	High	High	High	High	1	
FALSE	High	Master Prq P22262	heterogen	0	278.425	77	34	180	32	353	37.4	8.95	407.22	34	metabolic	cytoplasm; DNA bindi	P00076, F3181	3181	ENSG000001	HNRP2A1	7			mRNA Pro	XBP1(S) ac	10	0.963	0.815160634	30.13	41543.4	43155.3	9.26	12.34	High	High	High	High	High	High	1	
FALSE	High	Master Prq P51588	hepatoma	0	126.367	61	15	52	14	240	26.8	4.73	128.69	15	cell differe	cytoplasm; DNA bindi	P00065, 3068	3068	ENSG000001	HDNF9	6			Gene and i	4	0.962	0.039792886	1.56	12605	13238.2	4.78	3.82	High	High	High	High	High	High	1		
FALSE	High	Master Prq P55265-1	Double-str	0	107.513	23	24	45	24	1226	136	8.65	91.05	24	cell differe	cytoplasm; catalytic	ai	P00035, F103	103	ENSG000001	ADAR	1	Influenza A		OS deamin	12	0.962	0.050761731	2.07	11652.5	11950.1	5.21	5.53	High	High	High	High	High	High	1	
FALSE	High	Master Prq P83881	60S riboso	0	12.767	25	4	5	4	106	12.4	10.58	11.6	4	cell organ; cytoplasm; protein	bir	P00035	6173	ENSG000001	PSA4	3	Ribosome	Cytoplasm	Peptide ch	34	0.962	0.355672456	7.26	2404.2	2572.7	13.42	7.21	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q08Z19	BH3-intera	0	10.683	14	2	3	2	195	22	5.44	10.01	2	cell death; cytoplasm		P06193	637	ENSG000001	BID	22																				

FALSE	High	Master Prq Q60488-1	Long-chain	0	45.847	19	9	12	7	711	79.1	8.38	36.04	9	cell differe	cytoplasm; catalytic ac	P00501, 2182	ENSG000001	ACSL4	X	Peroxisom	Fatty Acid	Synthesis c	16	0.958	0.234391454	4.73	1810.9	1890.3	1.26	5.07	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q60488-1	Program	0	122.729	36	22	35	22	868	96	6.52	75.5	22	cell death; cytoplasm; protein bi	P00501, 2182	ENSG000001	ACSL4	X	Endocytos	Budding ar		9	0.958	0.276738013	4.24	5522.7	5766.1	1.06	3.04	High	High	High	High	High	High	High	1	
FALSE	Medium	Master Prq P49642	DNA prim	0.024	1.521	2	1	1	1	420	49.9	8.21	2.29	1	cell organ; membrane; catalytic ac	P01896, 5557	ENSG000001	PRIM1	12	Metabolic	Retinol/as	Activation	32	0.958	0.434024242	11.24	657.3	686.4	8	2.19	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P51570	galactinol	0	21.485	21	6	6	6	392	42.2	6.46	15.52	6	metabolic; cytoplasm; catalytic ac	P08544, 2584	ENSG000001	GALK1	17	Metabolic	Galactose c		10	0.958	0.444336683	11.66	658.4	691	10.59	2.01	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P11940-1	polyadeny	0	203.942	50	33	102	22	636	70.6	9.5	199.74	33	metabolic; cytoplasm; protein bi	P00076, 26986	ENSG000001	PABPC1	8	mRNA sur	Translator	AUF1 (hnR	24	0.958	0.478616063	12.44	16114.1	16815.9	5.18	4.43	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9NVU2	ADP-ribos	0	19.783	24	4	5	4	186	21.5	8.43	7.36	4	cell division; cytoplasm; catalytic ac	P00025, 55207	ENSG000001	ARL8B	3				0	0.958	0.638775973	46.58	681.3	804.2	54.92	9.65	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q12874	splicing fa	0	79.644	26	10	18	10	501	58.8	5.38	58.31	10	cell organ; nucleus; metal ion	P111931, F 10946	ENSG000001	F3A3	1	Spliceosom	Exercise in	mRNA Spli	7	0.958	0.692441446	2.86	3906.1	3968	14.52	1.86	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q43427	Acidic fibr	0.002	3.608	4	1	1	1	364	41.9	6.48	0	1	regulation; membrane; protein bi	P05427, 9158	ENSG000001	FBP	11				0	0.958	0.844412296	4.11	490.4	507.3	10.13	2.81	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P54727	UV exciso	0	63.457	26	9	23	8	409	43.1	4.84	66.31	9	cell organ; cytoplasm; DNA bindi	P00240, F 5887	ENSG000001	NAD23B	9	Nucleotide	Joseph d		13	0.958	0.900642115	16.43	3564.1	3720.2	17.34	1.39	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9GVP9-1	THO comp	0	14.128	6	4	5	4	657	75.6	4.98	11.23	4	cell death; cytoplasm; DNA bindi	P00531, F 9984	ENSG000001	THOC1	18	Spliceosom	Cleavage o		11	0.958	0.971216644	40.31	1681.4	1754.4	21.94	9.4	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P62333	26S protea	0	128.137	47	16	35	16	389	44.1	7.49	110.05	16	cell organ; cytoplasm; catalytic ac	P00004, F 5706	ENSG000001	PSMCG	14	Epstein-Ba	Proteasom	Regulation	152	0.957	0.069998828	2.29	14535.7	14817	3.07	1.98	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P49915	GMP synt	0	164.002	54	29	61	29	693	76.7	6.87	177.69	29	metabolic; cytoplasm; catalytic ac	P00117, F 8833	ENSG000001	GMP5	3	Metabolic	Purine ribc		7	0.957	0.165501114	1.68	13454.4	13842.9	1.95	3.84	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q01844	RNA-bindi	0	75.157	15	7	23	7	656	68.4	9.33	76.71	7	metabolic; cytoplasm; metal ion	P00076, F 2130	ENSG000001	EWSR1	22	Transcripti			1	0.957	0.265499649	3.75	8406	9079.8	3.97	6.74	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9UHX1-1	poly(U)-bi	0	69.101	28	12	19	12	559	59.8	5.29	61.83	12	cell death; nucleus	P00076, F 22827	ENSG000001	PUF60	8, CHR_H	Spliceosom	mRNA Spli	5	0.957	0.365897986	8.59	8566.9	8948.3	11.59	2.8	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq P08397-1	porphobili	0	22.55	14	3	4	3	361	39.3	7.18	17.2	3	metabolic; cytoplasm; catalytic ac	P01375, F 3145	ENSG000001	HMB5	11, CHR_H	Metabolic	Heme Bios	Heme bios	6	0.957	0.58828505	30.84	104.3	109	23.29	16.44	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q06830	peroxired	0	246.775	82	20	165	16	199	22.1	8.13	369.04	20	cell prolif; cytoplasm; antioxiand	P00578, F 5052	ENSG000001	PRDX1	1	Peroxisom	Androgen	TP53 Regu	15	0.957	0.635566479	4.03	41411.7	39795.5	6.46	5.1	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P46379-1	Large rrib	0	44.109	10	8	15	8	1132	119.3	5.6	47.87	8	cell death; cytoplasm; protein bi	P00240, F 7917	ENSG000001	BAG6	6, CHR_H			0	0.957	0.636715398	28.4	1575.9	1645.9	39.84	4.66	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq P43246-1	DNA misri	0	111.458	26	18	34	18	934	104.7	5.77	89.1	18	cell death; membrane; catalytic ac	P00488, F 4436	ENSG000001	MSH2	2	Colorectal	Rack/Pact1	Defective f	20	0.957	0.826546096	2.5	6177.7	6229.5	4.88	3.48	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q14839	Chromodo	0	20.454	4	4	4	3	1912	217.9	5.86	12.63	4	cell organ; cytoplasm; catalytic ac	P00176, F 1108	ENSG000001	CHD4	12	Viral carci	ERCC6 (CS		21	0.957	0.921918792	39.83	725.6	759.6	27.11	5.74	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q02790	Peptidyl-pi	0	128.024	64	23	44	22	459	51.8	5.43	102.2	23	cell organ; cytoplasm; catalytic ac	P00254, F 2288	ENSG000001	FKBP4	14	Estrogen s	Androgen	Attenuatio	8	0.956	0.091173601	3.34	14830.5	15594.1	2.92	6.04	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P55786	purinomy	0	103.585	31	20	36	20	919	103.2	5.72	97.64	20	metabolic; cytoplasm; catalytic ac	P01433, F 9520	ENSG000001	NPEPP5	17		Antigen pr		4	0.956	0.160117764	5.05	8480.3	8616.6	1.68	3.83	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q95298-1	NADH deH	0.001	4.42	7	1	3	1	119	14.2	98.6	2.14	1	cell organ; cytoplasm; catalytic ac	P06374, 4718; 1001	ENSG000001	NDUFC2	11	Alzheimer's	Electron Tr	Neutrophil	16	0.956	0.166177614	5.2	642.5	671.9	5.04	1.19	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9UDV8	Mucosa-as	0	6.499	3	2	2	2	824	92.2	5.73	4.06	2	cell differe; cytoplasm; catalytic ac	P00047, F 10892	ENSG000001	MALT1	13	NF-kappa B	Cell Rece	CLEC7A/in	20	0.956	0.28312258	1.44	92.2	103.9	12.51	5.82	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q92598	Heat shock	0	204.681	44	31	61	27	858	96.8	5.39	171.97	31	metabolic; cytoplasm; enzyme re	P00012	ENSG000001		13	Protein prc	Scavengin		8	0.956	0.312045697	6.58	17821.5	18466.2	10.68	2.5	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9NS43	prolyl 3-hy	0	10.591	7	4	4	4	542	63.2	5.11	4.65	4	cell organ; cytoplasm; catalytic ac	P110637, F 55239	ENSG000001	OGG1D1	22				0	0.956	0.322376011	7.11	833.8	874.2	6.11	0.83	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P30046	D-dapach	0.003	3.476	7	1	2	1	118	12.7	7.3	0	1	metabolic; cytoplasm; catalytic ac	P01187	ENSG000001	DDT	16	CHR_H			0	0.956	0.356502444	2.78	111.7	128.4	31.22	7.77	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P34806-1	Serine hyd	0	51.863	28	8	10	7	483	53	7.71	37.48	8	cell organ; cytoplasm; catalytic ac	P00464	ENSG000001	SHMT1	17	Glyoxylate	Folate Met	Metabolis	18	0.956	0.35897439	9.29	652.5	683.2	8.21	4.19	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q93731	Importin-7	0	85.277	19	16	26	15	1038	119.4	4.82	67.23	16	defense re; cytoplasm; enzyme re	P03810, F 10527	ENSG000001	IP07	11				0	0.956	0.614466341	21.82	6071	6098.6	15.28	8.83	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9B978-1	Uncharact	0	5.017	1	1	2	1	1806	196.6	8.47	6.23	1		P15327	ENSG000001	KIAA1671	22				0	0.956	0.62673633	38.53	299.7	313.6	48.42	3.21	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q98257	Quinone o	0	69.45	48	12	20	12	329	35.2	8.44	58.54	12	cell organ; cytoplasm; catalytic ac	P00107, F 1429	ENSG000001	CRS2	5				0	0.956	0.645069251	6.1	4219.3	4158.8	6.04	4.7	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P35052	Glypican-1	0.002	4.189	2	1	1	1	558	61.6	7.3	2.73	1	cell differe; cytosol;eni	P01153	ENSG000001	GPC1	2	Proteoglyc	VEGFA-VEC	Defective f	29	0.956	0.647811114	15.62	907.6	877.9	19.25	11.72	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q2747	WD40 rep	0	29.524	17	6	12	6	513	57.5	7.18	41.48	6	cell organ; cytoplasm; protein bi	P00400	ENSG000001	SMU1	9				0	0.956	0.701812685	4.22	4724.5	4944.3	14.08	3.63	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q99215	Leucine-4f	0	94.107	19	18	26	18	1176	134.4	7.3	72.38	18	cell comm; cytoplasm; catalytic ac	P00133, F 51520	ENSG000001	LARS	5	Aminoacyl	Cytosolic s		9	0.956	0.793605108	13.08	4934.1	5161.3	16.16	5.48	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q96014	Protein AB	0	7.552	11	2	2	2	210	22.3	6.4	3.05	2	metabolic; cytoplasm; catalytic ac	P00561, F 84836	ENSG000001	ABHD148	3		Cytosolic s		4	0.956	0.865625086	63.63	491.8	572.7	45.45	15.39	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P30740	Leukocyte	0	31.653	21	7	13	7	379	42.7	6.28	27.23	7	regulation; cytoplasm; enzyme re	P00079	ENSG000001	SERPINC1	16	Amoebasi	Neutrophil		4	0.956	0.914556758	8.6	1652.1	1651.5	3.68	10.07	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9BG00	Mvb-bindin	0	128.38	25	26	35	26	1328	148.8	9.28	91.9	26	cell comm; cytoplasm; catalytic ac	P04031, F 10514	ENSG000001	MYBBP1A	17		Energy Me	B-WICH co	5	0.955	0.025435491	1.84	8553.7	8826.4	3.84	3.39	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P07814	Bifunction	0	340.821	41	54	106	53	1512	170.5	7.33	308.99	54	cell organ; cytoplasm; catalytic ac	P04058, F 2058	ENSG000001	EP85	1	Aminoacyl	Parkinsons	tRNA mod	16	0.955	0.121362673	0.95	29787.9	31702.7	3.4	1.67	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9UHA3	Probable r	0	16.964	21	3	4	3	163	19.6	9.98																											

FALSE	High	Master Prq Q75477	erlin-1 [OS]	0	27.951	22	6	6	3	346	38.9	7.87	17.73	6	metabolic; endoplasmic reticulum	protein	bi	P11445, 10613	ENSG000001	ERLIN1	10			ABC family	6	0.951	0.339327129	5.36	282.5	320.3	8.27	14.83	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q818W8	Calcium hc	0	33.642	11	6	9	6	916	103.63	9.04	22.52	6	cellular hsc cytoplasm;	protein	bi	P10585, 10523	ENSG000001	CHEP1	19	Spliceosom		mRNA Spli	5	0.951	0.455059513	15.86	933.2	983.5	17.37	7.36	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q818W8	Iron-sulfur	0	7.969	19	2	2	2	129	14.2	9.07	2.69	2	cell organ; mitochondrion	metal ion	bi	P105121, 81689	ENSG000001	ISCA1	19			Mitochondr	2	0.951	0.595113836	17.43	626.5	652	10.67	17.3	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P35270	Septaplines	0	16.005	19	4	5	4	261	28	8.05	13.43	4	metabolic; cytoplasm;	catalytic ac	bi	P100066, 6697	ENSG000001	SPR	2	Folate bios		eNOS activ	6	0.951	0.699375068	26.99	253.9	266.4	12.56	9.61	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q818W8	Membrane	0	6.663	9	1	1	1	233	23.8	4.88	5.86	1	regulation; cytoplasm;	protein	bi	P100373, 10424	ENSG000001	PGRM2	4				0	0.951	0.823828411	8.36	91.3	90.9	4.79	9.05	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P23919	thymidylat	0	19.499	29	7	9	7	212	23.8	8.27	8.38	7	cell differe; cytoplasm;	catalytic ac	bi	P100406, 1841	ENSG000001	DYRK4	10	Pyrimidine		Interconve	5	0.951	0.458889274	2.6	1318.1	1338.3	8.32	14.69	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q818W8	Ribosome	0	28.662	30	10	16	10	353	41.4	9.92	30.33	10	cell organ; nucleus	RNA bindi	bi	P100427, 55299	ENSG000001	BRX1	5			Gastric car	1	0.951	0.885884015	17.07	2366.5	2489.4	10.41	6.11	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q16891	MICOS con	0	41.904	15	10	14	10	758	83.6	6.48	34.62	10	cell organ; membrane	protein	bi	P109731, 10989	ENSG000001	NMMT	2			Cristae for	3	0.951	0.998185905	4.38	2781.3	2831.9	8.3	4.33	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q91807	UPF0160 f	0	43.471	28	8	12	8	376	42.4	6.67	31.22	8	response i; mitochondrion		bi	P103690, 60314	ENSG000001	C12orf10	12				0	0.95	0.15660261	2.21	4304.9	4370.8	2.26	3.61	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q818W8	alpha-keto	0	9.842	7	2	2	2	505	58.2	5.22	5.18	2	metabolic; nucleus	catalytic ac	bi	P112933, 79968	ENSG000001	CTD16	16			F/OB Revers	4	0.95	0.229330769	6.47	105.1	110.6	11.02	6.17	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q95861-1	317[2,5'-bi	0	9.053	8	1	1	1	308	33.4	5.69	3.81	1	metabolic; cytosol	catalytic ac	bi	P100459, 10380	ENSG000001	BPNT1	1	Metabolic		Cytosolic v	6	0.95	0.550221698	8.11	44.1	45.4	3.5	10.61	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q96GX5-1	Serine/thr	0.001	4.259	2	2	2	1	879	97.3	5.99	0	2	cell divisio; cytoplasm;	catalytic ac	bi	P100069, F 84930	ENSG000001	MASTL	10	Amino su		Glycolysis	5	0.95	0.61170361	16.12	224.7	244.5	21.62	11.11	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q818W8	Serine/arg	0	74.698	18	15	21	15	904	102.3	11.84	40.58	15	metabolic; cytosol;nu	DNA bindi	bi	P104180, 10250	ENSG000001	SRRM1	1	mRNA sur	mRNA Pro	Cleavage o	14	0.95	0.617665909	5.63	6097.9	6131.4	2.9	7.22	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q818W8	Polymeras	0	12.703	7	2	2	2	421	46.1	9.99	4.85	2	metabolic; cytoplasm;	protein	bi	P100076, F 84271	ENSG000001	POLDIP3	22			Cleavage o	9	0.95	0.626042726	6.79	269.5	281.6	18.14	11.25	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P35580	Myosin-10	0	92.505	12	18	25	9	1976	228.9	5.54	64.64	18	cell organ; cytoplasm;	catalytic ac	bi	P100063, F 4628	ENSG000001	MYH10	17	Salmonella	Regulation	RHO GTPa	18	0.95	0.694347357	13.47	1767.3	1855.7	24.31	3.19	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P47813	NFATC2-in	0	7.446	4	1	2	1	419	45.8	6.6	9.98	1	metabolic; cytoplasm;	protein	bi	P115176, 84901	ENSG000001	NFATC2IP	16				0	0.95	0.69966973	17.49	328.1	329.5	9.57	6.95	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P47813	Eukaryotic	0	64.435	55	9	28	9	144	16.5	5.24	65.59	9	metabolic; cytosol	protein	bi	P101176, 1964; 107	ENSG000001	EIF1AX; LO X	1	RNA trans	Translation	Formation	13	0.949	0.101192287	3.13	13262.4	13981.4	7.17	3.29	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P10644	cAMP-dep	0	17.818	17	5	5	4	381	43	5.35	13.62	5	cell organ; cytoplasm;	catalytic ac	bi	P100027, F 5573	ENSG000001	PRKAR1A	1			Insulin sign	33	0.949	0.489597575	23.36	567.1	613	23.15	16.78	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q15427	Splicing fac	0	17.358	9	2	4	4	424	44.4	8.56	14.99	2	metabolic; nucleus;sp	protein	bi	P100076, F 10262	ENSG000001	SF3B4	1	Spliceosom	mRNA Pro	mRNA Spli	7	0.949	0.570440958	5.24	655.2	641.1	4.89	8.76	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P46926	glucosami	0	25.884	24	4	5	4	289	32.6	6.92	12.96	4	metabolic; cytoplasm;	catalytic ac	bi	P101182, 10007	ENSG000001	GNDA1	5	Amino su		Glycolysis	6	0.949	0.667747732	19.78	1522.4	1831.9	19.73	10.76	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P54619-1	5'-AMP-ac	0	13.453	12	3	4	3	331	37.6	6.92	7.3	1	cell comm; cytosol;me	catalytic ac	bi	P100478, F 5571	ENSG000001	PRKAG1	12	Adipocytol	AMP-activ	Translocat	36	0.949	0.680665222	27.87	741.1	827.9	43.58	7.54	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q13631-1	Myotubulu	0.003	3.186	2	1	2	1	665	74.6	7.14	5.97	3	metabolic; cytoplasm;	catalytic ac	bi	P100283, F 8776	ENSG000001	MTMR1	1	Metabolic		Synthesis c	8	0.949	0.869965175	4.23	379.2	394.9	4.68	10.01	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q07157	Tight junc	0	34.067	5	7	8	7	1748	195.3	6.7	20.42	7	cell comm; cytoplasm;	protein	bi	P100018, F 7082	ENSG000001	TIP1	15	Adherens j		c-src medi	23	0.948	0.080362926	1.48	1146.8	1210.3	3.12	0.66	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q15054	DNA polyn	0	8.555	5	2	2	2	466	51.4	9.35	5.86	2	cell organ; cytoplasm;	catalytic ac	bi	P100597, F 10714	ENSG000001	POLD3	11	Base excis	Homologous	Mismatch	53	0.948	0.20733172	3.86	1451.5	1571	1.81	7.65	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9Y3U8	60S ribos	0	24.507	30	5	12	5	105	12.2	11.59	26.04	5	cell organ; cytoplasm;	RNA bindi	bi	P101158, 25873	ENSG000001	RL36	19	Ribosome		Cytoplasm; Peptide ch	34	0.948	0.387257222	12.23	6079	5990	15.71	5.88	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P48147	prolyl end	0	53.763	23	13	17	13	710	80.6	5.86	44.21	13	metabolic; cytoplasm;	catalytic ac	bi	P100267, F 5550	ENSG000001	PREP	6	Renin-angi			1	0.948	0.395877237	1.34	3030.8	3163.4	1.07	4.04	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9UKV8	Protein aris	0	15.576	5	3	3	3	859	97.1	0.19	12.35	3	cell organ; cytoplasm;	catalytic ac	bi	P102170, F 27161	ENSG000001	AGO2; EIF	8			Post-trans	26	0.948	0.402693708	5.45	997.9	1053.1	1.07	5.17	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q60518	ran-bindin	0	14.282	6	5	8	3	1105	124.6	5.01	10.47	5	transport; cytoplasm;	protein	bi	P112755, F 26953	ENSG000001	RANBP6	9				0	0.948	0.459769032	19.33	145.6	162	19.9	15.2	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P25685	dnaI homc	0	30.375	25	8	11	8	340	38	8.63	20.71	8	cell organ; cytoplasm;	catalytic ac	bi	P100210, F 3337	ENSG000001	DNAI1B	19	Influenza A	NP22	Trans MAPK6/M	13	0.948	0.65302278	16.66	1926.9	2031.8	6.98	5.91	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P19532	Transcript	0	5.308	4	3	3	3	575	61.5	5.58	2.28	3	metabolic; cytosol;nu	DNA bindi	bi	P100060, 7030	ENSG000001	TFE3	X	Transcript		TGF-beta f	2	0.948	0.726901828	22.96	1469.6	1549.6	21.75	13.83	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9Y320	Thioredoxin	0	14.926	21	4	4	4	296	34	8.69	8.12	4	cellular hsc membrane		bi	P100085, 51075	ENSG000001	TMX2	11				0	0.948	0.871949682	18.55	469	508	19.59	4.1	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q08211	Atp-depen	0	299.525	46	50	116	50	1270	140.9	6.84	311.12	50	cell death; cytoplasm;	catalytic ac	bi	P100035, F 1660	ENSG000001	DHXR1	10			mRNA Pro	TRAFF6 me	34	0.948	0.889350727	0.65	23857.3	23833.1	5.18	4.91	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q99210	Cleavage a	0	10.943	6	4	5	4	782	88.4	5.11	6.6	4	metabolic; membrane	protein	bi	P100753, F 53981	ENSG000001	CPSF2	14	mRNA sur	mRNA Pro	mRNA 3'-e	16	0.947	0.115540265	0.29	794.7	921	8.73	8.39	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q96525	2-aminoet	0.002	3.561	9	1	1	1	270	29.7	6.04	2.2	1	metabolic; cytosol;me	catalytic ac	bi	P107847, 84890	ENSG000001	ATG10	10	Taurine an		Degradat	6	0.947	0.22237296	0.38	235.4	268.6	15.38	7.4	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q43847-1	Nardilytin	0	39.984	9	8	12	8	1150	131.5	5	34.37	8	cell organ; cell surface	catalytic ac	bi	P100675, F 4898	ENSG000001	NDR1; NRI	1				0	0.947	0.259807642	6.04	4156.4	4387.3	3.53	2.12	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q98XU9	N-alpha-ac	0	51.102	18	12	20	12	866	101.2	7.42	31.1	12	cell differe; cytoplasm;	catalytic ac	bi	P112569, F 80155	ENSG000001	NAAL5	4				0	0.947	0.289154678	3.75	5658.8	5976.1	1.94	3	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P35080-2	Isomorf mb	0	14.812	30	4	7	3	140	15.1	6.1	17.11	4	cell																										



FALSE	High	Master	PrC Q9NR9F	DNA polyn	0	9.235	18	3	3	3	147	16.8	4.74	2.67	3	cell organ	nucleus	catalytic	ai	P00808	54107	ENS00000	POL3	9	Purine met	Gap-filling	43	0.943	0.725496012	15.33	53	56.3	7.43	7.19	High	High	High	High	High	High	High	1	
FALSE	High	Master	PrC Q9UN52	COP9 sign	0	35.793	22	6	8	6	423	47.8	6.65	24.88	6	cell organ	cytoplasm	protein bi	ai	P01399	8533	ENS00000	COP3	17		Cargo reco	13	0.943	0.851913573	1.74	1334	1374.7	14.76	4.22	High	High	High	High	High	High	High	1	
FALSE	High	Master	PrC Q9UN52	Talin-1 [O]	0	295.816	30	50	78	47	2541	269.6	6.07	213.94	50	cell organ	cell surface	protein bi	ai	P00373	7094	ENS00000	TUN1	9	Rap1 signa	Integrin-m	SEMA3A li	43	0.942	0.048374845	1.11	13001.7	13374.2	3.65	3.42	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q9NZ74	Zinc finger	0	11.484	6	3	4	3	707	78.5	4.87	9.23	3	metabolic	cytosol	metal ion	ai	P00098	55596	ENS00000	ZCCHC	12			0	0.942	0.109451339	4.05	674	729.9	1.23	3.62	High	High	High	High	High	High	High	1	
FALSE	High	Master	PrC Q12894	Interferon	0.003	2.875	3	1	1	1	506	54.8	7.94	3.34	1	nucleus	protein bi	ai	P04836	7866	ENS00000	IFR2	3			0	0.942	0.181340942	1.51	248.4	278.9	6.45	4.89	High	High	High	High	High	High	High	1		
FALSE	High	Master	PrC P18621	60S riboso	0	99.348	57	12	47	11	184	21.4	10.17	96.23	12	cell organ	cytosol	protein bi	ai	P00337	6139	ENS00000	KPL17	18	Ribosome	Cytoplasm	Peptide ch	34	0.942	0.187248976	4.13	14103	14702.6	6.17	5.55	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q43175	D-3-phosph	0	164.462	51	21	65	21	533	56.6	6.71	149.23	21	metabolic	cytosol	catalytic	ai	P00389	76227	ENS00000	PGDH	9	Glycine, se	Trans-sulf	Serine bio	9	0.942	0.243136595	7.23	17389	18356.9	8	1.36	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC P05141	ADP/ATP i	0	116.820	50	19	62	8	298	32.8	9.69	107.77	19	regulation	membrane	protein bi	ai	P00153	292	ENS00000	SLC25A5	X	HTLV-I infe	Electron Tr	Nip-medi	15	0.942	0.24432548	2.49	5154.9	5469.8	9.75	4.64	High	High	High	High	High	High	High	1
FALSE	Medium	Master	PrC Q60725	protein-s-i	0.012	1.939	3	1	1	1	284	31.9	7.96	1.91	1	cell organ	endoplasm	catalytic	ai	P04140	72343	ENS00000	ICMT	1	Terpenoid		Gamma cat	4	0.942	0.921533913	24.1	505.6	544.6	21.46	1.34	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q15294	UDP-N-ace	0	25.929	7	5	6	5	1046	116.9	6.7	18.85	5	cell death	cytoplasm	catalytic	ai	P00515	18473	ENS00000	OGT	X	Other type	Extracell	HAT's acety	10	0.942	0.062460596	0.59	1875.2	2016	1.89	1.98	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC P56945	Breast can	0	31.504	13	6	7	6	870	93.3	5.67	20.08	6	cell divisio	cytoplasm	protein bi	ai	P00018	17954	ENS00000	BCAR1	1	Focal adhe	Integrin-m	pi30CAs li	29	0.941	0.073930245	3.51	1104.8	1219.5	5.76	7.54	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q0DMV8	heat shock	0	417.339	73	44	242	23	641	70	5.66	643.81	44	cell organ	cytoplasm	catalytic	ai	P00012	17304; 330	ENS00000	HSPA18; H	6; CHR_ HS	Longevity +	Apoptosis	AUF1 (thr	38	0.941	0.107537728	4.29	36993	38224.8	1.67	3.59	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q9H2M9	Rab3 GTPa	0	8.014	2	2	2	2	1393	155.9	5.62	5.74	2	regulation	cytoplasm	enzyme re	ai	P014655	17582	ENS00000	RAB3GAP2	1			COP1-inde	7	0.941	0.201543886	7.4	423.5	431.8	2.4	6.63	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC P53999	Activated f	0	151.962	65	13	63	13	127	14.4	9.6	229.65	13	cell organ	nucleus	catalytic	ai	P02229	10923	ENS00000	SUB1	5				0	0.941	0.301813001	10.15	30734.2	30514	18.28	10.34	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q9UGV2	protein NC	0	19.556	18	4	4	4	375	41.4	5.31	13.1	4	cell differe	cytoplasm		ai	P00561	175446	ENS00000	NRD63	10				0	0.941	0.537668586	7.85	402.1	419.5	43.37	2.08	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q9UKK3	Poly (ADP	0	11.023	1	2	2	2	1724	192.5	5.66	5.12	2	cell death	cytoplasm	catalytic	ai	P00092	17143	ENS00000	PARP4	23	Apoptosis;	NAD+ bio	Nicotinam	8	0.941	0.602453745	78.16	399	424.2	76.05	20.79	High	High	High	High	High	High	High	1
FALSE	Low	Master	PrC Q60293	Zinc finger	0.054	1.164	1	1	1	1	1989	226.2	8.13	0	1	metabolic	nucleus	metal ion	ai	P08317	17196441	ENS00000	ZFC3H1	12				0	0.941	0.632254374	25.69	167.4	177.9	39.17	12.76	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q9CYR8	Pyrolyne-s	0	6.051	7	1	1	1	274	28.6	7.72	4.95	1	metabolic	cytoplasm	catalytic	ai	P03807	1765263	ENS00000	PGYR1	8; CHR_ HS	Biosynthes	Urea cycle	Amino acid	7	0.941	0.76322369	24.53	152.9	162.8	7.91	13.45	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC P78318	Immunoglob	0	6.908	8	2	2	2	339	39.2	5.38	5.77	2	regulation	cytoplasm	enzyme re	ai	P04177	3476	ENS00000	IGBP1	X				0	0.941	0.768498497	4.29	624.3	663.7	20.81	2.19	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q07096	Sorbitol de	0	24.13	22	6	6	6	357	38.3	7.97	13.19	6	cellular cor	cytosol	catalytic	ai	P01007	176652	ENS00000	SORD	15	Pentose ara	Polyol Pat	Catabolism	9	0.941	0.862709609	8.16	852.7	906.1	15.48	4.18	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q9H3U1	Protein un	0	44.55	11	9	12	8	944	103	6.07	29.67	9	cell differe	cytoplasm	protein bi	ai	P00515	175588	ENS00000	UNC5A	15				0	0.94	0.105511831	1.37	1046.5	1113.2	1.03	2.21	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q13045-1	protein fil	0	32.506	7	9	16	9	1269	144.7	6.05	25.27	9	cell organ	cytoplasm	protein bi	ai	P00626	172314	ENS00000	FIL1	17; CHR_ HS				0	0.94	0.170855745	6.44	2301.7	2417.5	3.7	4	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC P40763	Signal tran	0	90.242	31	15	21	5	770	88	6.3	50.23	15	cell differe	cytoplasm	DNA bindi	ai	P00017	176774	ENS00000	STAT3	17	Jak-STAT si	IL-5 Signa	Interleukin	106	0.94	0.185426579	4.01	3930.6	4068.3	13.51	4.36	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q95400	CD2 antige	0	29.497	23	6	7	6	341	37.6	4.61	17.34	6	cell organ	cytoplasm	protein bi	ai	P00213	10421	ENS00000	CD2BP2	16	mRNA Pro	mRNA Spli		5	0.94	0.217311498	2.15	2353.9	2756.1	9.21	6.88	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q75821	Eukaryotic	0	30.766	21	7	13	7	320	35.6	6.13	41.93	7	metabolic	cytoplasm	protein bi	ai	P00076	178666	ENS00000	EIF3G	19	RNA trans	Translation	Formation	13	0.94	0.290323371	0.31	3673.4	4378.8	18.61	10.66	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC P52701	DNA mism	0	110.432	22	22	26	22	1360	152.7	6.9	67.24	22	cell organ	chromoso	catalytic	ai	P00488	172956	ENS00000	MSH6	2	Colorectal	Signaling	P Defective f	14	0.94	0.300638552	10.74	6726.6	6891.3	3.85	7.25	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q9B2G1	Ras-relate	0	15.052	5	1	3	1	259	29	7.88	8.72	1	cell organ	cytoplasm	catalytic	ai	P00025	178371	ENS00000	RAB34	17				3	0.94	0.343302867	12.39	258.6	263.9	9.04	4.16	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC P33992	DNA replic	0	72.745	27	16	20	16	734	82.2	83.7	42.58	16	cell divisio	membrane	catalytic	ai	P00493	174174	ENS00000	PCNA	22	Cell cycle;	Cell Cycle	M/G1 Tran	25	0.94	0.360658616	8.76	5877.3	5904.4	5.96	7.68	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q9C97C	Isocitronin	0.001	4.286	5	1	1	1	298	32.2	7.39	4.41	1	metabolic	cytoplasm	catalytic	ai	P00857	51015	ENS00000	ISOC1	1				0	0.94	0.418521697	15.72	599.1	594.9	11.96	5.72	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC P62899	60S riboso	0	31.889	44	9	26	9	125	14.5	10.54	29.77	9	cell organ	cytosol	me	protein bi	P01198	6150	ENS00000	RPL31	2	Ribosome	Cytoplasm	Peptide ch	34	0.94	0.473179998	4.41	7216.6	7810.2	1.06	7.56	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q9NUQ2	1-acyl-sn-g	0	7.761	6	1	1	1	364	42	9.1	4.68	1	cell differe	endoplasm	catalytic	ai	P01553	55326	ENS00000	AGPAT5	8	Glycerolip	Triacylgly	Synthesis c	10	0.94	0.605054401	5.17	92.2	99.1	30.43	0.64	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC P49755	Transmem	0	34.04	31	7	11	7	219	25	7.44	26.91	7	cell organ	endoplasm	protein bi	ai	P01105	10972	ENS00000	TMED10	14	mRNA Pro	COP1-depe		14	0.94	0.605575582	25.03	3763.6	3848.4	18.59	4.91	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC P26599	Polypyrim	0	199.942	62	21	63	21	531	57.2	9.17	222.91	21	metabolic	membrane	protein bi	ai	P00076	175725	ENS00000	PTBP1	19				11	0.94	0.683369892	7.05	12136.3	12911.4	4.31	6.04	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q61602	La-related	0	43.733	10	9	16	9	1096	123.4	8.82	39.45	9	cell profile	cytoplasm	protein bi	ai	P05383	23367	ENS00000	LARP1	1				0	0.94	0.595093229	16.06	3988.2	4243.1	12.88	6.58	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q16643	drebilin [O]	0	67.143	21	10	20	10	649	71.4	4.55	59.79	10	cell commu	cytoplasm	protein bi	ai	P00241	1627	ENS00000	DBN1	5				0	0.94	0.960466835	11.53	2571.3	2736.7	11.04	7.52	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC P62851	40S riboso	0	44.222	60	12	37	12	125	13.7	10.11</																														

FALSE	High	Master Prq Q00341-1	Vigilin [OS]	0	121.959	28	29	47	29	1268	141.4	6.87	93.17	29	metabolic; cytoplasm; protein bi	P00013, F 3069		HDLBP	2				HDL cleave	4	0.935	0.567304003	1.18	9054	9538.6	6.73	1.57	High	High	High	High	High	High	High	1	
FALSE	Low	Master Prq Q06566	thioridol cr	0.063	1.098	2	1	1	1	551	62	5.55	1.76	1	transport; endoplasm; transporte	P05834, F 23155	ENSG00000	CLCC1	1						0	0.935	0.616962064	11.98	591.5	637.5	9.5	4.38	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q00031	Chydori ct	0.003	3.386	5	1	1	1	241	287	9.88	3.11	1	metabolic; nucleus; protein bi	29080	ENSG00000	CCDC59	12				Surfactant	6	0.935	0.745934238	0.88	681.6	722.7	13.39	5.48	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P49591	Serine-4Rf	0	34.868	22	10	11	10	514	587	6.43	20.37	10	metabolic; cytoplasm; catalytic a	P00587, F 6301	ENSG00000	SARS	1				Selenocyst	9	0.935	0.810219399	17.08	5139.1	5273.4	12.52	9.27	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q08123	IRNA Cytic	0	180.057	43	29	54	29	767	86.4	6.77	130.1	29	cell division; cytoplasm; catalytic a	P01189, F 54888	ENSG00000	USN2	5				tRNA mod	3	0.935	0.864552847	2.34	15231.9	15615.7	8.27	3.59	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q09501	ESF1 homc	0	15.426	6	5	5	5	851	98.7	5.11	6.28	5	metabolic; nucleus; RNA bindi	P08159	ENSG00000	ESF1	20					0	0.935	0.904826744	38.75	56.4	62.9	30.63	13.04	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q096C4	PDZ and U	0	30.364	17	6	8	6	596	63.9	8.21	27.51	6	cell growth; cytoplasm; metal ion	P08412, F 10611	ENSG00000	PDMS	4				Neurinin	3	0.935	0.944477743	19.49	1231.6	1235.8	15.28	13.84	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P04075	fructose-bi	0	334.226	85	31	217	25	364	39.4	8.09	634.7	31	cell organ; cytoplasm; catalytic a	P00274	ENSG00000	ALDOA	16				Glycolysis; Glycolysis; Platelet de	21	0.934	0.129094909	0.59	56668	62412.6	6.2	2.48	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P05067-1	Amyloid-b	0	16.227	4	3	3	3	770	86.9	4.82	2.48	3	cell comm; cell surface; DNA bindi	P00014, F 351	ENSG00000	APP	21				Serotonerg Alzheimer's Post-trans	69	0.934	0.129676982	6.64	337.5	382.6	10.49	6.84	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q16706	Alpha-mar	0	12.276	2	2	4	2	1144	131.1	7.58	8.93	2	cell organ; Golgi/mer; catalytic a	P01074, F 4124	ENSG00000	MAN2A1	5				N-Glycan bi	12	0.934	0.394798578	14.32	1213.2	1425.2	16.57	8.9	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q93062-1	RNA-bindi	0	8.718	18	2	2	2	196	21.8	8.07	6.96	2	metabolic; cytoplasm; protein bi	P00076, F 11030	ENSG00000	RBPM5	8				Exercise-in	1	0.934	0.45744637	0.17	138.7	148.5	6.89	1.02	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9UHA4	regulator c	0	9.5	23	1	1	1	124	13.6	7.34	6.31	1	metabolic; endosome; enzyme re	P08923	ENSG00000	LAMTOR3	4				MAPK sign	28	0.934	0.520488906	23.27	306	327.6	11.11	10.1	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q13309-1	S-phase kin	0	10.294	11	2	2	2	424	47.7	7.11	7.91	2	cell comm; cytoplasm; catalytic a	P00646, F 6502	ENSG00000	SKP2	5				Small cell i	39	0.934	0.665259911	14.21	109.2	116.9	2.67	11.48	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9Y6M5	zinc transp	0	11.994	9	4	5	4	507	55.3	6.48	8.54	4	cellular ho; cytoplasm; protein bi	P01545	ENSG00000	SLC30A1	1				Mineral ab	8	0.934	0.861914201	7.78	427	457	15.51	4.2	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q15286	Ras-relate	0	24.236	22	5	13	4	201	23	8.29	28.26	5	cell organ; cytosol;eni; catalytic a	P00006, F 11021	ENSG00000	RAB35	12				Endocytosi	9	0.933	0.114564949	2.47	4087	4454.5	5.76	2.54	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q075879	Glutamyl-L	0	16.366	7	2	2	2	557	61.8	8.63	6.24	2	cell organ; mitochondr; catalytic a	P02637, F 5188	ENSG00000	PET112; G	4				Metabolic	2	0.933	0.28264506	6.41	70.7	75.8	8.92	2.36	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q8NAV1-1	Pre-mRNA	0	8.172	7	2	2	2	312	37.5	9.96	2.69	2	cell organ; membrane; protein bi	P03371	ENSG00000	PRPF38A	11				Spliceosom	6	0.933	0.305469563	11.79	1150	1247.2	4.74	6.35	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P05067-1	Zinc finger	0.001	4.249	3	1	1	1	310	34.1	8.07	3.17	1	regulation; Golgi/mer; DNA bindi	7542	ENSG00000	ZFP11	11					0	0.933	0.35198118	12.5	504.8	540.9	26.87	5.39	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P50454	Serpin H1	0	86.937	38	11	29	11	418	46.4	8.69	76.13	11	cell organ; cytoplasm; enzyme re	P00079	ENSG00000	SERPINH1	14				Endothcon; Collagen bi	4	0.933	0.376110204	11.29	6833.6	7286.9	4.56	6.04	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q096C4	selenoprot	0	12.426	20	2	2	2	189	21.2	9.7	2.09	2	cellular ho; cytoplasm; antioxidant	P06936	ENSG00000	VIMF; SELI	15				Protein prc	7	0.933	0.407190928	4.47	1277.2	1368.9	10	2.89	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9H875	PKR-inter	0.003	3.302	5	1	1	1	184	21	9.79	2.53	1	metabolic; nucleus; enzyme re	P06658	ENSG00000	PKRIP1	7					0	0.933	0.47467105	0.27	606.1	598.9	6.71	8.89	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P46199	Translatior	0	5.314	2	1	1	1	727	81.3	7.15	2.3	1	cell organ; mitochondr; catalytic a	P00009, F 4528	ENSG00000	MTF2	2				Mitochondr	4	0.933	0.620597851	1.95	564.8	566.3	4.36	6.92	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q5H9R7-1	Serine/thr	0	13.015	5	4	4	4	873	97.6	4.6	6.13	4	cell organ; cytoplasm; protein bi	P04499	ENSG00000	PPR361	11				COPII (Coa	8	0.933	0.708304368	0	74	75.9	13.25	7.7	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P00870	Vimentin j	0	330.729	82	46	210	42	466	53.6	5.12	497.27	46	cell differe; cytoplasm; protein bi	P00038, F 7431	ENSG00000		20				MicroRNA; Allograft R; interleukin	20	0.933	0.746657982	17.57	52803.7	56611.2	10.69	5.99	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q69YN2-1	CWF19-like	0	18.798	11	4	4	4	538	60.6	7.24	9.95	4	catalytic a	P04676, F 55280	ENSG00000	CWF19L1	10					0	0.933	0.760093238	10.97	617.8	662.2	21.67	4.75	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q15018	BRISC com	0	15.96	10	3	3	3	415	46.9	6.21	9.24	3	cell divisio; cytoplasm; protein bi	P00621	ENSG00000	FAM1758; U	10				Metallopro	4	0.933	0.935830131	50.97	596.4	639.3	30.59	16.48	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P62314	Small nucle	0	8.722	17	1	2	1	119	13.3	11.56	8.09	1	metabolic; cytoplasm; protein bi	P01423	ENSG00000	SNRPD1	18				Spliceosom; mRNA Proc; snRNP Ass	10	0.932	0.051177321	0.66	262.1	271.8	2.45	3.18	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q00701	UDP-glucos	0	136.99	52	20	44	20	494	55	7.12	129.19	20	metabolic; cytosol;nu; catalytic a	P00884, F 7358	ENSG00000	UGDH	4				Ascorbate; Glucuronid Form	10	0.932	0.055096237	3.07	12779.4	13503.6	1.01	3.29	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P61513	60S riboso	0	30.007	47	5	20	5	92	10.3	10.43	49.16	5	cell organ; cytosol;nu; metal ion	P01780	ENSG00000	RLP37A	2				Ribosome; Cytoplasm; Peptide ch	34	0.932	0.058820166	1.88	12059.4	13232	2.63	2.09	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P07187	T-complex	0	175.394	53	23	55	23	556	60.3	6.11	147.6	23	cell organ; cytoplasm; nucleotide	P00018	ENSG00000	TCPI	6				BBSome-r	18	0.932	0.900514049	2.39	13456.7	14898.8	3.99	2.99	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P38606	V-profilin p	0	10.527	40	17	28	17	617	68.3	5.52	90.76	17	cellular ho; cytosol;mer; catalytic a	P00006, F 523	ENSG00000	ATP6V1A	3				Synaptic ve	20	0.932	0.111963138	3.56	7215.7	7852.9	3.99	2.35	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q09471-1	Prefoldin s	0	38.526	59	9	14	9	154	17.3	6.33	39.71	9	metabolic; cytoplasm; protein bi	P02996	ENSG00000	PFMS	12				Prefoldin r	5	0.932	0.172829998	3.62	3151.2	3379.8	2.67	6.28	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9H832	Ubiquitin-n	0	20.205	8	3	9	3	354	38.2	5.62	20.22	3	cell death; cytoplasm; catalytic a	P00179, F 65264	ENSG00000	UBE2Z	7				Ubiquitin n	9	0.932	0.427343266	18.43	815.4	899.9	25.33	11.46	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9UH65	Switch-ass	0	23.767	12	7	10	7	585	69	5.87	13.49	7	cell organ; cytoplasm; DNA bindi	P03075, F 23075	ENSG00000	SWAP70	11					0	0.932	0.432807477	9.66	3355.6	3600.1	1.45	7.9	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9NWU2	Glucose-in	0	9.801	10	1	2	1	228	26.7	4.97	9.25	1	nucleus; protein bi	P08513, F 54994	ENSG00000	GID8	20					0	0.932	0.568341408	46.84	349.7	451.5	34.05	31.81	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q00933	Putative RI	0	49.479	20	8	24	5	392	46.5	10.01	67.29	8	cell organ; cytosol;sp; protein bi	P01394	ENSG00000	LYC12	1					0	0.932	0.687698415	4.97	3730.3	4053.2	13.01	3.11	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q075165	Dnal homc	0	8.117	1	2	2	2	2243	254.3	6.74	4.87	2	cell differe; cytosol;eni; protein bi	P00226, F 23317	ENSG00000	DNAIC13	3				Neutrophil	3	0.932	0.894097057	18.28	200.2	214.9	17.39	9.9	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q57457-1	e3 ubiquiti	0	108.872	6	20	24	20	5183	57.3	6.04	58.7	20	metabolic; cytoplasm; catalytic a	P00207, F 23352	ENSG00000	UBRA	1				Viral cardir	7	0.932	0.92637052	10.81													

FALSE	High	Master	PrC Q9NSD9	Phenylalanine	0	18.968	10	6	8	6	589	66.1	6.84	12.75	6	cell organ	cytoplasm; catalytic ac	P03483, F 10056	ENSG000001 FARS8	2	Aminoacyl-tRNA synthetase	Amino Acyl Cytosolic tRNA synthetase	6	0.927	0.705544246	39.19	1421.5	1533	17.69	14.59	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC P61313-1	60S ribosomal protein L13	0	65.517	10	11	28	11	204	24.1	11.62	53.14	11	cell organ	cytosol; membrane protein	P00827, F 6138	ENSG000001 RPL15	3	Ribosome	Cytoplasmic Peptide chain	34	0.927	0.912333629	1.66	8781.3	9412	5.08	7.6	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q06787	synaptophysin	0	21.653	11	6	8	5	632	71.1	7.42	29.88	6	metabolic	chromosome; protein	P00013, F 2332	ENSG000001 FMRL1	X	RNA transport	Serotonin	2	0.927	0.948756472	11.21	1993	2150.1	19.16	1.3	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q00221	NF-kappa-B	0	4.794	6	1	1	1	500	52.8	6.68	4.41	1	regulation	cytoplasm; protein	P00023, F 4794	ENSG000001 NFkBIE	6	B cell receptor	TNF alpha Activation	14	0.926	0.009700853	1.04	63.1	67.1	4.77	4.83	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q00483	Cytochrome c	0	10.623	46	4	9	4	81	9.4	9.38	10.01	4	metabolic	membrane; catalytic ac	P06522, F 4697	ENSG000001 NDUF4A	7	Parkinson's disease	Electron Transport	17	0.926	0.015876867	1.83	3277.7	3612.1	9.06	9.07	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q75153	Clustring	0	43.827	11	10	13	10	1309	146.6	6.13	32.45	10	cell organ	cytoplasm; protein	P112807, F 23277	ENSG000001 CLUH; KIAA1127	11	Translational		1	0.926	0.136478175	7.08	4640.5	4956.8	1.49	4.35	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC P62861	40S ribosomal protein S19	0	10.724	31	2	8	2	59	6.6	12.15	8.42	2	cell organ	cytosol; ribosomal	P04758, F 2197	ENSG000001 RPS19	17	Ribosome	Cytoplasmic Peptide chain	37	0.926	0.170557844	8.55	846.9	915.7	3.77	3.89	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q95140	Mitofusin-1	0	6.975	3	2	3	2	757	86.3	6.98	3.16	2	cell common	cytoskeleton; catalytic ac	P000350, F 9927	ENSG000001 MFN2	1	NOD-like receptor	Factors involved in	5	0.926	0.263589698	8.17	435	485.6	14.16	5.32	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q96K91	exocyst complex subunit 1	0	6.945	4	2	3	2	924	10.4	6.9	7.11	2	cell organ	cytosol; membrane protein	P01813, F 55770	ENSG000001 EXOC2	6	Ras signaling	Raila down Translocation	12	0.926	0.517300965	18.32	315	340.3	4.27	9.93	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q96K91	Histidine H1	0	54.729	79	8	20	8	126	13.8	6.95	48.73	8	cell death	cytoplasm; catalytic ac	P01230, F 3094	ENSG000001 HNT7	5			0	0.926	0.662058696	9.16	4944.4	5430.1	32.73	0.98	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q99661-1	Kinesin-like	0	18.069	7	4	4	3	725	81.3	7.83	3.48	4	cell division	chromosome; catalytic ac	P00225, F 11004	ENSG000001 KIF2C	1	Regulation	COPII-dependent	28	0.926	0.759134525	8	126.2	136.3	13.18	14.62	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC P17066	Heat shock protein 70	0	85.763	21	12	66	1	643	71	6.14	135.69	12	cell organ	cytoplasm; catalytic ac	P00012, F 3310	ENSG000001 HSPA6	6	Estrogen signaling	Neurotrophin	20	0.926	0.802018115	72.11	65.5	68.1	46.31	40.04	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC P11172	uridine 5'-phosphate decarboxylase	0	24.906	17	6	6	6	480	52.2	7.24	15.53	6	metabolic	cytoplasm; catalytic ac	P00156, F 7372	ENSG000001 UMP5	3	Pyrimidine	Fluoropyrimidine	8	0.925	0.028391724	2.35	1155.4	1249	10.72	8.18	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC P08237	ATP-dependent	0	96.69	33	17	27	14	780	85.1	7.99	65.71	17	cell organ	cytoplasm; catalytic ac	P00365, F 5213	ENSG000001 PFKFB3	12	Central carbon metabolism	Glycolysis	16	0.925	0.148689739	1.19	5521.8	6001.2	3.38	6.23	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q95363	phenylalanine	0	10.716	8	3	3	3	451	52.3	7.46	19.9	3	metabolic	cytoplasm; catalytic ac	P01409, F 10667	ENSG000001 FARS2	6	Aminoacyl-tRNA synthetase	Mitochondrion	5	0.925	0.338909043	12.57	484.2	523.2	16.73	5.86	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q9Y5A9-1	YTH domain	0	37.994	13	5	7	4	579	62.3	8.79	20.29	5	cell organ	cytoplasm; protein	P04146, F 51441	ENSG000001 YTHDF2	1			0	0.925	0.868956991	0.41	1031.5	1072.9	7.02	5.27	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q13362	Serine/threonine	0	9.585	8	4	4	4	524	61	6.87	4.61	4	metabolic	chromosome; enzyme	P01603, F 5527	ENSG000001 PPP2R3C	14	PI3K-Akt signaling	Focal Adhesion Beta-catenin	74	0.925	0.968042879	42.49	588.1	635.9	23.8	12.79	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q96K91	60S ribosomal protein L13	0	59.985	71	12	29	12	165	17.8	9.42	66.86	12	cell organ	cytosol; membrane protein	P00298, F 6136	ENSG000001 RPL12	3	Ribosome	Cytoplasmic Peptide chain	34	0.924	0.086199992	0.72	6427.4	6942.2	5.02	3.28	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q92499	ATP-dependent	0	83.078	24	17	31	17	740	82.4	7.23	61.12	17	cell organ	cytoplasm; catalytic ac	P00270, F 1653	ENSG000001 DDXL1	X			5	0.924	0.165456466	1.7	7754.1	8699.2	10.31	2.95	High	High	High	High	High	High	High	1	
FALSE	High	Master	PrC Q92499	negative regulation of	0.005	2.554	12	1	2	1	68	7	9.42	48.91	1	metabolic	cytoplasm; protein	550643	ENSG000001 LOC5064	X			0	0.924	0.461307705	21.66	431.2	470	3.96	12.24	High	High	High	High	High	High	High	1	
FALSE	High	Master	PrC Q96A83	isochorin	0	20.429	34	3	3	3	205	22.3	7.77	9.59	3	metabolic	cytoplasm; catalytic ac	P00857, F 7963	ENSG000001 ISOC2	9			0	0.924	0.578528908	38.36	342.8	370.8	24.88	18.3	High	High	High	High	High	High	High	1	
FALSE	High	Master	PrC P62258-1	14-3-3 protein	0	185.021	69	23	108	20	255	29.4	4.74	275.99	23	cell organ	cytoplasm; protein	P00244, F 7531	ENSG000001 YWHAH	17	CHRNA1	Cell Cycle; Regulation	65	0.924	0.649932811	5.13	31793.6	34221	10.15	2.98	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q15381-1	Nuclear	0	20.746	4	2	3	2	856	95	6.48	9.92	2	metabolic	membrane; catalytic ac	P00004, F 4931	ENSG000001 NNL1	1	Ribosome		1	0.924	0.762624893	41.34	355.4	384.8	16.25	16.98	High	High	High	High	High	High	High	1	
FALSE	High	Master	PrC P18859	ATP synthase	0	46.922	56	6	18	6	108	12.6	9.52	53.67	6	cell organ	membrane; catalytic ac	P05511, F 522	ENSG000001 ATP5B	21	Huntington's disease	Electron Transport	14	0.924	0.804783901	7.15	3569.3	3861.1	5.79	8.28	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q8BIW2	GRIP and	0	9.85	3	3	3	3	1684	195.8	5.14	4.54	3	cell organ	cytoplasm; protein	P00363, F 9648	ENSG000001 GCC2	2	Deregulation	Retrospect	5	0.924	0.920819917	0.13	91.8	85	49	10.58	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q75534	cold shock	0	117.867	34	29	52	29	798	88.8	6.25	97.14	29	metabolic	cytoplasm; DNA binding	P00313, F 7812	ENSG000001 CSD1	1			0	0.923	0.048795239	4.35	9900.2	10588.4	3.38	3.83	High	High	High	High	High	High	High	1	
FALSE	High	Master	PrC Q75643-1	US small nuclear	0	347.713	36	59	102	59	2136	244.8	6.06	265.46	59	cell difference	membrane; catalytic ac	P00270, F 23020	ENSG000001 SNRP200	2	Spliceosome	mRNA Splicing	6	0.923	0.053744089	0.45	22452.9	24518.3	3.25	5.8	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q9NR56-1	Muscle	0	21.515	16	5	8	5	388	41.8	8.9	19.36	5	cell difference	cytoplasm; metal ion	4154	ENSG000001 MBNL1	1	Adipogenesis		1	0.923	0.06117799	4.32	2289.6	2448.5	5.1	3.43	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q8BWU0	Nuclear	0	32.895	6	4	5	4	1156	128.9	5.1	24.05	4	cell difference	chromosome; protein	P03177, F 55746	ENSG000001 NUP133	1	RNA transport	Rev-mediated	77	0.923	0.09151602	0.88	802.1	825.3	4.3	5.53	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q515H3	WD repeat	0	10.189	4	3	3	3	913	101.3	5.45	5.49	1	metabolic	cytoplasm; protein	P00400, F 54521	ENSG000001 WDRA4	X	Endocytosis		1	0.923	0.224792443	2.46	550.9	683.5	11.08	10.85	High	High	High	High	High	High	High	High	1
FALSE	Medium	Master	PrC P46020-1	Phosphorylation	0.011	2.038	1	1	1	1	1223	137.2	6.19	26.1	1	metabolic	cytosol; membrane; catalytic ac	P00723, F 5255	ENSG000001 PHKA1	X	Insulin signaling	Glycogen Phosphorylation	8	0.923	0.258334081	9.04	107.3	116.3	5.36	3.11	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC P31949	protein S13	0	52.699	56	6	34	6	105	11.7	7.12	63.51	6	regulation	cytoplasm; metal ion	P00036, F 6282	ENSG000001 S100A11	X	Neutrophin		3	0.923	0.258342911	7.23	8397.9	9016.8	26.81	6.33	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q8NE71-1	ATP-binding	0	88.636	20	14	26	14	845	95.9	6.88	58.42	14	defense	cytoplasm; catalytic ac	P00005, F 23	ENSG000001 ABCF1	6	CHRNA1	ABC-family	2	0.923	0.566573272	13.85	7167.5	7768.7	9.5	3.88	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC P62258-1	caveolin-1	0	19.128	12	4	6	4	390	43.5	5.6	14.72	4	metabolic	cytoplasm; protein	P15237, F 284119	ENSG000001 PTFR	17	CHRNA1	RNA Polymerase	3	0.923	0.667936115	27.1	953.4	1019	12.36	9.05	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC P27708	CAD protein	0	172.691	19	32	43	28	2225	242.8	6.46	112.66	32	metabolic	cytoplasm; catalytic ac	P00117, F 790	ENSG000001 CAD	2	Metabolic	Endothelial Pyrimidine	9	0.922	0.007513926	0.95	9671.4	10423.8	1.03	0.87	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC Q9P209	Pre-mRNA	0	219.729	25	47	66	47	2335	273.4	8.84	161.32	47	cell organ	membrane; catalytic ac	P01398, F 10594	ENSG000001 PRPF8	17	CHRNA1	mRNA Processing	7	0.922	0.078585636	1.5	16488.1	17494.8	5.57	4.4	High	High	High	High	High	High	High	High	1
FALSE	High	Master	PrC P61306	Ras-related	0	51.151	50	9	15	9	215	23.9	6.21	43.58	9	cell organ	cytosol; membrane; catalytic ac	P00009, F 51552	ENSG000001 RAB1A	1	AMPA signaling	Focal Adhesion Translocation	18	0.922	0.4421267219	18.11	67												

FALSE	High	Master Prq P23368-1	NAD-depen	0	40.837	17	6	9	6	584	65.4	7.61	18.43	6	metabolic; mitochondr	catalytic ac	P100390, F 4200	ENSG000001ME2	18	Pyruvate m		Major pat	2	0.917	0.595597634	41.63	256.3	279.4	14.25	25.29	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q00541-1	Pescadillo	0	35.746	12	7	15	7	588	68	7.33	30.6	7	cell organ; chromos	protein br	P100333, F 23481	ENSG000001PE1	22				4	0.917	0.66326341	8.83	4356.5	4899.5	14.42	2.09	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P04264	Keratin, ty	0	135.172	39	20	53	17	644	66	8.12	151.58	20	cell death; cytoskele	catalytic ac	P100338, F 3848	ENSG000001KRT1	12	Corbiculo	TGF-beta r	Formation	7	0.917	0.775680047	7.06	13840.5	14594.2	28.74	8.74	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P61081	NEDD8-con	0	45.395	60	10	18	10	183	20.9	7.69	40.07	10	metabolic; cytoplasm	catalytic ac	P100179	ENSG000001UEB2M	19	Ubiquitin r			19	0.917	0.787491253	2.6	7054	7669.9	10.49	2.23	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P74441	Eukaryotic	0	67.929	21	15	18	15	907	102.73	7.14	46.06	15	cell death; cytosol-me	protein br	P100200, F 1982	ENSG000001EFA62	11	RNA trans	Exercise-in	ISG15 anti	8	0.916	0.0274144238	2.26	2346.4	2562.6	2.64	4.72	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P22392-3	isoform 3	0	159.949	83	18	93	3	267	30.1	8.92	263.54	18	cell organ; cytoplasm	catalytic ac	P100334	65-4364, 4l	ENSG000001NME1-NM	17	Purine met	Nucleotide		4	0.916	0.038895432	3.46	3273.9	3488.7	4.17	5.38	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P07868	Cathepsin d	0	35.702	18	5	10	5	339	37.8	6.3	31.88	5	cell differe	extracellular	catalytic ac	P100112, F 1508	ENSG000001C5E8	8	Antigen pr	Collagen d		17	0.916	0.144299637	3.76	1655.3	1844.7	3.2	6.99	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P51003	Poly(A) pol	0	8.432	3	2	2	2	745	82.8	7.37	0	2	metabolic; cytoplasm	catalytic ac	P100305, F 10914	ENSG000001PAP0LA	14	mRNA sur	mRNA Pro	Cleavage a	13	0.916	0.162706636	7.34	1175.7	1250.7	9.77	2.83	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P49902	Cytosolic p	0	18.281	11	5	5	5	561	64.9	6.14	11.32	5	metabolic; cytoplasm	catalytic ac	P105761	22978	ENSG000001NTSC2	10	Metabolic	Abacavir r		10	0.916	0.173933777	7.45	1411.4	1541.6	1.75	7.6	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9P2W2	WW doma	0	33.272	15	7	11	7	641	70	8.38	16.73	7	metabolic; cytoplasm	DNA bindi	P109429	51729	ENSG000001CBP21	12	Spliceosor	mRNA Spli		5	0.916	0.189734089	1.4	1564.4	1697.5	4.07	1.45	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P38919	Eukaryotic	0	108.22	49	18	54	15	411	46.8	6.73	117.25	18	metabolic; cytoplasm	catalytic ac	P100270, F 9775	ENSG000001EFA4A3	17	mRNA sur			27	0.916	0.244348884	7.34	8834.1	10292.5	10.15	8.75	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9Y2P8	RNA 3'-ter	0	7.253	4	1	1	1	373	40.8	9.26	3.64	1	metabolic; nucleus	catalytic ac	P101137, F 10171	ENSG000001RCL1	9	Ribosome	Major pat		6	0.916	0.445041643	23.53	157.7	176.4	12.31	11.09	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q96F47	tRNA (ade	0	9.751	11	2	3	2	289	31.4	7.36	12.45	2	metabolic; nucleus	catalytic ac	P108704, F 115708	ENSG000001TRMT61A	14	tRNA mod			3	0.916	0.468591838	17.48	899.4	981.5	10.42	3.58	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P17844	probable p	0	151.992	40	31	75	22	614	69.1	8.92	152.04	31	cell differe	cytoplasm; catalytic ac	P100270, F 1655	ENSG000001DDX5	17	Proteoglyc	mRNA Spli		7	0.916	0.717539147	2.44	18016.1	19672.6	6.4	5.37	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P52209	6-phospho	0	141.746	51	18	39	18	483	53.1	7.23	137.1	18	metabolic; cytoplasm	catalytic ac	P100393, F 5226	ENSG000001PGD	1	Carbon me	Pentose Ph	Pentose ph	9	0.915	0.023510528	2.77	11625.7	12680	1.83	0.69	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P83731	60S riboso	0	57.577	41	9	30	9	157	17.8	11.25	71.67	9	cell organ; cytoplasm	protein br	P101246	6152	ENSG000001RPL24	3	Ribosome	Cytoplasm	Peptide ch	34	0.915	0.155970389	2.6	17751.4	19069.8	22.73	8.25	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9GZL7	ribosome i	0	41.061	21	6	11	6	423	47.7	5.9	31.16	6	cell prolif	nucleus	protein br	P104000, F 55759	ENSG000001WDR12	1		Major pat		4	0.915	0.196640487	8.78	4137.2	4783.8	8.15	6.82	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P83731	60S riboso	0	57.577	41	9	30	9	157	17.8	11.25	71.67	9	cell organ; cytoplasm	protein br	P101246	6152	ENSG000001RPL24	3	Ribosome	Cytoplasm	Peptide ch	34	0.915	0.155970389	2.6	17751.4	19069.8	22.73	8.25	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9GZL7	ribosome i	0	41.061	21	6	11	6	423	47.7	5.9	31.16	6	cell prolif	nucleus	protein br	P104000, F 55759	ENSG000001WDR12	1		Major pat		4	0.915	0.196640487	8.78	4137.2	4783.8	8.15	6.82	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P83731	60S riboso	0	57.577	41	9	30	9	157	17.8	11.25	71.67	9	cell organ; cytoplasm	protein br	P101246	6152	ENSG000001RPL24	3	Ribosome	Cytoplasm	Peptide ch	34	0.915	0.155970389	2.6	17751.4	19069.8	22.73	8.25	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9GZL7	ribosome i	0	41.061	21	6	11	6	423	47.7	5.9	31.16	6	cell prolif	nucleus	protein br	P104000, F 55759	ENSG000001WDR12	1		Major pat		4	0.915	0.196640487	8.78	4137.2	4783.8	8.15	6.82	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P83731	60S riboso	0	57.577	41	9	30	9	157	17.8	11.25	71.67	9	cell organ; cytoplasm	protein br	P101246	6152	ENSG000001RPL24	3	Ribosome	Cytoplasm	Peptide ch	34	0.915	0.155970389	2.6	17751.4	19069.8	22.73	8.25	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9GZL7	ribosome i	0	41.061	21	6	11	6	423	47.7	5.9	31.16	6	cell prolif	nucleus	protein br	P104000, F 55759	ENSG000001WDR12	1		Major pat		4	0.915	0.196640487	8.78	4137.2	4783.8	8.15	6.82	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P83731	60S riboso	0	57.577	41	9	30	9	157	17.8	11.25	71.67	9	cell organ; cytoplasm	protein br	P101246	6152	ENSG000001RPL24	3	Ribosome	Cytoplasm	Peptide ch	34	0.915	0.155970389	2.6	17751.4	19069.8	22.73	8.25	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9GZL7	ribosome i	0	41.061	21	6	11	6	423	47.7	5.9	31.16	6	cell prolif	nucleus	protein br	P104000, F 55759	ENSG000001WDR12	1		Major pat		4	0.915	0.196640487	8.78	4137.2	4783.8	8.15	6.82	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P83731	60S riboso	0	57.577	41	9	30	9	157	17.8	11.25	71.67	9	cell organ; cytoplasm	protein br	P101246	6152	ENSG000001RPL24	3	Ribosome	Cytoplasm	Peptide ch	34	0.915	0.155970389	2.6	17751.4	19069.8	22.73	8.25	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9GZL7	ribosome i	0	41.061	21	6	11	6	423	47.7	5.9	31.16	6	cell prolif	nucleus	protein br	P104000, F 55759	ENSG000001WDR12	1		Major pat		4	0.915	0.196640487	8.78	4137.2	4783.8	8.15	6.82	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P83731	60S riboso	0	57.577	41	9	30	9	157	17.8	11.25	71.67	9	cell organ; cytoplasm	protein br	P101246	6152	ENSG000001RPL24	3	Ribosome	Cytoplasm	Peptide ch	34	0.915	0.155970389	2.6	17751.4	19069.8	22.73	8.25	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9GZL7	ribosome i	0	41.061	21	6	11	6	423	47.7	5.9	31.16	6	cell prolif	nucleus	protein br	P104000, F 55759	ENSG000001WDR12	1		Major pat		4	0.915	0.196640487	8.78	4137.2	4783.8	8.15	6.82	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P83731	60S riboso	0	57.577	41	9	30	9	157	17.8	11.25	71.67	9	cell organ; cytoplasm	protein br	P101246	6152	ENSG000001RPL24	3	Ribosome	Cytoplasm	Peptide ch	34	0.915	0.155970389	2.6	17751.4	19069.8	22.73	8.25	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9GZL7	ribosome i	0	41.061	21	6	11	6	423	47.7	5.9	31.16	6	cell prolif	nucleus	protein br	P104000, F 55759	ENSG000001WDR12	1		Major pat		4	0.915	0.196640487	8.78	4137.2	4783.8	8.15	6.82	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P83731	60S riboso	0	57.577	41	9	30	9	157	17.8	11.25	71.67	9	cell organ; cytoplasm	protein br	P101246	6152	ENSG000001RPL24	3	Ribosome	Cytoplasm	Peptide ch	34	0.915	0.155970389	2.6	17751.4	19069.8	22.73	8.25	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9GZL7	ribosome i	0	41.061	21	6	11	6	423	47.7	5.9	31.16	6	cell prolif	nucleus	protein br	P104000, F 55759	ENSG000001WDR12	1		Major pat		4	0.915	0.196640487	8.78	4137.2	4783.8	8.15	6.82	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P83731	60S riboso	0	57.577	41	9	30	9	157	17.8	11.25	71.67	9	cell organ; cytoplasm	protein br	P101246	6152	ENSG000001RPL24	3	Ribosome	Cytoplasm	Peptide ch	34	0.915	0.155970389	2.6	17751.4	19069.8	22.73	8.25	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9GZL7	ribosome i	0	41.061	21	6	11	6	423	47.7	5.9	31.16	6	cell prolif	nucleus	protein br	P104000, F 55759	ENSG000001WDR12	1		Major pat		4	0.915	0.196640487	8.78	4137.2	4783.8	8.15	6.82	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P83731	60S riboso	0	57.577	41	9	30	9	157	17.8	11.25	71.67	9	cell organ; cytoplasm	protein br	P101246	6152	ENSG000001RPL24	3	Ribosome	Cytoplasm	Peptide ch	34	0.915	0.155970389	2.6	17751.4	19069.8	22.73	8.25	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q9GZL7	ribosome i	0	41.061	21	6	11	6	423	47.7	5.9	31.16	6	cell prolif	nucleus	protein br	P104000, F 55759	ENSG000001WDR12	1		Major pat		4	0.915	0.196640487	8.78	4137.2	4783.8	8.15	6.82</								

FALSE	High	Master Prq Q9Y5M8	signal reco	0	57.496	37	9	20	9	271	29.7	9.04	48.24	9	regulation	cytoplasm;	nucleotide	P00009, F 58477	ENSG00000	SRPR8	3	Protein exp	XBPI1 [5]	ac	7	0.906	0.025316635	2.99	4697.5	5262.9	2.35	1.48	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq P08579	U2 small n	0	20.786	16	4	10	3	225	25.5	9.72	19.47	4	metabolic	nucleus;	protein bi	P00076, F 6629	ENSG00000	SNRPB2	20	Spliceosom	mRNA Pro	mRNA Spli	6	0.906	0.108072079	1.11	1269.2	1414.2	1.87	8.56	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q9N12-1	Helicase 9	0	14.631	4	4	4	4	1246	137.7	6.06	7.81	4	metabolic	cytoplasm;	catalytic a	P00270, F 6499	ENSG00000	SKIVL2	6	RNA degra	mRNA dec	8	0.906	0.122816304	1.42	1324.5	1516.1	12.61	3.95	High	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q00232-1	26s proteo	0	70.477	31	11	17	11	456	52.9	7.65	56.88	11	metabolic	cytoplasm;	catalytic a	P01399	5718	ENSG00000	MSO12	17	Epstein-Ba	Proteasom	Regulat	153	0.906	0.139614748	10.05	5784.2	6106.8	9.99	3.44	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9NY12-1	H/ACA ribz	0	19.577	32	5	7	5	217	22.3	10.92	12.08	5	cell organ	nucleus	protein bi	P04041	54433	ENSG00000	GAR1	4	Ribosome	rRNA mod	5	0.906	0.149385463	0.54	1833.1	2000.6	1.29	5.2	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq P56556	NADH deh	0	5.67	12	2	3	2	154	17.9	10.14	6.93	2	cell organ	membrane	catalytic a	P05347, F 4700	ENSG00000	NDOUF4	22	Metabolic	Electron Tr	Complex I	13	0.906	0.293463233	17.02	1015.8	1147.3	4.99	9.32	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq P19338	Nucleolin	0	370.239	54	59	198	59	710	76.6	4.7	403.77	59	regulation	cytoplasm;	DNA bindi	P00000	NCL	6	ENSG00000	NC	2	Pathogeni	Major pat	7	0.906	0.446762056	5.64	71671.6	75455.5	7.17	5.05	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q6P57-1	Acylglyoxy	0	6.016	17	2	2	2	224	24.8	7.39	4	2	metabolic	cytoplasm;	catalytic a	P01557	81899	ENSG00000	FAH01	16	Tyrosine m		2	0.906	0.611235136	34.27	199.2	219.8	14.13	12.64	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q13167-1	Cullin-2 [O	0	13.7	9	6	7	6	745	86.9	6.92	6.75	6	metabolic	cytosol	catalytic a	P00888, F 8453	ENSG00000	CUL2	10	Renal cell	Oxygen-de	20	0.906	0.72487696	18.58	1187.7	1375.8	23.77	5.88	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q99623	Prohibitin	0	65.537	37	12	32	12	299	33.3	9.83	70.59	12	cell organ	cell surface	protein bi	P01145	11331	ENSG00000	PRB2	12	Processing		3	0.905	0.026127178	2.9	9511.2	10868.6	4.47	4.64	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q9Y273	guanine de	0	77.435	41	12	21	12	454	51	5.68	53.1	12	metabolic	cytosol	catalytic a	P01978, F 9615	ENSG00000	GDA	9	Purine met	Purine cat	6	0.905	0.08123649	4.12	3439.2	3829.4	7.5	1.05	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q9NG88	Fructose-2	0	5.682	6	1	1	1	270	30	7.69	2.48	1	cell death;	cytoplasm;	catalytic a	P00300	57103	ENSG00000	CL2orf5, T	12	Central car	TP53 Regu	7	0.905	0.117157696	4.22	151.8	176.3	8.31	3.16	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q15102	Platelet-ac	0	19.824	29	5	7	5	231	25.7	6.84	13.71	5	metabolic	cytoplasm;	catalytic a	P00657, F 5050	ENSG00000	PAFAH1B3	19	Metabolic	COPH-ind	7	0.905	0.129292920	3.18	1054.5	1182.8	7.69	3.19	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq P78417	Glutathion	0	43.623	39	10	22	10	241	27.5	6.6	29.28	10	cellular ho	cytoplasm;	antioxidan	P00043, F 9446	ENSG00000	GSTO1	10	Glutathion	Myometri	Gene and	20	0.905	0.148424647	10.4	5826.6	6441.2	3.13	4.72	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q13418	Integrin-lir	0	8.92	8	3	3	3	452	51.4	8.07	6.82	3	cell organ	cytoplasm;	catalytic a	P00023, F 3611	ENSG00000	ILK	11	Endometri	Integrin-m	Localizati	15	0.905	0.322303383	13.72	783.5	825.8	5.53	8.92	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9H2J4	phosducin	0	15.006	14	3	4	3	239	27.6	4.84	5.42	3	cell death;	cytoplasm;	catalytic a	P00214	79031	ENSG00000	PDL3	2	Endocytos		0	0.905	0.388928011	22.74	484.5	576.1	17.51	16.97	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q13596	Sorting net	0	39.934	16	7	13	5	522	59	5.15	26.83	7	cell organ	cytoplasm;	protein bi	P00787, F 6642	ENSG00000	SNX1	15	Endocytos		1	0.905	0.463750599	25.24	1384.5	1424	17.56	5.09	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq P04114	apolipopro	0.004	2.683	0	1	1	1	4563	515.3	7.05	2.18	1	cell organ	cytoplasm;	protein bi	P01347, F 338	ENSG00000	APOB	2	Vitamin di	Selenium P	Post-transl	46	0.905	0.50956131	25.89	231.8	261.4	8.29	13.22	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q04391-1	band 4.1-l	0	39.09	11	9	10	9	1005	112.5	5.44	23.01	9	cell divisio	cytoplasm;	protein bi	P00373, F 2037	ENSG00000	EPB41L2	6	Tight junct	Neurexins	4	0.905	0.673198918	5.8	2279.2	2460.2	12.61	1.78	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q9NBZ7-1	UOP-glucu	0	7.559	6	1	2	1	420	47.5	8.94	6.63	1	cell organ	cytoplasm;	catalytic a	P01073, F 80146	ENSG00000	UKX1	2	Amino sug		2	0.905	0.818517763	72.39	30	27.4	69.88	21.31	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q9S169	NADH deh	0	14.774	30	4	4	4	186	21.8	6.8	10.05	4	cell organ	endoplasm	catalytic a	P05821	4714	ENSG00000	NDUFB8	10	Metabolic	Electron Tr	Mitochond	15	0.905	0.925769083	0.21	559	592.9	3.6	13.44	High	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prq Q06210-1	glutamine	0	115.608	32	16	33	16	699	78.8	7.11	105.52	16	metabolic	cytosol	catalytic a	P00110, F 2673	ENSG00000	GFTT1	2	Amino sug		17	0.904	0.036557284	2.39	6802.6	7592.8	8.15	3.42	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq P0406-1	glyceralde	0	489.219	84	30	391	30	335	36	8.46	1150.36	30	cell death;	cytoplasm;	catalytic a	P00044, F 2597	ENSG00000	GAPDH	12	Glycolysis	Cori Cycle	Glucose	15	0.904	0.17524628	40.49	119900.5	134791.1	12.25	2.48	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q14684	Ribosomal	0	21.867	8	5	8	5	758	84.4	9.76	12.61	5	metabolic	cytosol;nu	protein bi	P05997	23076	ENSG00000	RL18B	21	0	0.904	0.245310651	15.24	630	696.7	8.61	2.27	High	High	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq Q9Y306	mitochond	0	13.239	22	3	11	3	152	16.9	8.79	21.84	3	cell death;	endoplasm	protein bi	P014852, F 51024	ENSG00000	F51	7	0	0.904	0.270212051	6.58	3361.6	4047	10.42	16.76	High	High	High	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq P78330	phosphose	0	7.634	12	2	2	2	225	25	5.69	4.12	2	metabolic	cytoplasm;	catalytic a	P00102, F 5723	ENSG00000	PSPH	7	Carbon me	Trans-sulf	Serine bio	9	0.904	0.55652586	7.28	836	872.2	8.33	7.29	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P61353	60S riboso	0	37.717	55	8	25	8	136	15.9	10.56	42.41	8	cell organ	cytosol;me	RNA bindi	P00467, F 6155	ENSG00000	RLP27	17	Ribosome	Cytoplasm	Peptide ch	34	0.903	0.020882019	1.66	15073.5	17270.1	10.08	10.25	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P68366	Tubulin al	0	223.338	53	21	139	4	448	49.9	5.06	475.12	21	cell organ	cytoplasm;	catalytic a	P00091, F 7277	ENSG00000	TUBAA4	2	Gap juncti	Pathogeni	COPH-ind	76	0.903	0.251318614	13.75	3102.1	3409.9	13.86	2.15	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q9Y4E8	ubiquitin c	0	17.942	5	4	4	4	981	12.3	5.22	11.26	4	cell organ	cytoplasm;	catalytic a	P00443, F 9958	ENSG00000	USP15	12	UCH pro		10	0.903	0.289565845	7.25	1095.3	1222.3	10.95	1.85	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq P09234	U1 small n	0	29.146	30	4	8	4	159	17.4	9.67	29.44	4	cell organ	nucleus;	metal ion	P06220	6631	ENSG00000	SNRPC	6	Spliceosom	mRNA Spli	5	0.903	0.569597046	32.6	2106.9	2052.6	19.5	11.79	High	High	High	High	High	High	High	High	High	1	
FALSE	Low	Master Prq Q9NFMA	adenylate	0.057	1.136	1	1	1	1	1077	119.7	7.47	2.4	1	metabolic	cytoplasm;	catalytic a	P00211, F 196883	ENSG00000	ADCY4	14	GABAergic	Myometri	Adenylate	78	0.903	0.589734664	45.5	133	141.1	67.04	11.46	High	High	High	High	High	High	High	High	High	1	
FALSE	Low	Master Prq Q9GNR2	Integrator	0.057	1.136	1	1	1	1	710	82.2	7.44	0	1	metabolic	nucleus	protein bi	55174	ENSG00000	INTS10	8	RNA polyr		3	0.903	0.894182177	24.52	92.2	102.8	22.13	7.84	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q14697-1	Neutral al	0	200.716	38	33	100	1	944	106.8	6.14	257.85	33	metabolic	endoplasm	catalytic a	P01055, F 23193	ENSG00000	GANAB	19	N-Glycan b	Calnexin/c	8	0.902	0.039522859	3.55	1462.2	1577.7	4.59	2.27	High	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq P04029	60S riboso	0	61.622	50	14	42	14	203	23.6	10.93	60.98	14	cell organ	cytoplasm;	RNA bindi	P00572	23521	ENSG00000	RLP13A	11	Ribosome	Cytoplasm	Peptide ch	34	0.902	0.040760631	2.02	16708.5	18529.4	4.01	7.34	High	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prq P09488	Glutathion	0	25.538	34	7	9	7	218	25.7	6.7	16.83	7	metabolic	cytoplasm;	catalytic a	P00043, F 2944	ENSG00000	GSTM1	1	Platinum d	Glutathion	Glutathion	15	0.902	0.055234041	2.38	3303.9	3844	6.5	3.47	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q0A096	RNA-bindin	0	11.956	7	3	3	3	593	64.1	7.68	5.63	3	cell death;	nucleus	RNA bindi	P00076, F 54502	ENSG00000																								

FALSE	High	Master Pcr F21291	Cysteine ai	0	97.343	67	9	29	9	193	20.6	8.57	105.9	9	nucleus	metal ion I	P00412	1465	ENSG000001	CSRP1		Mecp2 acn MTP1 actv	4	0.896	0.99138503	8.55	10484.9	11710.7	25.46	9.82	High	High	High	High	High	High	1			
FALSE	High	Master Pcr F10155-1	60 kDa SS-	0	16.757	9	4	5	4	538	60.6	8.03	7.44	4	cell organ cytoplasm	metal ion I	P05731	6738	ENSG000001	TROV2			1	0.895	0.022865705	3.4	280.8	325.9	7.38	6.51	High	High	High	High	High	High	1			
FALSE	High	Master Pcr F49321	Nuclear aa	0	189.936	45	28	56	28	788	85.2	43	150.25	28	cell organ cytoplasm	protein bin	P00515	F_4678	ENSG000001	NASR	1		0	0.895	0.02999053	3.83	11271	12596.6	6.08	2.82	High	High	High	High	High	High	1			
FALSE	High	Master Pcr Q14929	histone aa	0	21.167	18	5	7	5	419	49.5	5.69	14.69	5	cell organ cytoplasm	catalytic a	P01394	8520	ENSG000001	HAT1	2	Alcoholism	HATS acety	4	0.895	0.032406411	0.05	1146.8	1335	2.99	4.4	High	High	High	High	High	High	1		
FALSE	High	Master Pcr P05198	Eukaryotic	0	61.209	42	11	23	11	315	36.1	5.08	10.11	11	cell commu cytoplasm	protein bin	P00575	F_1965	ENSG000001	EF2S1	14	Herpes sim Translatior	Formation	25	0.895	0.121982893	7.68	5983.4	6539.4	1.68	6.05	High	High	High	High	High	High	1		
FALSE	High	Master Pcr Q15008	265 proteas	0	35.16	23	7	13	7	389	45.5	5.62	42.07	7	metabolic cytosol/ex	catalytic a	P01399	F_9861	ENSG000001	PSMD6	3	Epstein-Ba	Proteasom Regulation	153	0.895	0.169122783	11.62	4310.4	5041.9	6.76	7.37	High	High	High	High	High	High	1		
FALSE	High	Master Pcr P05198	Annekin A	0	294.477	83	38	161	38	339	38.6	7.75	394.61	38	cell organ cytoplasm	cell surfac	enzyme re	P00519	302	ENSG000001	ANXA2	15		12	0.895	0.264519036	18.3	55761.2	57348.8	1.22	7.81	High	High	High	High	High	High	1		
FALSE	High	Master Pcr QZM281-1	AP2-assoc	0	9.076	4	2	2	2	961	103.8	6.6	4.05	2	cell organ cytoplasm	catalytic a	P00609	F_22848	ENSG000001	AAL1	2		4	0.895	0.275442354	2.45	270.4	294.3	7.21	11.72	High	High	High	High	High	High	1			
FALSE	High	Master Pcr F30484	HLA class I	0	26.336	20	6	17	2	362	40.4	6.62	24.61	6	regulation cell surfac	protein bin	P01025	F_3106	ENSG000001	HLA-B	6		15	0.895	0.313444546	5.19	137.0	190.5	25.14	26.85	High	High	High	High	High	High	1			
FALSE	High	Master Pcr P62847-1	40S riboso	0	36.827	31	5	17	5	133	15.4	10.78	55.88	5	cell organ cytosol/me	protein bin	P01282	G_2239	ENSG000001	RPS24	10	Ribosome	Cytoplasmic Peptide ch	38	0.895	0.593570341	9.58	6433.9	7189.3	8.1	7.68	High	High	High	High	High	High	1		
FALSE	High	Master Pcr QN6092	Coordinate	0	4.672	7	1	3	1	184	20.1	1		1	cell organ cytosol/me	protein bin	P11540	S_5352	ENSG000001	CPSC5	17		3	0.895	0.894728374	49.21	611.7	681.2	42.62	3.54	High	High	High	High	High	High	1			
FALSE	High	Master Pcr P09906-1	Ieukotrien	0	68.848	25	12	20	12	61.2	69.2	61.8	54.76	12	metabolic cytoplasm	catalytic a	P01433	F_4048	ENSG000001	LTA4H	12	Metabolic	Cyclooxygenase II	11	0.894	0.028804927	4.74	624.6	696.24	2.13	2.57	High	High	High	High	High	High	1		
FALSE	High	Master Pcr P62888	60S riboso	0	87.388	67	7	50	7	115	12.8	9.63	122.8	7	cell organ cytoplasm	protein bin	P01248	G_6156	ENSG000001	RP138	8	Ribosome	Selenium H	Peptide ch	35	0.894	0.054842452	5.25	15415.9	17245.9	1.02	5.24	High	High	High	High	High	High	1	
FALSE	High	Master Pcr QGN84-1	rRNA metit	0	8.95	9	3	4	3	353	38.6	7.94	8.4	3	metabolic mitochond	catalytic a	P00588	F_79922	ENSG000001	MRM1	17	CHR_H	rRNA mod	4	0.894	0.282131814	16.03	381.6	426.9	7.22	11.78	High	High	High	High	High	High	1		
FALSE	High	Master Pcr F49841-1	Glyogen s	0	15.225	9	2	3	2	420	46.7	8.78	8.16	2	cell differe cytoplasm	catalytic a	P00606	F_2932	ENSG000001	GSK3B	3	Dopamine H5-Signal	Regulation	124	0.894	0.392711034	24.16	634.6	710.2	11.81	10.32	High	High	High	High	High	High	1		
FALSE	High	Master Pcr Q14914	Prostaglan	0	9.54	7	1	1	1	329	35.8	8.29	6.41	1	metabolic cytoplasm	catalytic a	P00617	G_22949	ENSG000001	PTGR1	9	NR2 path	Synthesis c	7	0.894	0.551068341	26.54	474	536.5	0.67	21.45	High	High	High	High	High	High	1		
FALSE	High	Master Pcr QBQV4	Nuclear cl	0	6.771	4	1	1	1	516	58.4	7.49	4.74	1	metabolic membrane	protein bin	P013914	F_79050	ENSG000001	NOC12	12		Major pat	5	0.894	0.68088412	56.13	48.4	54.1	29.12	23.26	High	High	High	High	High	High	1		
FALSE	High	Master Pcr P09661	U2 small n	0	47.761	38	9	17	9	255	28.4	8.62	30.49	9	metabolic nucleoscy	protein bin	P121799	F_6627	ENSG000001	SNRPA1	2	Spliceosom mRNA Pro	Gene and	11	0.893	0.014369005	1.57	3178	3507.2	5.32	6.63	High	High	High	High	High	High	1		
FALSE	High	Master Pcr Q9H12	39S riboso	0	16.022	13	3	4	3	332	37.5	8.4	15.04	3	metabolic membrane	catalytic a	P00636	G_65080	ENSG000001	MRPL44	2		Mitochond	6	0.893	0.070606088	6.96	1176.9	1249.1	4.29	6.79	High	High	High	High	High	High	1		
FALSE	High	Master Pcr F32119	Peroxired	0	63.507	51	11	37	10	198	21.9	5.97	80.08	11	cell commu cytoplasm	antioxidan	P005678	F_7001	ENSG000001	PRDX2	1		Selenium H	TP53 Regu	12	0.893	0.073414428	2.36	9503.8	11150.5	5.06	4.24	High	High	High	High	High	High	1	
FALSE	High	Master Pcr Q9Y388-1	Oligobion	0	42.906	46	9	11	9	237	26.8	6.87	25.19	9	metabolic cytoplasm	catalytic a	P00929	G_25996	ENSG000001	REK02	11		Ribosome	1	0.893	0.070310777	1.64	4558.2	4949.4	2.4	3.65	High	High	High	High	High	High	1		
FALSE	High	Master Pcr F49770	Translatio	0	8.531	11	3	3	3	351	39	6.16	5.76	3	metabolic cytoplasm	nucleotide	P01008	G_8892	ENSG000001	EF2R2	14	RNA trans	Translator	Recycling c	8	0.893	0.125507066	7.66	214	228.6	6.07	10.99	High	High	High	High	High	High	1	
FALSE	Medium	Master Pcr P61803	Dolichyl-d	0.034	1.374	9	1	1	1	113	12.5	7.08	0	1	cell death endoplasm	catalytic a	P01209	G_1603	ENSG000001	DAI1	14	Protein prc	Asparagin	6	0.893	0.938727284	4.61	161	180.3	3.32	8.49	High	High	High	High	High	High	1		
FALSE	High	Master Pcr Q9Y580	rRNA poly	0	7.287	3	3	4	4	961	104.3	5.27	4.94	4	cell division cytoplasm	catalytic a	P00533	F_9150	ENSG000001	CDTP1	18		RNA elonga	25	0.893	0.933666041	5.05	578.9	597.9	13.45	8.83	High	High	High	High	High	High	1		
FALSE	High	Master Pcr Q9UR04	Brain-spec	0	14.874	10	4	4	4	511	56.8	8.68	7.01	4	cell organ cytoplasm	protein bin	P010018	G_55971	ENSG000001	BAIAP211	7			0	0.892	0.098688701	1.33	907.7	1017.7	5.65	9.07	High	High	High	High	High	High	1		
FALSE	High	Master Pcr P62750	60S riboso	0	65.561	54	11	46	11	156	17.7	10.45	91.51	11	cell organ cytoplasm	protein bin	P00276	F_6147	ENSG000001	RP124	17		Ribosome	Cytoplasm	Peptide ch	34	0.892	0.095803911	2	1235.5	13426.6	4.98	1.29	High	High	High	High	High	High	1
FALSE	High	Master Pcr F52943	Cyteline-e	0	24.509	25	2	3	2	208	22.5	8.72	15.38	2	regulation	metal ion I	P00412	1397	ENSG000001	CRP23	14			0	0.892	0.11447801	9.1	759.6	806.9	4.01	9.42	High	High	High	High	High	High	1		
FALSE	High	Master Pcr Q92799	Ribosomal	0	18.666	18	3	3	3	244	26.7	9.17	8.85	3	metabolic cytoplasm	catalytic a	P01587	G_10436	ENSG000001	ENG1	12	Ribosome	Major pat	6	0.892	0.246486268	14.29	756.4	909.6	11.55	10.13	High	High	High	High	High	High	1		
FALSE	High	Master Pcr P62280	40S riboso	0	48.295	53	10	28	10	158	18.4	10.3	64.51	10	cell differe cytoplasm	protein bin	P00366	G_6205	ENSG000001	RPS11	19	Ribosome	Cytoplasm	Peptide ch	38	0.892	0.324439667	13.24	12213.8	13700.2	1.91	10.49	High	High	High	High	High	High	1	
FALSE	High	Master Pcr Q9H782	Ribosome	0	7.676	6	2	3	2	306	35.6	9.99	4.62	2	cell organ nucleu	RNA bindi	P00447	G_84154	ENSG000001	RPF2	6			0	0.892	0.408204179	11.9	176.9	198.3	10.88	4.73	High	High	High	High	High	High	1		
FALSE	High	Master Pcr P47755	F-actin-cap	0	38.499	40	8	12	6	286	32.9	5.85	26.19	8	cell organ cytoskelet	protein bin	P01267	G_830	ENSG000001	CAFP2A	7	Endocytosi	COP1-ind	22	0.892	0.505988609	17.01	699	708	7.82	12.79	High	High	High	High	High	High	1		
FALSE	High	Master Pcr Q136740	ATP-deph	0	25.456	27	4	4	4	277	30.7	8.09	22.54	4	cell organ mitochond	catalytic a	P00574	G_8192	ENSG000001	CLP2	19			0	0.892	0.567207942	36.3	2209.9	2460.2	17.65	10.88	High	High	High	High	High	High	1		
FALSE	High	Master Pcr P62244	40S riboso	0	29.676	61	9	12	9	130	14.8	10.13	21.14	9	cell organ cytoplasm	protein bin	P01040	G_6210	ENSG000001	RPS15A	16	Ribosome	Cytoplasmic Peptide ch	38	0.891	0.019713999	1.59	5950.8	6608.3	5.5	10.5	High	High	High	High	High	High	1		
FALSE	High	Master Pcr Q62441	Eukaryotic	0	37.661	26	11	16	11	585	64.9	8.87	44.03	11	cell organ cytoplasm	protein bin	P00862	G_83939	ENSG000001	EF2A	3		Phytodyn	2	0.891	0.045840124	5.05	3802.1	4154.5	5.86	5.77	High	High	High	High	High	High	1		
FALSE	High	Master Pcr P83916	Chromoso	0	27.55	30	4	7	3	185	21.4	49.3	13.06	4	regulation chromos	protein bin	P00385	F_10951	ENSG000001	CBX1	17			0	0.891	0.071278653	7.91	22.8	24.2	17.17	15.11	High	High	High	High	High	High	1		
FALSE	High	Master Pcr Q00762	Ubiquitin	0	14.896	23	3	5	3	179	19.6	7.37	10.26	3	cell division cytoplasm	catalytic a	P00179	F_11065	ENSG000001	UBC2	10	Ubiquitin n	Gastric Car	Inactivation	39	0.891	0.103072313	8.13	2231.7	2436.2	4.67	4.02	High	High	High	High	High	High	1	
FALSE	High	Master Pcr F49458	Signal rec	0	20.798	40	4	9	4	86	10.1	7.97	14.98	4	cell organ cytoplasm	protein bin	P005486	G_6726_653	ENSG000001	SRP	1	Protein ext	SRP-deph	4	0.891	0.281753346	19.51	4864.3	4871.8	17.83	7.96	High	High	High	High	High	High	1		
FALSE	High	Master Pcr QGNR12-1	PDZ and I	0	10.178	7	3	6	3	457	49.8	8.41	11.54	3	cell differe cytoplasm	metal ion I	P00412	G_9260	ENSG000001	POLM17	5	EBV LMP1	RET sign	4	0.891	0.957789027	26.86	1734.4	1946.9	25.85	5.41	High	High	High	High	High	High	1		
FALSE	High	Master Pcr Q96F06																																						

FALSE	High	Master Prq	P04844-1	Dolichyl-di	0	101.079	38	13	21	13	631	69.2	5.69	81.01	13	metabolic; endoplasmic reticulum	protein bi	P05817	6185	ENSG000001	RPN2	20	Protein pr	Proteasom	Asparagin	9	0.881	0.446492142	31.36	5108.9	5695.2	18.04	9.41	High	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq	Q18N129	Protein cat	0	5.098	8	1	1	1	248	28.3	4.64	4.35	1	regulation	cytosol	protein bi	P11938	245812	ENSG000001	CNPY4	7				0	0.881	0.503583029	62.1	19.8	25.8	70.28	44.2	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q75937	Dnal hom	0	30.173	23	6	10	6	253	29.8	9.06	20.51	6	metabolic; cytosol	nu	protein bi	P00226	22826	ENSG000001	DNAIC8	1	mRNA Pro	mRNA Spli	5	0.88	0.1621498	13.69	3158.6	3587.7	9.55	2.24	High	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq	Q96055	Transcript	0	6.794	5	1	1	1	360	41.7	9.32	4.69	1	cell organ	mitochond	catalytic a	P12836	79736	ENSG000001	TFT1	17			0	0.88	0.224797593	13.79	88.3	100.3	18.18	1.48	High	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq	Q96286	NAD-depe	0	18.435	9	6	7	6	747	81.6	4.67	11.2	6	cell comm	chromoso	catalytic a	P02146	23411	ENSG000001	SERF	10	MicroRNA; Androgen	SIRT1 nega	26	0.88	0.330563803	18.08	1073.5	1646.5	30.2	24.47	High	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq	Q96766	ubiquitin c	0	19.769	5	5	5	5	1375	157.2	5.08	10.02	5	metabolic; cytoplasm	catalytic a	P00443	55031	ENSG000001	USP47	11			Ub-specific	4	0.88	0.881026495	28.1	263.8	299.8	22.34	10.74	High	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq	Q96766	protein arg	0	57.133	40	12	17	12	361	41.5	54.3	55.88	12	cell organ	cytoplasm; catalytic a	P05175	3276	ENSG000001	PRMT1	19	FoxO signa	Energy Me	17	0.88	0.90681456	4.65	5563.3	5951.9	18.65	5.36	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq	Q46783	40S riboso	0	50.487	53	12	47	11	165	18.9	10.15	71.54	12	cell organ	cytoplasm; protein bi	P03051	6204	ENSG000001	RP510	6	Ribosome	Cytoplasm	Peptide ch	38	0.879	0.023464425	1.52	15171.8	17440.5	3.96	6.22	High	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq	Q13408	Cytoskele	0	8.54	1	2	4	2	2032	22.4	7.8	7.58	2	cell divisio	chromoso	protein bi	P12348	9783	ENSG000001	OXAP5	11			Regulation	28	0.879	0.037754293	6.21	1338	1585.2	12.03	8.94	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q60900	Proteasom	0	88.587	60	14	45	14	246	27.4	6.76	105.17	14	metabolic; cytoplasm; catalytic a	P00227	5687	ENSG000001	PSMA6	14	Proteasom	Proteasom	Regulation	150	0.879	0.130004718	10.9	11682.7	13294.9	8.52	2.14	High	High	High	High	High	High	High	High	High	1			
FALSE	Medium	Master Prq	Q19477	ribokinase	0.015	1.754	2	1	1	1	322	34.1	5.05	0	1	metabolic; cytoplasm; catalytic a	P00294	64080	ENSG000001	RBK5	2	Pentose ph	Pentose ph	4	0.879	0.195608084	9.91	69.8	83.5	9.97	9.35	High	High	High	High	High	High	High	High	High	1				
FALSE	High	Master Prq	Q10181	Splicing fa	0	32.64	31	6	14	6	240	27.9	8.81	37.43	6	metabolic; nucleus;spi	metal ion	P00076	7307; 102	ENSG000001	U2AF1; LO	21	Shigellos; mRNA Pro	Cleavage o	14	0.879	0.501517434	7.73	3041.1	3155.6	8.75	10.31	High	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q45974-1	Ubiquitin c	0	17.322	7	6	7	6	858	95.7	5.03	11.98	6	metabolic; cytosol:vai	catalytic a	P00443	78078	ENSG000001	USP5	12			Synthesis c	6	0.878	0.018128712	3.7	2879.3	3282.6	5.02	5.28	High	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q05639	Elongation	0	216.024	54	24	134	12	463	50.4	9.03	325.4	24	metabolic; cytoplasm; catalytic a	P00009	1917	ENSG000001	EEF1A2	20	Legionello	Translatio	Eukaryotic	6	0.878	0.064742723	4.31	11879.3	13533.5	2.58	4.64	High	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q52888	thimet olig	0	31.174	14	8	11	8	689	78.8	6.05	21.74	8	metabolic; cytoplasm; catalytic a	P01432	7064	ENSG000001	THOP1	19	Renin-angi	Antigen pr	6	0.878	0.140605809	12.04	1618.1	1884.7	2.1	8.04	High	High	High	High	High	High	High	High	High	High	1			
FALSE	High	Master Prq	Q96H51-1	Serine/thr	0	7.515	7	2	4	2	289	32	8.68	3.9	2	cell comm	membrane	catalytic a	P00300	192111	ENSG000001	PGAM5	12	TNF signa		1	0.878	0.147424334	7.54	2253.5	2565.3	4.68	3.56	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q15833-1	Syntaxin-b	0	13.127	6	3	3	3	593	66.4	5.55	9.35	3	regulation	cytosol:ext	protein bi	P00995	6813	ENSG000001	STXBP2	19	Insulin Sig	Platelet de	9	0.878	0.157593743	1.97	900.8	1006	7.86	1.87	High	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q18Y51	Peptidase	0.006	2.446	2	1	1	1	436	47.7	5.85	2.46	1	metabolic; cytosol	catalytic a	P01546	135293	ENSG000001	PM2002	6				0	0.878	0.160455091	12.21	327.1	373.6	3.92	6.68	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q9NY26	Zinc transp	0	4.991	4	1	1	1	324	34.2	5.92	2.04	1	transport	endoplasm	protein bi	P02335	27173	ENSG000001	SLC3A1	9	NRF2 path	Zinc infl	9	0.878	0.289537667	5.56	368.8	435.6	24.15	16.78	High	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q50579	methionin	0	36.007	19	7	13	7	478	52.9	5.82	39.59	7	metabolic; cytoplasm; catalytic a	P00557	10988	ENSG000001	METAP2	12			Signaling b	5	0.878	0.379427303	25.4	1680.9	1914.8	12.21	5.92	High	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q96572	protein IW	0	21.332	7	5	5	5	819	91.9	4.69	10.49	5	metabolic; nucleus	DNA bindi	P05297	55677	ENSG000001	IWS1	2			Formation	5	0.877	0.009135963	0.51	690	796.4	8.07	8.87	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q9JIA5-1	tRNA (ade)	0	12.132	9	3	3	3	497	55.8	7.55	8.93	3	metabolic; nucleus	RNA bindi	P04189	51605	ENSG000001	LMF2	20			tRNA mod	3	0.877	0.19894515	16.94	102.3	110.6	13.67	3.11	High	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q92621	Nuclear pc	0	56.476	8	15	18	15	2012	227.8	6.19	29.63	15	cell organ	membrane	protein bi	P11894	23165	ENSG000001	NUP205	7	RNA trans	Rev-media	64	0.877	0.524461588	10.17	1442	1645.1	27.71	12.55	High	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q9BWX9	Selenoact	0	10.505	19	2	2	2	145	16.2	5.54	6.78	2	metabolic; cytoplasm; protein bi	P08806	140606	ENSG000001	SELM; SELI	22			Selenium I	2	0.877	0.560820081	52.9	299.7	358	28.32	27.77	High	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q96005-1	Cleft lip a	0	5.659	3	2	2	2	669	76	6.3	1.97	2	cell differe	membrane	protein bi	P05602	1209	ENSG000001	CLPTM1	19				0	0.877	0.692476931	34.32	724.6	902.1	34.22	9.5	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q99460	26S prote	0	54.793	21	13	17	13	953	105.8	6.39	35.59	13	metabolic; cytosol:ext	catalytic a	P01851	5707	ENSG000001	PM2005	12	Epstein-Ba	Proteasom	Regulation	153	0.876	0.071959369	7.97	2472.4	2821.4	2.99	8.71	High	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q62854	40S riboso	0	27.452	37	4	10	4	115	13	11	16.03	4	cell organ	cytosol:me	protein bi	P01283	6231; 101	ENSG000001	RP52; LO1; LO2; 20; 4		Ribosome	Cytoplasm	Peptide ch	38	0.876	0.339428233	11.54	2784.2	3180.6	7.18	42.45	High	High	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q9UGP4	LM domai	0	6.465	4	1	1	1	676	72.1	6.65	3.63	1	cell organ	cytosol; metal ion	P00412	8994	ENSG000001	LSMD1	3	Hippo sign		7	0.876	0.386340071	20.14	159.6	182.3	11.56	5.38	High	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q97546	Calcium-bi	0	19.879	6	3	6	1	678	74.7	8.38	16.26	3	metabolic; membrane	metal ion	P00153	8604	ENSG000001	SLC2A12	2			Gluccone	6	0.876	0.42699645	29.77	233.3	266.5	15.54	5.54	High	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q9BUH6	Protein PA	0	22.93	30	4	4	4	204	21.6	5.48	17.77	4	metabolic; nucleus	protein bi	P115384	286257	ENSG000001	COrf142	9				0	0.876	0.622066379	25.11	445.5	508.6	57.06	8.92	High	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q9NIU7	ATP-dep	0	38.682	23	8	8	8	478	53.9	6.58	23.44	8	metabolic; cytoplasm; catalytic a	P00270	55308	ENSG000001	DDX19A	16				0	0.876	0.814087767	15.36	1091.5	1218.5	20.08	4.51	High	High	High	High	High	High	High	High	High	High	1		
FALSE	High	Master Prq	Q9ULW3	activator c	0.003	3.273	10	1	1	1	272	31.1	9.88	2.58	1	cell differe	nucleus	DNA bindi	P14259	29777	ENSG000001	ABT1	6				0	0.876	0.838113354	18.76	296.4	282.7	29.49	11.22	High	High	High	High	High	High	High	High	High	High	1
FALSE	High	Master Prq	Q49381	T-complex	0	197.659	58	33	91	33	545	60.5	6.49	219.99	33	cell organ	cytoplasm; nucleotide	P00118	7203	ENSG000001	CTC3	1			BBSome-r	13	0.875	0.109696819	1.95	30105.3	33824.7	5.08	1.89	High	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q32969	60S riboso	0	40.484	52	9	23	9	192	21.9	9.95	39.96	9	cell organ	cytoplasm; protein bi	P00347	6133	ENSG000001	ALM49	4	Ribosome	Cytoplasm	Peptide ch	34	0.875	0.186021672	15.96	5804.9	6632.7	8.88	2.66	High	High	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Prq	Q49748-1	Very long-	0	162.981	45	24	58	24	655	70.3	8.75	120.55	24	cell differe	cytosol:me	catalytic a	P00441	4737	ENSG000001	ACADVL	17	Metabolic	Fatty Acid	Beta oxid	15	0.875	0.250784313	18.77															

[illegible]



FALSE	High	Master Prc Q53H12	Acylglyceri	0	13.613	13	4	5	4	422	47.1	8.09	7.43	4	cell organ	cytosol:met	catalytic a	P000781	55750	ENSG00000	AGK	7	Glycerolip		Signaling b	10	0.836	0.122546648	5.61	425.8	555.2	8.04	13.33	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc Q98067	Glutamate	0	17.992	9	3	6	3	446	49.4	4.92	14.19	3	cell organ	chromoso	DNA bindi	P00400	83743	ENSG00000	GRWD1	19				0	0.836	0.254638118	10.78	1491.3	1766.7	11.25	3.65	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc Q9BX40	protein L5F	0	20.838	15	2	2	2	385	42	9.69	14.03	2	developm		RNA bindi	P09532	149986	ENSG00000	SLM148	20			0	0.836	0.297609116	11.73	373.8	387.2	13.71	14.74	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9W176	alcohol de	0	24.347	14	6	8	6	374	39.7	7.49	18.65	6	metabolic	cytoplasm	catalytic a	P00007	128	ENSG00000	ADHS	4	Metabolis	Folate-Ac	Ethanol ox	15	0.835	0.009090969	4.32	206.3	244.4	1.41	2.41	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc Q96555-1	ATPase WI	0	26.454	9	4	6	4	665	72.1	6.1	15.17	4	metabolic	membrane	catalytic a	P00004	56897	ENSG00000	WNRP1	6			0	0.835	0.230065108	23.68	848.8	1018	20.4	12.61	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9H443	Serine/thr	0	6.569	1	2	2	2	2382	250.6	6.34	4.21	2	metabolic	cytoplasm	catalytic a	P00069	65125	ENSG00000	WNK1	12		Stimuli-ser	3	0.835	0.33101191	32.34	310.1	361	72.6	6.45	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q42064	Isomorf 4	0	32.702	7	7	8	7	1477	163	8.53	5.66	7	cell divisi	chromoso	protein bi	P03985	73332	ENSG00000	CLASP1	2		Regulation	1	0.835	0.739204847	5.78	2271.1	2568.6	44.11	3.6	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q60271	C-jun-ami	0	10.046	4	3	3	3	1321	146.1	5.15	2.68	3	cell differe	cytoplasm	protein bi	P09744	9043	ENSG00000	IPAG9	17		COO in my	3	0.834	0.016098348	5.57	318.6	388.3	6.41	2.26	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9Y6D9	mitotic spi	0	19.805	9	5	5	5	718	83	5.92	10.05	5	cell divisio	chromoso	protein bi	P05557	8379	ENSG00000	MAD1L1	7	Progester	Cell Cycle	Amplificat	20	0.834	0.0164638	4.33	909.4	1090.3	3.2	6.45	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc P61619	Protein tra	0	18.483	13	6	9	6	476	52.2	8.06	17.54	6	cell growth	cytosol:eni	protein bi	P00344	29927	ENSG00000	SEC61A1	3	Vibrio chol	ER-Phagoc	Ion transp	15	0.834	0.149834894	7	269.5	361.2	12.78	12.3	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc Q9NTM9	Copper ho	0.003	3.118	4	1	1	1	273	29.3	8.18	2.22	1	cell organ	cytoplasm	metal ion	P03932	51076	ENSG00000	CUTC	10		Ion transp	3	0.834	0.413707786	16.42	882.6	1019	22.6	5.74	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc P15328	Folate rec	0	58.803	37	9	33	9	257	29.8	7.97	92.8	9	cell comm	cell surfac	receptor a	P03024	2348	ENSG00000	FORL1	11	Antifolate	Folate Met	COPI-medi	13	0.833	0.245527256	5	11285.4	12810.6	4.36	10.61	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc P40121	Macrophia	0	66.737	34	9	19	9	348	38.5	6.19	49.57	9	cell organ	cytoplasm	protein bi	P00626	822	ENSG00000	CAPG	2		TYROBP Ca	1	0.833	0.343992498	17.79	2753.6	3484.1	19.34	3.69	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q885Q4	Adhesion c	0.002	4.019	2	1	1	1	1221	136.6	7.87	1.66	1	cell differe	membrane	protein bi	P00002	57211	ENSG00000	GPR126	A 6			0	0.833	0.352248152	34	15.9	19.5	5.14	31.47	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc P43490	nicotinin	0	13.881	10	3	3	3	491	55.5	7.15	12.55	3	cell comm	cytoplasm	catalytic a	P04095	10135	ENSG00000	NAMPT	7	Nicotinate	Adipogene	BMAL1:Cl	14	0.833	0.458840002	50.38	245.9	328.9	20.2	29.01	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc P55211-1	caspace-9	0	11.037	9	2	3	2	416	46.3	6.05	5.51	2	cell death	cytoplasm	catalytic a	P00619	F 842	ENSG00000	CASP9	1	Parkinso	Nucleotide	AKT phosph	68	0.833	0.497119888	9.01	450.2	517.3	19.46	2.9	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc Q14653-1	Golgi SNAF	0	13.18	22	3	3	3	212	24.8	8.06	5.61	3	cell organ	cytosol:eni	protein bi	P12352	9570	ENSG00000	GOSR2	17		SNARE int	16	0.832	0.361621896	8.36	40.1	47.8	6.76	17.37	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc P37198	nuclear po	0	9.907	6	3	3	3	522	53.2	5.31	8.31	3	cell death	cytoplasm	protein bi	P05064	23636	ENSG00000	NUP62	19	RNA trans	Rev-medi	64	0.832	0.386265113	38.94	374.3	431.3	25.98	14.84	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q96JP2	Unconvect	0.002	4	1	1	1	1	1530	167	4.81	3.25	1	cytoplasm	catalytic a	P00063	F 80022		LOC10313	17			0	0.832	0.389088083	40.08	274.9	348.9	13.26	20.77	High	High	High	High	High	High	High	1			
FALSE	High	Master Prc P31946	14-3-3 pro	0	111.212	58	15	60	6	246	28.1	4.83	120.32	15	cell organ	cytoplasm	protein bi	P00244	7529	ENSG00000	YWHAB	20	Hippo sign	Cell Cycle	MAP2K an	68	0.831	0.138441114	1.69	3747.2	4333.7	3.71	9.16	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc Q9U03-1	Vacuolar p	0	9.218	3	1	1	1	782	86	6.47	5.02	1	cell organ	cytosol:eni	protein bi	P04124	F 738	ENSG00000	VP551	11		Retrogredi	4	0.831	0.50423883	53.24	254.6	321.5	21.76	26.45	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9ADA7-1	Ubiquitin-i	0	19.544	8	8	9	8	1052	117.9	6.14	10.02	8	metabolic	cytoplasm	catalytic a	P00899	F 55236	ENSG00000	UBAA6	4	Ubiquitin r	Synthesi c	9	0.831	0.75491019	3.33	1546.8	1888.5	44.49	2.97	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc P62910	60S riboso	0	64.331	52	11	38	11	135	15.9	11.33	9.7	11	cell organ	cytosol:me	RNA bindi	P01655	6161	ENSG00000	RLP32	3	Ribosome	Cytoplasm	Peptide ch	34	0.833	0.033162028	3.95	12664	14236.1	8.17	5.6	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc Q92P75	Ubiquitin c	0	16.716	4	3	5	5	1121	122.6	9.67	10.77	3	metabolic	nucleus	catalytic a	P00443	F 57602		USP96	17			0	0.83	0.060573681	6.15	357.4	446.4	13.88	8.99	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q06869-1	Endothelia	0	11.88	27	4	7	4	148	16.4	9.95	12.58	4	cell differe	cytoplasm	catalytic a	P01381	F 8721	ENSG00000	CDP5	9			0	0.83	0.673300504	6.89	1805.4	2164	13.59	10.79	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9GZ21-1	N-alpha-ac	0	45.413	53	10	13	10	169	19.4	8.81	28.92	10	cell organ	cytoplasm	catalytic a	P00583	F 80218	ENSG00000	NAASO	3	Metapathw		1	0.83	0.890373695	20.28	1280.5	1444	34.51	5.93	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q07866-1	Kinesin liq	0	8.946	5	3	4	1	573	65.3	6.2	8.99	3	cell organ	cytoplasm	catalytic a	P08317	F 3831	ENSG00000	KLC1	14	Salmonella	COPI-depe	16	0.829	0.070264592	12.61	174.8	227	9.68	5.15	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q96066	RNA pseu	0	8.64	7	3	3	3	427	47.4	8.41	3.56	3	cell organ	mitochond	catalytic a	P01416	80324	ENSG00000	PUS1	12		tRNA mod	3	0.829	0.132067583	7.4	1104.5	1398.8	14.21	4.47	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q76094	Signal rec	0	43.497	16	8	11	8	671	74.6	9.26	31.84	8	cell organ	cytoplasm	protein bi	P08492	F 6731	ENSG00000	SRP72	4	Protein exp	SRP-depen	4	0.829	0.176866871	0.41	2888.3	3510	1.82	22.99	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc P03001	Ras-relate	0	11.979	13	2	2	2	218	23.5	6.95	6.84	2	cell differe	membrane	catalytic a	P00071	F 6237	ENSG00000	RRAS	19	Proteotexy	G Protein S	SEMAP4 m	28	0.829	0.438644774	30.17	438.7	513.3	15.78	11.47	High	High	High	High	High	High	High	1	
FALSE	Low	Master Prc P35125-1	Ubiquitin c	0.05	1.197	1	1	1	1	1406	158.6	7.71	2.03	1	metabolic	cytoplasm	catalytic a	P00443	F 9098	ENSG00000	USP6	17			0	0.828	0.386302574	40.66	713.8	880.7	19.08	20.46	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc P49720	proteasom	0	22.576	24	4	9	4	205	22.9	6.55	19.01	4	metabolic	cytoplasm	catalytic a	P00227	5691	ENSG00000	PSMB3	17	CHR_H	Proteasom	Proteasom	Regulation	150	0.827	0.134486788	13.08	2895.8	3502.5	18.8	1.21	High	High	High	High	High	High	High	1
FALSE	High	Master Prc Q9NU15	Repressor	0	5.23	6	1	1	1	291	33.1	7.25	30.8	1	defence re	cytoplasm	protein bi	P15135	55337	ENSG00000	CIR6196	6			0	0.827	0.387919164	39.18	238.9	270.1	21.74	12.08	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9Y5X1	Sorting nei	0	17.825	10	3	3	3	595	66.6	5.58	10.35	3	cell divisio	cytoplasm	protein bi	P15149	F 51429	ENSG00000	SNX9	6		Golgi Asso	6	0.827	0.414660083	47.97	149	204.1	34.07	28.67	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc Q9NR94	Succinate c	0	6.349	25	2	2	2	125	14.6	9.07	7.4	2	cell organ	mitochond		P05347	F 57001	ENSG00000	ACN9	SDH	7			0	0.827	0.595500351	19.39	94	103.5	6.77	29.84	High	High	High	High	High	High	High	1	
FALSE	High	Master Prc Q9T591	Small subu	0	24.461	3	6	8	6	2785	318.2	7.39	16.1	6	metabolic	cytoplasm	protein bi	P07539	27340	ENSG00000	UTP20	12		Major patf	5	0.826	0.053933416	7.73	1515.7	1840.6	11.48	9.48	High	High	High	High	High	High	High	1		
FALSE	High	Master Prc P62249	40S riboso	0	51.504	72	13	31	13	146	16.4	10.21	52.05	13	cell organ	cytosol:me	protein bi	P00380	6217	ENSG00000	RP516	16	Ribosome	Cytoplasm	Peptide ch	38	0.826	0.06101151	11.26	11018.8	13344.9	6.23	2.36	High								

FALSE	Medium	Master Prq Q13632-1	Program	0.011	2.019	3	1	1	1	344	38.6	5.38	1.66	1	cell death; cytoplasm; DNA bindi	P101753, F 5134	ENSG000001 PCD2	6						0	0.806	0.040371787	12.94	860	1067.7	18.28	8.63	High	High	High	High	High	High	1
FALSE	High	Master Prq Q12965	uncoment	0	75.927	16	13	20	13	1108	127	8.92	56.38	13	cell differ; cytoplasm; catalytic a	P00018, F 4643	ENSG000001 MYO1E	15		Primary Fo				1	0.806	0.155375488	1.88	4513.9	5601	6.63	5.34	High	High	High	High	High	High	1
FALSE	High	Master Prq Q09H5	Ankyrin re	0	22.348	8	4	5	4	726	80.9	8.41	17.48	4	metabolic; cytoplasm; catalytic a	P000233, F 55139	ENSG000001 ANKRF1	2						0	0.806	0.165906294	16.44	340.1	422	8.56	7.12	High	High	High	High	High	High	1
FALSE	High	Master Prq Q09532	Ubiquitin	0	19.912	8	4	4	4	703	77.9	8.24	11.02	4	cell comm; cytoplasm; catalytic a	P00089, 10533	ENSG000001 ATG7	3		Autophagy	Nanopartic	Signaling b		15	0.806	0.997022955	0.29	95.2	118.3	36.14	3.55	High	High	High	High	High	High	1
FALSE	High	Master Prq Q5998	Actin-relat	0	8.705	17	3	5	3	168	19.7	6.43	6.62	3	cell organ; cytoplasm; protein bi	P00586, 10093	ENSG000001 APC4	3		Shigellosi	Pathogen	EBH-m	23	0.805	0.016594978	3.25	1276	1611.2	3.96	2.45	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q21266	glutathion	0	70.253	50	12	24	12	225	26.5	5.54	65.88	12	metabolic; cytoplasm; catalytic a	P00043, F 2947	ENSG000001 GSTM3	1		Drug meta	NRF2 pat	Glutathion	12	0.805	0.0509477	0.12	5974	7238.7	6.93	1.51	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q43719	HIV Tat-sp	0	17.644	9	7	7	7	755	85.8	4.4	11.7	7	cell organ; nucleus;sp	P000828, F 27336	ENSG000001 HTATSF1	X					0	0.805	0.774198691	2.87	2010.4	2344.8	46.77	5.89	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q23230	cytidine di	0	27.286	45	5	9	5	146	16.2	6.92	31.7	5	cell organ; cytosol;enl	P00083, F 978	ENSG000001 CDA	1		Pyrimidine	Fluoropyri	Pyrimidine	11	0.804	0.167700521	22.93	2517.1	3248.5	11.12	11.88	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q08323-3	GTP-bindir	0.002	3.898	5	1	1	1	284	32.1	9.42	2.31	1	membrane; catalytic a	P00009, F 29083	ENSG000001 GTPBP8	3					0	0.804	0.24166406	20.15	144.1	179.4	15.67	21.01	High	High	High	High	High	High	1	
FALSE	Medium	Master Prq Q14925	Mitochond	0.026	1.481	4	1	2	1	209	21.9	8.6	3.94	1	transport	membrane; protein bi	P02466, 10027933	ENSG000001 TMEM23	10			Mitochond		2	0.804	0.258452996	16.17	1030.1	1282	45.91	12.89	High	High	High	High	High	High	1
FALSE	High	Master Prq Q09B78	transmem	0	9.066	9	2	4	2	246	26.2	5.72	4.02	2	metabolic; cytoplasm; protein bi	P02400, F 83590	ENSG000001 TMUB1	19					0	0.804	0.394893594	2.07	1630.1	1727	10.87	20.12	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q07020	60S riboso	0	37.675	42	7	14	7	188	21.6	11.72	27.9	7	cell organ; cytoplasm; RNA bindi	P000828, 6141	ENSG000001 RPL18	7			Ribosome	Cytoplasm; Peptide ch	34	0.802	0.072669139	10.59	4852.2	6036.2	4.31	6.62	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q53609	Geranylge	0.004	2.723	3	1	1	1	377	42.3	6.83	2.1	1	metabolic; cytoplasm; catalytic a	P00432, F 5229	ENSG000001 PGGT18	5					0	0.801	0.189704049	7.29	485.1	563.5	6.92	11.1	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q095747	Serine/thr	0	14.15	8	4	7	4	527	58	6.43	13.34	4	metabolic; cytoplasm; catalytic a	P00069, F 9943	ENSG000001 OXSR1	3					0	0.801	0.439313214	25.54	1793.6	2237.8	17.97	10.04	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q14744	Protein arg	0	23.115	14	7	10	7	637	72.6	6.29	12.71	7	cell organ; cytoplasm; catalytic a	P02475, F 10419	ENSG000001 PRMT5	14		RNA trans	snRNP Ass		13	0.799	0.104404727	9.42	2578.3	3154.6	22.08	4.81	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q095P6	Mannose-	0	14.349	15	3	4	3	360	39.8	6.61	12.88	3	metabolic; cytoplasm; catalytic a	P00132, F 29925	ENSG000001 GMPBP	8		Metabolic	Synthesis c		9	0.799	0.191673403	27.47	624.6	748.8	15.59	10.79	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q09WT1	p21-activa	0	18.722	10	4	5	4	392	43.9	8.91	17.61	4	cell profile; nucleus	protein bi	P00400, 55003	ENSG000001 PAK1P1	6					0	0.798	0.10153923	3.65	2461.2	3090.3	1.16	4.34	High	High	High	High	High	High	1
FALSE	High	Master Prq Q0547	2-(3-amin	0	4.727	7	2	2	2	489	52.1	5.53	1.83	2	metabolic; cytosol	catalytic a	P01866, 1802	ENSG000001 DHP2	1			Synthesis c		4	0.796	0.042554528	9.53	41.6	49.1	12.56	14.47	High	High	High	High	High	High	1
FALSE	High	Master Prq Q0UKD2	mRNA tur	0	33.24	32	8	9	8	239	27.5	8.29	15.13	8	cell organ; cytoplasm; protein bi	P00466, 51154	ENSG000001 MIRT04	0					0	0.796	0.048944268	12.7	1303.3	1695.4	6.45	8.35	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q0547	sphingolin	0	17.918	8	3	4	3	568	63.5	9.16	11.07	3	cell death; endoplasm	catalytic a	P00155, F 8879	ENSG000001 SGP1	10		Metabolic	Kennedy p	Sphingolip	8	0.796	0.620489259	8.18	446.8	564.2	75.1	17.79	High	High	High	High	High	High	1
FALSE	High	Master Prq Q02688	Acidic leuc	0	46.746	29	7	19	6	251	28.8	4.06	36.39	7	cell organ; cytoplasm; protein bi	P12179, F 10541	ENSG000001 ANP32B	9					0	0.795	0.150155283	2.19	4240.9	4765.5	9.49	8.04	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q093C6	Peptidyl-p	0	7.758	17	2	2	2	166	18.2	7.99	6.63	2	metabolic; spliceosom	catalytic a	P00160, 51645	ENSG000001 PPL1	6		Spliceosom	mRNA Spli		5	0.794	0.105854	14.43	304.4	474.3	17.51	20.19	High	High	High	High	High	High	1
FALSE	High	Master Prq Q15800	Methylste	0	5.535	5	1	1	1	293	35.2	7.23	4.21	1	metabolic; endoplasm	catalytic a	P04116, 6307	ENSG000001 MSMD1	4		Metabolic	Cholesterol	Cholesterol	7	0.794	0.167143133	8.48	60.7	72	13.22	3.88	High	High	High	High	High	High	1
FALSE	High	Master Prq Q13098	COP9 sign	0	12.091	7	3	4	3	491	55.5	6.74	8.42	3	cell organ; cytoplasm; enzyme re	P01399, F 2873	ENSG000001 GPS1	17			Cargo reco		13	0.793	0.013363064	2.51	552.5	696.7	5.97	8.7	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q68036	Ubiquitin	0	34.572	46	5	8	5	154	17.9	8.51	25.38	5	cell profile; cytoplasm; catalytic a	P00179, 7332	ENSG000001 UBE2L3	22		Ubiquitin r	Parkin-Ubi	Synthesis c	13	0.793	0.017584515	0.04	2503.9	3079.5	3.34	5.81	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q18077	60S riboso	0	51.537	53	8	33	8	110	12.5	11.06	7.38	8	cell organ; cytosol;me	protein bi	P01247, 6165	ENSG000001 RPL35A	3		Ribosome	Cytoplasm; Peptide ch	34	0.793	0.023037188	4.49	12175.5	15029.5	1.63	5.63	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q0UH09	Ubiquitin-2	0	24.363	7	3	7	2	624	65.7	5.22	16.17	3	metabolic; cytoplasm; protein bi	P00240, F 29978	ENSG000001 UBLN2	X		Protein prc	Cargo reco		5	0.793	0.114073387	16.17	861.1	970.7	15.45	18.92	High	High	High	High	High	High	1	
FALSE	High	Master Prq P00491	purine nuc	0	43.26	29	6	12	6	289	32.1	6.95	37.7	6	metabolic; cytoplasm; catalytic a	P01048, 4860	ENSG000001 PNP	14		Metabolic	Neurotro		13	0.792	0.113175413	19.3	2064.9	2605.6	12.01	5.87	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q0XQ6-1	nicotinate	0	24.155	13	5	5	5	538	57.5	5.68	11.55	5	metabolic; cytoplasm; catalytic a	P04095, 93100	ENSG000001 NAPRT1; N	8; CHR_ HS	Metabolic	NAD- bio	Neutrophil		11	0.791	0.039399158	5.98	2325.7	2756.8	3.98	7.71	High	High	High	High	High	High	1	
FALSE	Medium	Master Prq Q0H5X1-1	MP18 farr	0.024	1.527	7	1	1	1	160	18.3	4.88	0	1	cytoplasm; metal ion		84191	ENSG000001 FAM96A	6				0	0.791	0.116201213	9.25	397.8	538.2	9.87	12.35	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q09B6-1	U3 small n	0	10.832	5	3	3	3	771	87.9	7.87	8.12	3	metabolic; cytosol;nu	protein bi	P04615, 10813	ENSG000001 UTP14A	X		Ribosome	Major patf		6	0.79	0.024840803	11.23	358.7	498.2	13.17	10.34	High	High	High	High	High	High	1
FALSE	High	Master Prq Q09UC1-4	Malignant	0	30.651	27	3	5	3	181	20.5	8.82	20.97	3	cell organ; cytoplasm; protein bi	P01472, 28985	ENSG000001 QMUL1	X					0	0.79	0.125430411	14.88	1185.9	1218	17.5	16.25	High	High	High	High	High	High	1	
FALSE	High	Master Prq P0306-1	Guanine m	0	36.165	15	4	9	1	354	40.3	5.97	23.81	4	cell division; cytoplasm; catalytic a	P00025, F 2770	ENSG000001 GNA1	7		Morphine	Nicotine A	G alpha i	74	0.789	0.159387005	2.2	508.5	544.1	11.33	11.03	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q09UB5	Eukaryotic	0	39.626	40	7	9	7	218	25	4.93	21.03	7	metabolic; cytoplasm; protein bi	P01399, F 27335	ENSG000001 EF3K	19; CHR_ H	Formation				11	0.788	0.016983641	7.26	1419.4	1811.7	2.98	3.94	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q09Y81-3	Spermatog	0.002	3.595	3	1	1	1	493	57	7.4	2.31	1	cell differ; cytoplasm; protein bi	P09787, 63894	ENSG000001 VPAS39	4					0	0.787	0.153429958	21.95	44.4	57.5	1.78	15.36	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q16637	Survival m	0	9.751	11	2	2	2	294	31.8	6.55	2.96	2	cell organ; cytoplasm; protein bi	P00603, 6606; 660	ENSG000001 SMN1; SM	5; CHR_ HS	RNA trans	snRNP Ass		4	0.786	0.059249447	1.51	377.9	438.6	8.32	11.87	High	High	High	High	High	High	1		
FALSE	High	Master Prq Q06R06	Sperm-ass	0	2.504	1	1	1	1	1193	134.3	5	2.06	1	cell division; chromos	protein bi	10615	ENSG000001 SPG10	0				0	0.785	0.176685818	24.55	95.3	127.4	14.11	12.59	High	High	High	High	High	High	1	
FALSE	High	Master Prq P13645	Keratin, ty	0	70.192	22	10	21	9	584	58.8	5.21	64.63	10	cell death; cytoplasm; structural	P00038, F 3858	ENSG000001 KRT10	17		Staphylococ			0	0.785	0.549479997	2.74	5049.7	5726.1	15.06	6.66	High	High	High	High	High	High	1	
FALSE	High	Master Prq Q08162	Cap-specif	0	7.927	2	1	1	1	835	95.3	7.05	3.03	1	metabolic; cytosol;nu	catalytic a	P01585, F 23070																					

FALSE	High	Master Pcr P46781	40S riboso	0	56.222	53	15	36	15	394	22.6	10.65	59.62	15	cell organ	cytoplasm; protein	rib P00163, F 6203	ENSG000001	RP59	19; CHR, H	Ribosome	Cytoplasm	Peptide ch	39	0.724		0.000989031	2.43	13985.7	19309.8	6.57	3.25	High	High	High	High	High	High	High	High	1
FALSE	High	Master Pcr Q13547	histone de	0	20.195	13	4	5	3	482	55.1	5.48	8.62	4	cell differ	chromos	catalytic a	P008050	3065					95	0.724		0.072800163	90.46	18.6	25.8	41.89	31.87	High	High	High	High	High	High	High	High	1
FALSE	High	Master Pcr Q81574-1	YH1-asso	0	5.544	14	1	1	1	180	19.9	9.72	3.16	1	metabolic	cytoplasm; metal ion	P100641	10138					6	0.719		0.025290875	2.2	185.4	257.7	9.88	14.33	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Pcr P30041	Peroxired	0	132.57	64	16	59	16	224	25	6.38	129.79	16	cellular ho	cytoplasm; antioxidant	P005078, F 9588	ENSG000001	P006X	1		Metabolic	NR2F path	8	0.719		0.044470299	8.99	10976.2	15918.2	47.3	11.12	High	High	High	High	High	High	High	High	1
FALSE	High	Master Pcr P75834	5S proteo	0	22.42	25	4	4	4	226	24.4	6.1	1.94	4	cell death	cytoplasm; protein	P00023, F 5716	ENSG000001	PSM010	X		Proteasom	Neutrophil	150	0.718		0.009017521	1.46	2467.3	3435.6	18.4	9.13	High	High	High	High	High	High	High	High	1
FALSE	High	Master Pcr Q14950	Myosin reg	0	21.905	40	5	7	5	172	19.8	4.84	1.66	5	regulation	cytosol	metal ion	P100396, F 103910;	ENSG000001	MYL12B, N 18		Regulation	Human TH	22	0.718		0.036024574	7.50	243.5	3252.5	7.09	13.31	High	High	High	High	High	High	High	High	1
FALSE	High	Master Pcr P15941	myosin I (C	0	5.785	2	2	2	2	1255	12.2	7.47	2.12	2	metabolic	cytoplasm; DNA bindi	P00030, F 4582	ENSG000001	MUC1	1			18	0.718		0.069193485	12.03	257.9	408.3	9.27	19.73	High	High	High	High	High	High	High	High	1	
FALSE	High	Master Pcr Q5210	Protein Fak	0	19.194	8	2	6	1	330	37.2	6.29	17.24	2	regulation	cytoplasm; catalytic a	P102329	283742	ENSG000001	FAM988	15			3	0.716		0.010828214	1.23	934.5	1295	12.29	13.86	High	High	High	High	High	High	High	High	1
FALSE	High	Master Pcr Q36613	LanC-like p	0	6.043	7	2	3	3	399	45.3	7.75	6.05	3	metabolic	cytoplasm; metal ion	P105147	10314	ENSG000001	LANCL2	1			0	0.713		0.005597657	4.46	720	979.8	16.04	7.87	High	High	High	High	High	High	High	High	1
FALSE	High	Master Pcr Q436613	Protein reg	0	4.673	2	1	2	1	620	71.6	6.68	697	1	cell divisio	cytoplasm; protein	P03999	9055	ENSG000001	PRC1	15			4	0.711		0.177688788	37.02	115.2	178.2	16.62	20.84	High	High	High	High	High	High	High	High	1
FALSE	High	Master Pcr P53007	Tricarboxy	0	12.157	11	3	3	3	311	34	9.89	6.83	3	metabolic	membrane; transporte	P001513	6576	ENSG000001	SLC25A1	22			7	0.707		0.068609315	1.14	596.5	805	4.03	9.57	High	High	High	High	High	High	High	High	1
FALSE	High	Master Pcr P11908	ribose-pho	0	46.448	25	7	14	1	318	34.7	6.61	36.57	7	metabolic	cytoplasm; catalytic a	P00156, F 5634	ENSG000001	PRPF2	X		Metabolic	Nucleotide	10	0.703		0.004590656	4.8	2581.7	3596.9	13.11	5.71	High	High	High	High	High	High	High	High	1
FALSE	High	Master Pcr Q39132-P1	Negative e	0	10																																				

Table S2. Gene Ontology (GO) information, including the biological process, cellular component and molecular function, of differentially expressed proteins (DEPs) with  $|\text{FC}| \geq 1.2$  identified in A549 cells exposed to ZQX-1 (0.5  $\mu\text{M}$ ) under irradiation at 420 nm for 20 min following 4.0 h of incubation at 37 °C in the dark. \* NA: not available.

No.	Accession	Gene symbol	Protein name	FC (LZ vs.DZ)	Biological Process	Cellular Component	Molecular Function
1	Q86X55	CARM1	Histone-arginine methyltransferase CARM1	-1.49	cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	cytoplasm; cytosol; nucleus	catalytic activity; DNA binding; protein binding
2	O75815-1	BCAR3	Breast cancer anti-estrogen resistance protein 3	-1.49	regulation of biological process; response to stimulus	N.A.*	protein binding
3	P51153	RAB13	Ras-related protein Rab-13	-1.47	cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus;	cytosol; Golgi; endosome; membrane	catalytic activity; nucleotide binding; protein binding
4	P11908	PRPS2	ribose-phosphate pyrophosphokinase 2	-1.42	metabolic process	N.A.*	catalytic activity; metal ion binding; nucleotide binding; protein binding; metal ion binding; protein binding; receptor activity; signal transducer activity
5	O43813	LANCL1	Lan C-like protein 1	-1.40	regulation of biological process; response to stimulus	cytoplasm; membrane	catalytic activity; protein binding; RNA binding
6	Q52LJ0	FAM98B	Protein Fam 98b	-1.40	metabolic process; regulation of biological process	cytoplasm; nucleus	protein binding
7	O75832	PSMD10	26S proteasome non-ATPase regulatory subunit 10	-1.39	cell death; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus; transport	cytoplasm; cytoskeleton; cytosol; nucleus;	protein binding

8	O14950	MYL12B; MYL12A	Myosin regulatory light chain 12B	-1.39	regulation of biological process; response to stimulus	proteasome  cytosol	metal ion binding; protein binding
9	Q8IY57-1	YAF2	YY1-associated factor 2	-1.39	metabolic process; regulation of biological process	cytosol; nucleus	metal ion binding; protein binding
10	P30041	PRDX6	Peroxiredoxin-6	-1.39	cellular homeostasis; metabolic process; regulation of biological process; response to stimulus; transport	cytoplasm; cytosol; extracellular; membrane; nucleus; organelle lumen; vacuole	antioxidant activity; catalytic activity; protein binding
11	P46781	RPS9	40S ribosomal protein S9	-1.38	cell organization and biogenesis; metabolic process; regulation of biological process; transport	cytoplasm; cytosol; membrane; nucleus; ribosome	protein binding; RNA binding; structural molecule activity; translation regulator activity
12	P68104	EEF1A1	Elongation factor 1-alpha 1	-1.34	metabolic process; regulation of biological process; response to stimulus; transport	cytoplasm; cytosol; membrane; nucleus; organelle lumen	catalytic activity; nucleotide binding; protein binding; RNA binding
13	P62877	RBX1	E3 ubiquitin-protein ligase RBX1	-1.33	cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	cytoplasm; cytosol; nucleus	catalytic activity; metal ion binding; protein binding

14	Q12933	TRAF2	TNF receptor-associated factor 2	-1.32	cell death; cell organization and biogenesis; metabolic process; response to stimulus	cytoplasm; cytosol; membrane	catalytic activity; metal ion binding; protein binding; signal transducer activity
15	Q9UQ80	PA2G4	proliferation-associated protein 2G4	-1.32	cell proliferation; metabolic process; regulation of biological process; transport	cytoplasm; extracellular; membrane; nucleus; organelle lumen	DNA binding; protein binding; RNA binding
16	Q6PI48	DARS2	Aspartate-tRNA ligase, mitochondrial	-1.32	metabolic process	cytoplasm; mitochondrion; nucleus; organelle lumen	catalytic activity; nucleotide binding; protein binding; RNA binding
17	Q9H074	PAIP1	Polyadenylate-binding protein-interacting protein 1	-1.29	metabolic process; regulation of biological process	cytoplasm; cytosol	protein binding; RNA binding; translation regulator activity
18	Q06124	PTPN11	tyrosine-protein phosphatase non-receptor type 11	-1.29	cell differentiation; cell organization and biogenesis; cellular component movement; metabolic process; regulation of biological process; response to stimulus	cytoplasm; cytosol; mitochondrion; nucleus	catalytic activity; protein binding
19	Q9HCD5	NCOA5	Nuclear receptor coactivator 5	-1.28	metabolic process; regulation of biological process	cytoskeleton; nucleus	protein binding; RNA binding

20	Q9UBQ5	EIF3K	Eukaryotic translation initiation factor 3 subunit K	-1.27	metabolic process; regulation of biological process	cytoplasm; cytosol; membrane; nucleus	protein binding; RNA binding
21	Q6XQN6-1	NAPRT1; NAPRT	nicotinate phosphoribosyl transferase	-1.26	metabolic process; response to stimulus; transport	cytoplasm; cytosol; extracellular; organelle lumen	catalytic activity; protein binding
22	Q13098	GPS1	COP9 signalosome complex subunit 1	-1.26	cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	cytoplasm; cytosol; nucleus	enzyme regulator activity; protein binding
23	P68036	UBE2L3	Ubiquitin-conjugating enzyme E2 L3	-1.26	cell proliferation; metabolic process; regulation of biological process; response to stimulus	cytoplasm; cytosol; nucleus	catalytic activity; enzyme regulator activity; nucleotide binding; protein binding; RNA binding
24	P18077	RPL35A	60S ribosomal protein L35a	-1.26	cell organization and biogenesis; metabolic process; transport	cytosol; membrane; ribosome	protein binding; RNA binding; structural molecule activity
25	Q9BQC3	DPH2	2-(3-amino-3-carboxypropyl)histidine synthase subunit 2	-1.26	metabolic process	cytosol	catalytic activity; protein binding
26	Q9UKD2	MRTO4	mRNA turnover protein 4 homolog	-1.26	cell organization and biogenesis; metabolic process	cytoplasm; nucleus	protein binding; RNA binding

27	Q9NWT1	PAK1IP1	p21-activated protein kinase-interacting protein 1	-1.25	cell proliferation; regulation of biological process	nucleus	protein binding
28	P59998	ARPC4	Actin-related protein 2/3 complex subunit 4	-1.24	cell organization and biogenesis; regulation of biological process; response to stimulus	cytoplasm; cytoskeleton; cytosol	protein binding; structural molecule activity
29	Q16342-1	PDCD2	Programmed cell death protein 2	-1.24	cell death; metabolic process; regulation of biological process	cytoplasm; nucleus	DNA binding; metal ion binding; protein binding
30	Q8WX92	COBRA1; NELFB	Negative elongation factor B	-1.23	metabolic process; regulation of biological process	cytoplasm; nucleus	protein binding; RNA binding
31	Q86TI2	DPP9	Dipeptidyl peptidase 9	-1.23	metabolic process	cytoplasm; cytosol; nucleus	catalytic activity; protein binding
32	P63244	GNB2L1; RACK1	Receptor of activated protein C kinase 1	-1.23	cell death; cellular homeostasis; development; metabolic process; regulation of biological process; response to stimulus	cytoplasm; mitochondrion; nucleus; ribosome	enzyme regulator activity; protein binding; RNA binding;
33	Q92538	GBF1	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	-1.23	cell organization and biogenesis; cellular component movement; metabolic process; response to stimulus; transport	cytoplasm; cytosol; Golgi; mitochondrion; organelle lumen	protein binding
34	P40261	NNMT	Nicotinamide N-methyl transferase	-1.22	metabolic process; response to stimulus	cytoplasm; cytosol	catalytic activity



35	Q9Y508-1	RNF114	E3 ubiquitin-protein ligase RNF114	-1.22	cell differentiation; development; metabolic process; regulation of biological process	cytoplasm; cytosol; membrane; nucleus	catalytic activity; metal ion binding; protein binding
36	P23396-1	RPS3	40S ribosomal protein S3	-1.22	cell death; cell division; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus; transport	endoplasmic reticulum; mitochondrion; nucleus; ribosome	catalytic activity; DNA binding; protein binding; RNA binding;
37	Q7L1Q6-1	BZW1	Basic leucine zipper and W2 domain-containing protein 1	-1.22	metabolic process; regulation of biological process	cytoplasm; membrane	protein binding; RNA binding
38	O60256-1	PRPSAP2	Phosphoribosyl pyrophosphate synthase- associated protein 2	-1.22	metabolic process; regulation of biological process	N.A.*	catalytic activity; metal ion binding; protein binding
39	P26374	CHML	Rab proteins geranyl transferase component A 2	-1.21	metabolic process; regulation of biological process; response to stimulus; transport	cytoplasm; cytosol	catalytic activity; protein binding
40	P62910	RPL32	60S ribosomal protein L32	-1.20	cell organization and biogenesis; metabolic process; response to stimulus; transport	cytosol; membrane; ribosome	RNA binding; structural molecule activity
41	P00338-1	LDHA	L-lactate dehydrogenase A chain	-1.20	metabolic process; regulation of biological process	cytoplasm; nucleus	protein binding; RNA binding
No.	Accession	Gene symbol	Protein name	FC (LZ vs. DZ)	Biological Process	Cellular Component	Molecular Function

1	P56385	ATP5ME	ATP synthase subunit e, mitochondrial	1.20	cell organization and biogenesis; metabolic process; transport	membrane; mitochondrion	catalytic activity; transporter activity
2	P63165-1	SUMO1	Small ubiquitin-related modifier 1	1.20	cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	chromosome; cytoplasm; membrane; nucleus	catalytic activity; protein binding; RNA binding
3	Q5JTV8	TOR1AIP1	Torsin-1A-interacting protein 1	1.21	cell organization and biogenesis; regulation of biological process	membrane; nucleus	enzyme regulator activity; protein binding
4	Q9GZP4	PITHD1	PITH domain-containing protein 1	1.21	response to stimulus	nucleus	
5	Q92734-1	TFG	Protein TFG	1.22	cell organization and biogenesis; regulation of biological process; response to stimulus; transport	cytoplasm; endoplasmic reticulum;	protein binding; signal transducer activity
6	Q96EC8-1	YIPF6	Protein YIPF6	1.22	N.A.*	endoplasmic reticulum; Golgi;	protein binding
7	P14406	COX7A2	Cytochrome c oxidase subunit 7A2, mitochondrial	1.22	metabolic process; transport	membrane; mitochondrion	catalytic activity; transporter activity
8	O96008	TOMM40	Mitochondrial import receptor subunit TOM40 homolog	1.23	cell communication; metabolic process; response to stimulus; transport	cytosol; membrane; mitochondrion	protein binding; transporter activity
9	P19367-1	HK1	Hexokinase-1	1.23	cellular homeostasis; metabolic process; regulation of biological process	cytosol; membrane; mitochondrion	catalytic activity; nucleotide binding; protein binding

10	Q9Y3D9	MRPS23	28S ribosomal protein S23, mitochondrial	1.23	cell organization and biogenesis; metabolic process	cytoskeleton; mitochondrion; ribosome	protein binding; RNA binding;
11	O75175	CNOT3	CCR4-NOT transcription complex subunit 3	1.23	cell differentiation; development; metabolic process; regulation of biological process; response to stimulus	cytoplasm; cytosol; nucleus	protein binding
12	Q9UIJ7-1	AK3	GTP: AMP phosphotransferase AK3, mitochondrial	1.23	coagulation; metabolic process	mitochondrion; organelle lumen	catalytic activity; nucleotide binding; protein binding
13	Q6P1L8	MRPL14	39S ribosomal protein L14, mitochondrial	1.23	cell organization and biogenesis; metabolic process	membrane; mitochondrion; ribosome	RNA binding; structural molecule activity
14	P80303	NUCB2	Nucleobindin-2	1.24	N.A.*	endoplasmic reticulum; nucleus	DNA binding; metal ion binding; protein binding
15	Q9H089	LSG1	Large subunit GTPase 1 homolog	1.24	transport	cytoplasm; endoplasmic reticulum; nucleus	catalytic activity; nucleotide binding
16	Q9HDC9	APMAP	Adipocyte plasma membrane-associated protein	1.24	metabolic process	cell surface; endoplasmic reticulum;	catalytic activity
17	Q9BXT2	CACNG6	voltage-dependent calcium channel gamma- 6 subunit	1.25	regulation of biological process; transport	membrane	transporter activity

18	Q9BS26	ERP44	Endoplasmic reticulum resident protein 44	1.26	cellular homeostasis; metabolic process; regulation of biological process; response to stimulus; transport	endoplasmic reticulum; organelle lumen	catalytic activity; metal ion binding; protein binding
19	P09651-2	HNRNPA1	Isoform A1-A of Heterogeneous nuclear ribonucleoprotein A1	1.27	cell communication; metabolic process; regulation of biological process; response to stimulus; transport	cytoplasm; nucleus; spliceosomal complex	DNA binding; protein binding; RNA binding
20	P09874	PARP1	Poly [ADP-ribose] polymerase 1	1.27	cell death; cell differentiation; metabolic process; regulation of biological process; response to stimulus	membrane; mitochondrion; nucleus	catalytic activity; DNA binding; metal ion binding; nucleotide binding; protein binding; RNA binding
21	Q9UBS4	DNAJB11	DNAJ homolog subfamily B member 11	1.27	metabolic process; regulation of biological process	endoplasmic reticulum; nucleus; organelle lumen	protein binding
22	P01111	NRAS	GTPase NRas	1.27	cellular component movement; metabolic process; regulation of biological process; response to stimulus; transport	Golgi; membrane	catalytic activity; nucleotide binding; protein binding
23	Q8TDW7	FAT3	Protocadherin Fat 3	1.27	development	membrane	metal ion binding; protein binding

24	Q86VU5	COMTD1	Catechol O-methyl transferase domain-containing protein 1	1.28	metabolic process	membrane; mitochondrion	catalytic activity; protein binding
25	P56377	AP1S2	AP-1 complex subunit sigma-2	1.29	regulation of biological process; transport	cytosol; Golgi; membrane	protein binding; transporter activity
26	Q8NEY8-3	PPHLN1	Isoform 3 of Periphilin-1	1.30	metabolic process; regulation of biological process	chromosome; cytosol; Golgi	protein binding; RNA binding
27	Q8WWC4	C2orf47; MAIP1	m-AAA protease-interacting protein 1, mitochondrial	1.30	cell organization and biogenesis; cellular homeostasis; transport	membrane; mitochondrion; organelle lumen	protein binding
28	P07919	UQCRH	Cytochrome b-c1 complex subunit 6, mitochondrial	1.32	metabolic process; transport	membrane; mitochondrion	catalytic activity; protein binding; transporter activity
29	Q9NX40	OCIAD1	OCIA domain-containing protein 1	1.33	regulation of biological process	endosome; membrane; mitochondrion	protein binding
30	Q96AY3	FKBP10	Peptidyl-prolyl cis-trans isomerase FKBP10	1.35	cell organization and biogenesis; metabolic process	cytoplasm; endoplasmic reticulum; organelle lumen	catalytic activity; metal ion binding
31	Q9HD33-1	MRPL47	39S ribosomal protein L47, mitochondrial	1.38	cell organization and biogenesis; metabolic process	membrane; mitochondrion; ribosome	structural molecule activity

32	P50213-1	IDH3A	Isocitrate dehydrogenase 8 subunit alpha, mitochondrial	1.41	metabolic process	mitochondrion; nucleus; organelle lumen	catalytic activity; metal ion binding; nucleotide binding
33	Q8NHP8	PLBD2	Putative phospholipase B-like 2	1.41	metabolic process	organelle lumen; vacuole	catalytic activity
34	P14314	PRKCSH	Glucosidase 2 subunit beta	1.43	metabolic process; regulation of biological process; response to stimulus	endoplasmic reticulum; organelle lumen	metal ion binding; protein binding
35	P02788	LTF	Lactotransferrin	1.45	cellular homeostasis; defense response; metabolic process; regulation of biological process; response to stimulus; transport	cell surface; cytoplasm; extracellular; nucleus; organelle lumen	catalytic activity; DNA binding; enzyme regulator activity; metal ion binding; protein binding
36	Q9HCN8	SDF2L1	Stromal cell-derived factor 2-like protein 1	1.49	metabolic process; regulation of biological process; response to stimulus	endoplasmic reticulum; membrane; organelle lumen	catalytic activity; protein binding
37	P16403	HIST1H1C	Histone H1.2	1.58	cell organization and biogenesis; metabolic process; regulation of biological process	chromosome; nucleus	DNA binding; protein binding; RNA binding
38	Q96A26	FAM162A	Protein FAM162A	1.66	cell death; metabolic process; regulation of biological process; response to stimulus	cytosol; membrane; mitochondrion	protein binding

39	P23142-4	FBLN1	Isoform C of Fibulin-1	1.68	cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	extracellular	enzyme regulator activity; metal ion binding; protein binding; structural molecule activity
40	P21912	SDHB	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	1.68	metabolic process; transport	membrane; mitochondrion	catalytic activity; metal ion binding; protein binding
41	P69905	HBA2; HBA1	Hemoglobin subunit alpha	2.04	cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus; transport	cytosol; extracellular; membrane; organelle lumen	antioxidant activity; catalytic activity; metal ion binding; protein binding; transporter activity
42	P02765	AHSG	Alpha-2-HS-glycoprotein	2.51	defense response; metabolic process; regulation of biological process; response to stimulus; transport	extracellular; organelle lumen; Golgi;	enzyme regulator activity
43	P78562	PHEX	Phosphate-regulating neutral endopeptidase PHEX	3.70	cell communication; metabolic process; response to stimulus	endoplasmic reticulum; Golgi; membrane	catalytic activity; metal ion binding

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Table S3. Bioinformatics information and KEGG/Wiki/Reactome pathways of DNA damage repair proteins and DNA damage response proteins with a fold change (FC)  $\leq -1.20$  or of  $\geq 1.20$  identified in A549 cells exposed to ZQX-1 (0.5  $\mu$ M) under irradiation at 420 nm. \* NA: not available.

Accession	Gene Symbol	Protein name	FC (LZ vs. DZ)	KEGG pathways	Wiki pathways	Reactome pathways
P62877	RBX1	E3 ubiquitin-protein ligase	-1.33	nucleotide excision repair; HIF-1 signaling pathway; Ubiquitin mediated proteolysis; cell cycle; TGF-beta signaling pathway	TGF-beta signaling pathway;	DNA damage recognition in GG-NER; formation of incision complex in GG-NER; dual incision in GG-NER; formation of TC-NER pre-incision complex; Dual incision in TC-NER; Gap-filling DNA repair synthesis and ligation in TC-NER; recognition of DNA damage by PCNA-containing replication complex; NOTCH1 intracellular domain regulates transcription; Oxygen-dependent proline hydroxylation of Hypoxia-inducible factor Alpha; constitutive signaling by NOTCH1 HD+PEST domain mutants; Ubiquitination & Proteasome degradation; Neddylation;
Q13098	GPS1	COP9 signalosome complex subunit 1	-1.26	NA*	NA*	DNA Damage Recognition in GG-NER; formation of TC-NER Pre-Incision Complex; Neddylation; Cargo recognition for clathrin-mediated endocytosis
P63165-1	SUMO1	Small ubiquitin-related modifier 1	1.20	RNA transport	TP53 Network; TGF-beta Signaling Pathway;	SUMOylation of DNA damage response and repair proteins; Recruitment and ATM-mediated phosphorylation of repair and signaling proteins at DNA double strand breaks; Processing of DNA double-strand break ends G2/M DNA damage checkpoint; SUMOylation of DNA replication proteins; Nonhomologous End-Joining (NHEJ); Formation of Incision Complex in GG-NER;
P01111	NRAS	GTPase NRas	1.27	Apoptosis; Non-small cell lung cancer; Ras signaling pathway; PI3K-Akt signaling pathway;	DNA Damage Response (only ATM dependent);	Regulation of RAS by GAPs; SHC-mediated cascade:FGFR1/3/4; Signaling by high-kinase activity BRAF mutants; VEGFR2 mediated cell proliferation; RAF activation; Negative regulation of MAPK pathway; CER1 mediated MAPK activation; Downstream signal transduction; RAS signaling downstream of NF1 loss-of-function variants; RAS GTPase and MAP kinases;
P09874	PARP1	Poly [ADP-ribose] polymerase 1	1.27	Apoptosis; Base excision repair; NF-kappa B signaling pathway;	NAD metabolism; NAD+ biosynthetic pathways; Nanoparticle triggered regulated necrosis;	POLB-Dependent Long Patch Base Excision Repair; Dual Incision in GG-NER; Formation of Incision Complex in GG-NER; Downregulation of SMAD2/3:SMAD4 transcriptional activity; DNA Damage Recognition in GG-NER; HDR through MMEJ (alt-NHEJ); SUMOylation of DNA damage response and repair proteins



Table S4. Proteins associated with photodynamic therapy-induced signaling pathways.

Accession	Gene Symbol	Protein name	FC (LZ vs. DZ)	Biological process	Cellular component	Molecular function	KEGG pathways	Wiki pathways
<b>P00338-1</b>	LDHA	L-lactate dehydrogenase A chain	-1.20	metabolic process; regulation of biological process	cytoplasm; nucleus	protein binding; RNA binding	HIF-1 signaling pathway; metabolic pathways; pyruvate metabolism; glycolysis / gluconeogenesis; central carbon metabolism in cancer; cysteine and methionine metabolism; glucagon signaling pathway;	photodynamic therapy-induced HIF-1 survival signaling; glycolysis and gluconeogenesis; Cori cycle; amino acid metabolism;
<b>P19367-1</b>	HK1	Hexokinase-1	1.23	cellular homeostasis; metabolic process; regulation of biological process	cytosol; membrane; mitochondrion	catalytic activity; nucleotide binding; protein binding	HIF-1 signaling pathway; carbon metabolism; glycolysis / gluconeogenesis; fructose and mannose metabolism; galactose metabolism; amino sugar and nucleotide sugar metabolism; central carbon metabolism in cancer;	photodynamic therapy-induced HIF-1 survival signaling; Cori cycle; glycolysis and gluconeogenesis; glucuronidation
<b>Q9UBS4</b>	DNAJB11	DNA J homolog subfamily B member 11	1.27	metabolic process; regulation of biological process	cytoplasm; endoplasmic reticulum; nucleus; organelle lumen	protein binding	protein processing in endoplasmic reticulum	photodynamic therapy-induced unfolded protein response

**Table S5.** The enriched protein-protein (PPI) networks of the DEPs with  $|FC| \geq 1.2$  identified in A549 cells exposed to ZQX-1 under irradiation. The protein names in bold represent upregulation (↑) or downregulation (↓).

No.	Molecules in the network	Top associated diseases and functions of Network
1	ACTN1, ADAM17, ARHGEF5, BCR, CXCL8, DDX10, DSG1, DSP, <b>EEF1A1</b> ↓, EGF, EGFR, <b>FKBP10</b> ↑, <b>GPS1</b> ↓, GRB2, HBB, HK2, HSPA8, HSPD1, IGF1R, JUP, MVP, NFKB1, NFKBIA, PKM, PRKCD, <b>PTPN11</b> ↓, RAD50, RELA, <b>RPS3</b> ↓, S100A9, <b>SDHB</b> ↑, SHC1, STK11, <b>TRAF2</b> ↓, UBA52	Cell Death and Survival, Cellular Development, Organismal Injury and Abnormalities
2	TP53BP1, <b>UBE2L3</b> ↓	Hereditary Disorder, Organismal Injury and Abnormalities
3	CDKN1A, <b>CNOT3</b> ↑	Cell Morphology, Connective Tissue Development and Function
4	<b>AP1S2</b> ↑, SMARCA4	Cancer, Cell Cycle
5	<b>ATP5ME</b> ↑, SREBF1	Dermatological Diseases and Conditions, Developmental Disorder
6	Let-7, <b>NRAS</b> ↑, RHOB	Cancer, Hematological disease, immunological disease
7	BMI1, FOXM1, GLI1, <b>RACK1</b> ↓, SMO, PTCH1	Cancer, Organismal Injury and Abnormalities