

# Supplementary Figure S1

## Nucleotide comparison of *MT-ATP8* and *ATP5G1* MTS with codon-corrected and codon-optimized *ATP8* (o*ATP8*)\*

mtATP8	1	-----	0
oATP8	1	ATGCAGACCGCCGGGGCATTATTCATTTCTCCAGCTCTGATCCGCTGTTG	50
mtATP8	1	-----	0
oATP8	51	TACCAGGGGTCTAATCAGGCCTGTGTCTGCCTCCTTCTTGAATAGCCCAG	100
mtATP8	1	-----	0
oATP8	101	TGAATTCATCTAAACAGCCTTCCTACAGCAACTTCCCACTCCAGGTGGCC	150
mtATP8	1	-----	0
oATP8	151	AGACGGGAGTTCCAGACCAGTGTTGTCTCCCGGGACATTGACACGGCGAC	200
mtATP8	1	----ATGCCCCAACTAAATACTACCGTATGGCCCACCATAATTACCCCCA	46
oATP8	201	. GCGTATGCCCCAGCTGAACACCACAGTGTGGCCTACTATGATCACCCCAA	250
mtATP8	47	TACTCCTTACACTATTCCTCATCACCCAACTAAAAATATTAAACACAAAC	96
oATP8	251	. TGCTGCTGACACTGTTTCCTGATTACTCAGCTGAAGATGCTGAACACCAAT	300
mtATP8	97	TACCACCTACCTCCCTCACCAAAGCCCATAAAAATAAAAAATTATAACAA	146
oATP8	301	. TACCACCTGCCCCCTTCCCCAAAACCCATGAAGATGAAAACTATAATAA	350
mtATP8	147	ACCCTGAGAACCAAAATGAACGAAAATCTGTTTCGCTTCATTATTGCCCC	196
oATP8	351	. GCCCTGGGAACCTAAGTGACCAAAATCTGTAGCCTGCATAGCCTGCCAC	400
mtATP8	197	CACAATCC-----	204
oATP8	401	. . . . CTCAGTCACTCGAGCAGAACTCATCTCAGAAGAGGATCTGGCAGCAAAT	450
mtATP8	205	-----	204
oATP8	451	GATATCCTGGATTACAAGGATGACGACGATAAGGTTTAA	489

**Protein sequence comparison for nuclear translation of codon-corrected and codon-optimized *ATP8* (o*ATP8*), and mitochondrial translation for *MT-ATP8*.**

	ATP5G1 MTS	
oATP8	MQTAGALFISPALIRCCTRGLIRPVSAFLNSPVNSSKQPSYSNFPLQVARREFQTSVVS	60
mtATP8	-----	0
oATP8	RDIDTATRMPQLNNTTVWPTMITPMLLTFLITQLKMLNTNYHLPPSPKPMKMKNYNKPWE	120
mtATP8	-----MPQLNNTTVWPTMITPMLLTFLITQLKMLNTNYHLPPSPKPMKMKNYNKPWE	52
	Myc tag	FLAG tag
oATP8	PKWTKICSLHSLPPQSLEQKLISEEDLAANDILDYKDDDDKV	162
mtATP8	PKWTKICSLHSLPPQS-----	68

**Nucleotide comparison of *MT-ATP6* and *ATP5G1* MTS with recoded (codon-corrected) *ATP6* (r*ATP6*)\***

mtATP6	1	-----	0
rATP6	1	ATGCAGACCGCCGGGCATTATTCATTTCTCCAGCTCTGATCCGCTGTTG	50
mtATP6	1	-----	0
rATP6	51	TACCAGGGGTCTAATCAGGCCTGTGTCTGCCTCCTTCTTGAATAGCCCAG	100
mtATP6	1	-----	0
rATP6	101	TGAATTCATCTAAACAGCCTTCCTACAGCAACTTCCCACTCCAGGTGGCC	150
mtATP6	1	-----	0
rATP6	151	AGACGGGAGTTCAGACCAGTGTTGTCTCCCGGACATTGACACGGCGAC	200
mtATP6	1	----ACGAAAATCTGTTGCTTCATTGCCCCACAATCCTAGGCC	45
rATP6	201	GCGTAACGAAAATCTGTTGCTTCATTGCCCCACAATCCTAGGCC	250
mtATP6	46	TACCCGCCGAGTACTGATCATTCTATTTCCTCTATTGATCCCCACC	95
rATP6	251	TACCCGCCGAGTACTGATCATTCTATTTCCTCTATTGATCCCCACC	300
mtATP6	96	TCCAAATATCTCATCAACAACCGACTAATCACCACCCAACAATGACTAAT	145
rATP6	301	TCCAAATATCTCATCAACAACCGACTAATCACCACCCAACAATGCTAAT	350
mtATP6	146	CAAATAACCTCAAAACAAATGATAACCATACACAACACTAAAGGACGAA	195
rATP6	351	CAAATAACCTCAAAACAAATGATGACCATGCACAACACTAAAGGACGAA	400
mtATP6	196	CCTGATCTCTTATACTAGTATCCTTAATCATTTTTATTGCCACAACCTAAC	245
rATP6	401	CCTGCTCTCTTATGCTAGTATCCTTAATCATTTTTATTGCCACAACCTAAC	450
mtATP6	246	CTCCTCGGACTCCTGCCTCACTCATTTACACCAACCACCAACTATCTAT	295

rATP6	451	 CTCCTCGGACTCCTGCCTCACTCATTTACACCAACCACCCA ACTATCTAT	500
mtATP6	296	AAACCTAGCCATGGCCATCCCCTTATGAGCGGGCACAGTGATTATAGGCT ·	345
rATP6	501	GAACCTAGCCATGGCCATCCCCTTATGGCGGGCACAGTGATTATGGGCT	550
mtATP6	346	TTCGCTCTAAGATTAAAAATGCCCTAGCCCCTTCTTACCACAAGGCACA 	395
rATP6	551	TTCGCTCTAAGATTAAAAATGCCCTAGCCCCTTCTTACCACAAGGCACA	600
mtATP6	396	CCTACACCCCTTATCCCCATACTAGTTATTATCGAAACCATCAGCCTACT 	445
rATP6	601	CCTACACCCCTTATCCCCATCTAGTTATTATCGAAACCATCAGCCTACT	650
mtATP6	446	CATTCAACCAATAGCCCTGGCCGTACGCCTAACCGCTAACATTACTGCAG 	495
rATP6	651	CATTCAACCAATGGCCCTGGCCGTACGCCTAACCGCTAACATTACTGCAG	700
mtATP6	496	GCCACCTACTCATGCACCTAATTGGAAGCGCCACCCTAGCAATATCAACC 	545
rATP6	701	GCCACCTACTCATGCACCTAATTGGAAGCGCCACCCTAGCAATCTCAACC	750
mtATP6	546	ATTAACCTTCCCTCTACACTTATCATCTTCACAATTCTAATTCTACTGAC 	595
rATP6	751	ATTAACCTTCCCTCTACACTTATCATCTTCACAATTCTAATTCTACTGAC	800
mtATP6	596	TATCCTAGAAATCGCTGTGCGCTTAATCCAAGCCTACGTTTTACACTTC 	645
rATP6	801	TATCCTAGAAATCGCTGTGCGCTTAATCCAAGCCTACGTTTTACACTTC	850
mtATP6	646	TAGTAAGCCTCTACCTGCACGACAACACA----- 	674
rATP6	851	TAGTAAGCCTCTACCTGCACGACAACACACTCGAGCAGAAACTCATCTCA	900
mtATP6	675	-----	674
rATP6	901	GAAGAGGATCTGGCAGCAAATGATATCCTGGATTACAAGGATGACGACGA	950
mtATP6	675	----- 674	
rATP6	951	TAAGGTTTAA 960	

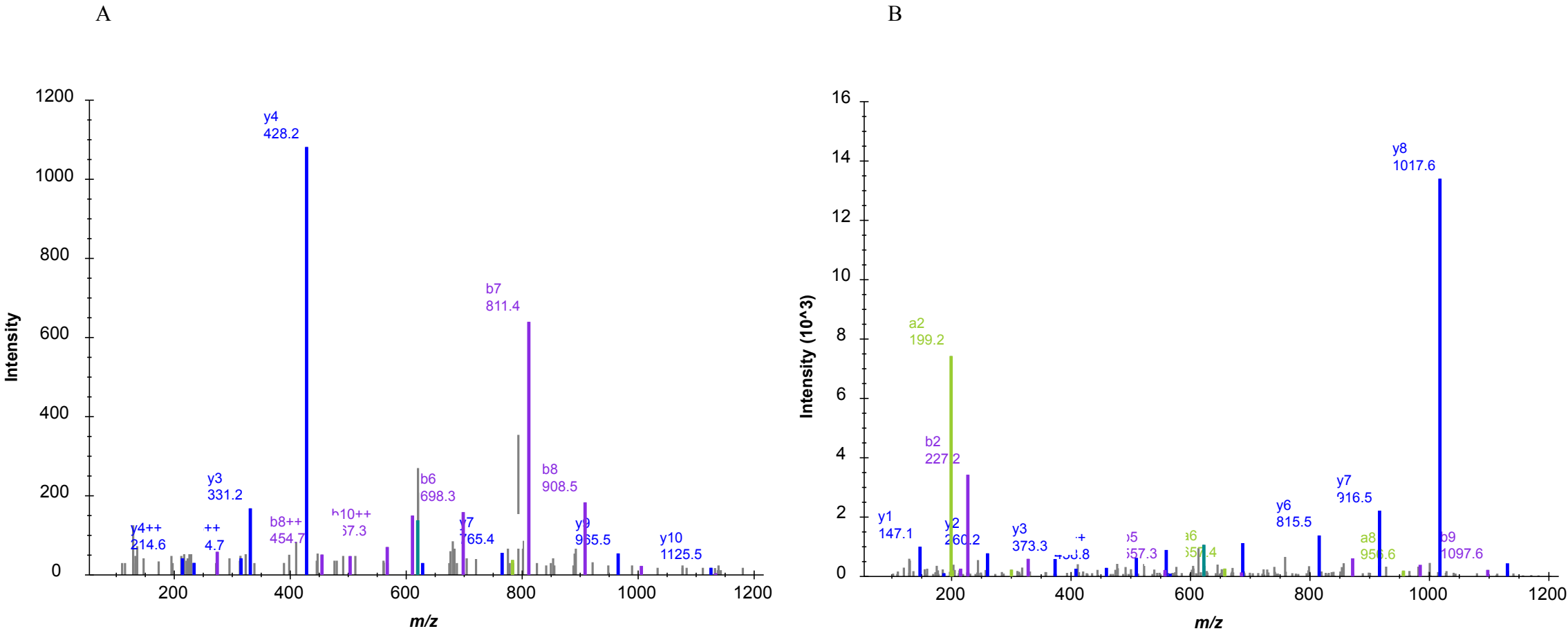
**Protein sequence comparison for nuclear translation of recoded *ATP6* (r*ATP8*), and mitochondrial translation for *MT-ATP6*.**

	ATP5G1 MTS	
rATP6	MQTAGALFISPALIRCCTRGLIRPVSASFVNSKQPSYSNFPLQVARREFQTSVVS	60
mtATP6	-----	0
<hr/>		
rATP6	RDIDTATRNENLFASFIAPTILGLPAAVLIILFPPLLIPTSKYLINNRLITTQQWLIKLT	120
mtATP6	-----MNENLFASFIAPTILGLPAAVLIILFPPLLIPTSKYLINNRLITTQQWLIKLT	53
<hr/>		
rATP6	SKQMMTMHNTKGRTWSLMLVSLIIFIATTNLLGLLPHSFTPTTQLSMNLAMAIPWAGTV	180
mtATP6	SKQMMTMHNTKGRTWSLMLVSLIIFIATTNLLGLLPHSFTPTTQLSMNLAMAIPWAGTV	113

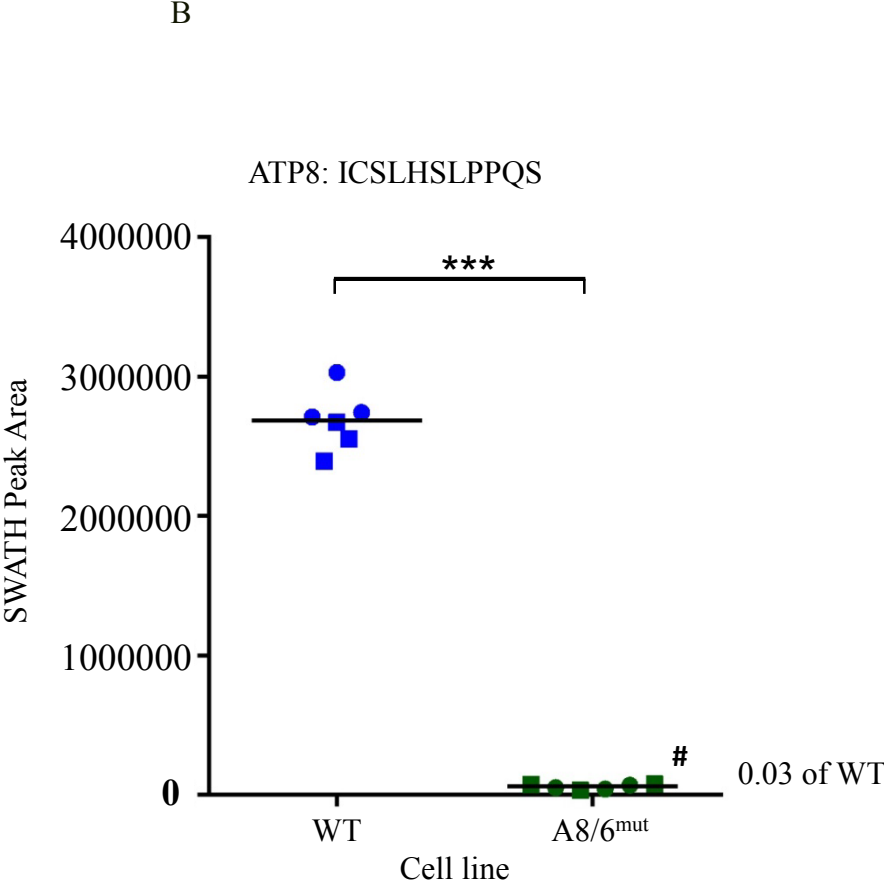
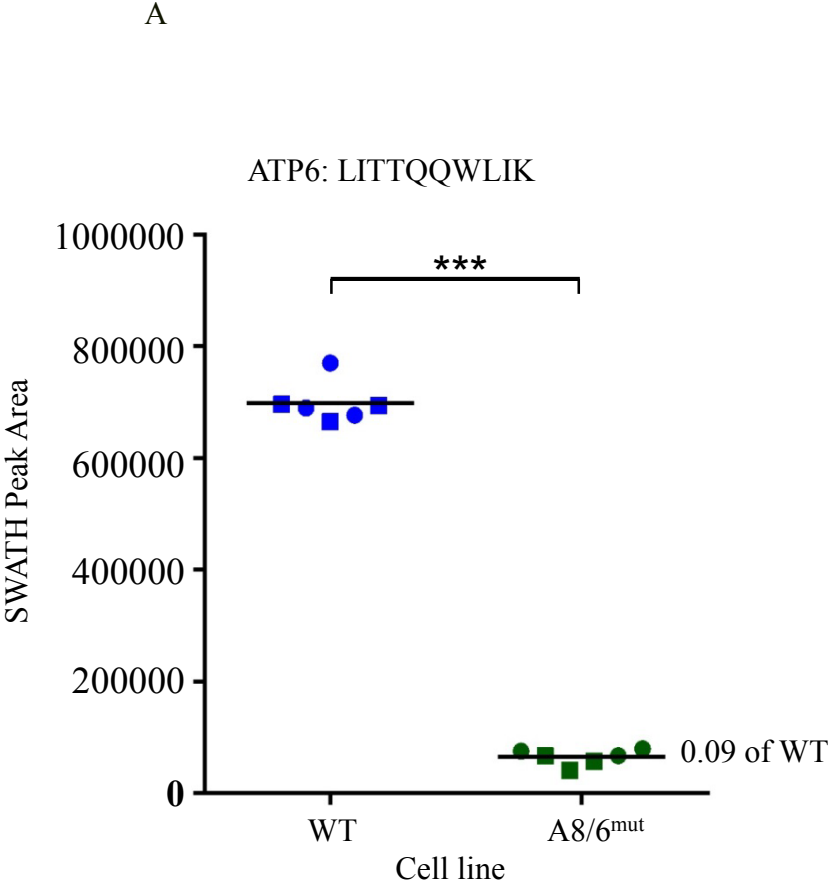
rATP6	IMGFRSRIKNALAHFLPQGTPTPLIPMLVIIETISLLIQPMALAVRLTANITAGHLLMHL	240
mtATP6	IMGFRSRIKNALAHFLPQGTPTPLIPMLVIIETISLLIQPMALAVRLTANITAGHLLMHL	173
		<u>Myc tag</u>
rATP6	IGSATLAMSTINLPSTLIIFTILILLTILEIAVALIQAYVFTLLVSLYLHDNTLEQKLIS	300
mtATP6	IGSATLAMSTINLPSTLIIFTILILLTILEIAVALIQAYVFTLLVSLYLHDNT-----	226
		<u>FLAG tag</u>
rATP6	EEDLAANDILDYKDDDDKV	319
mtATP6	-----	226

\*Nucleotides labelled in red indicate required coding for productive nuclear translation.

Supplementary Figure S2

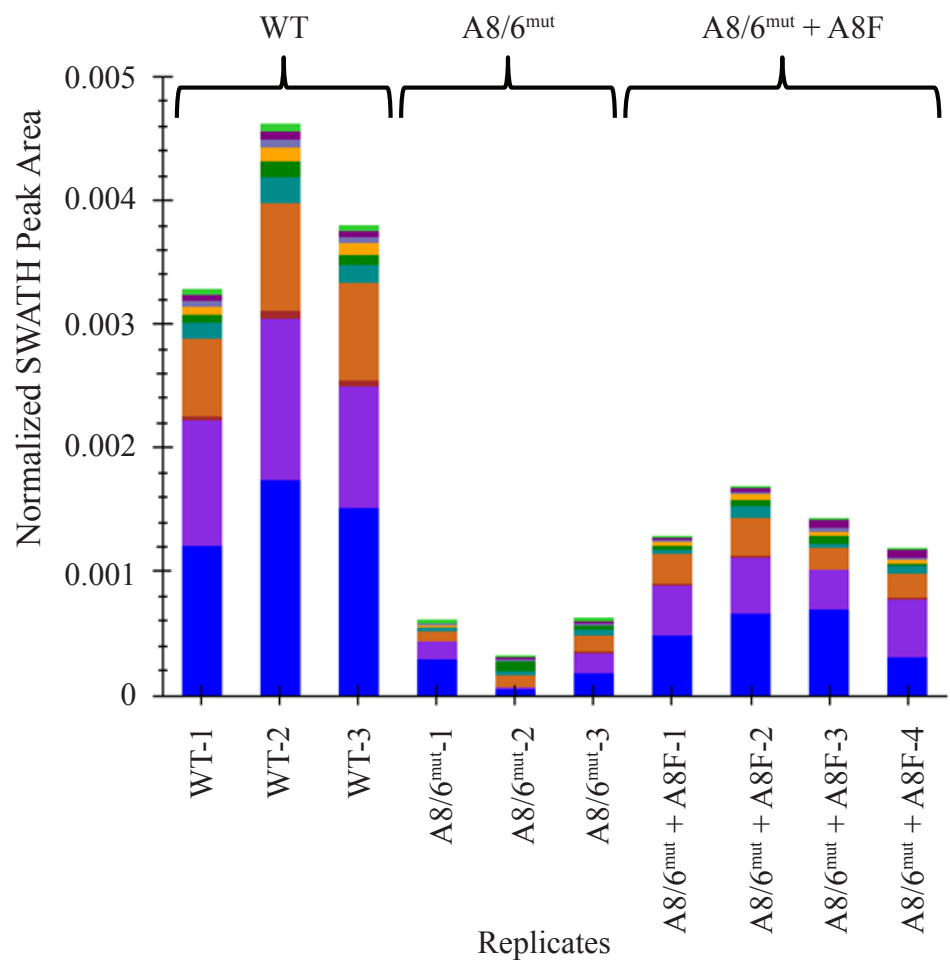


Supplementary Figure S3

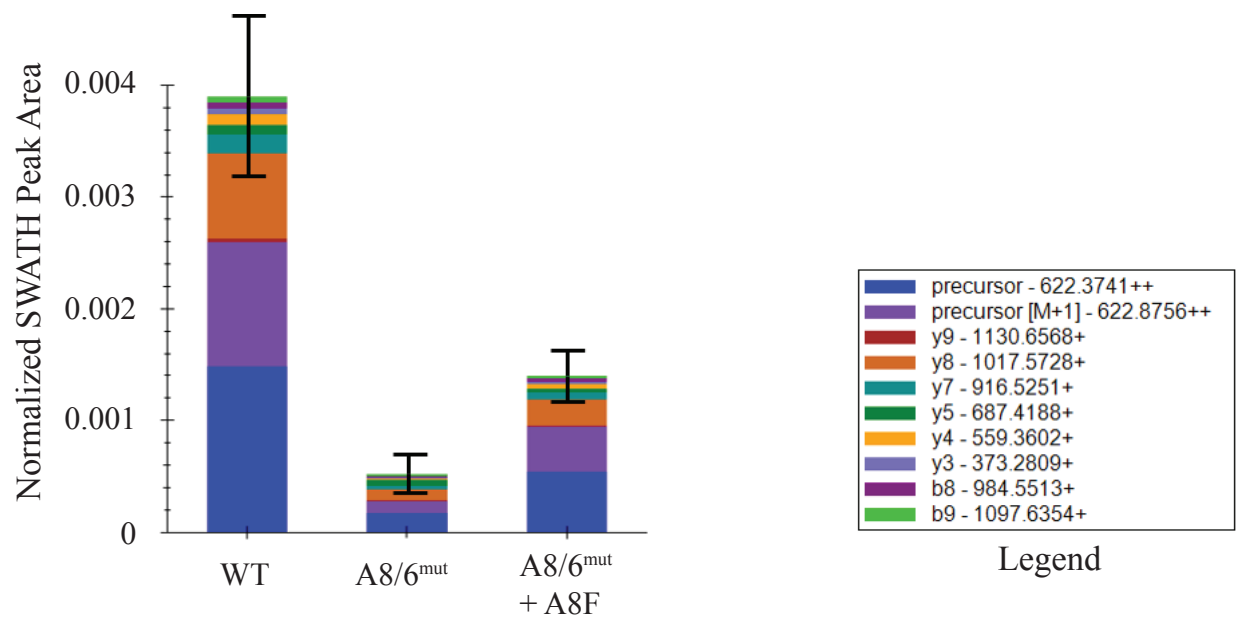


Supplementary Figure S4

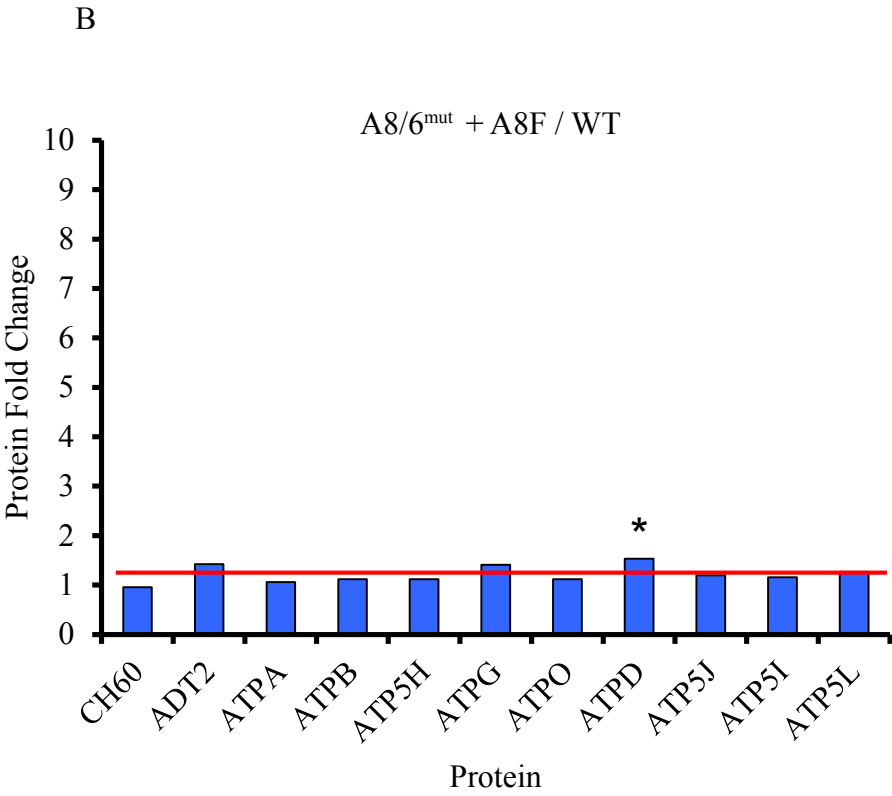
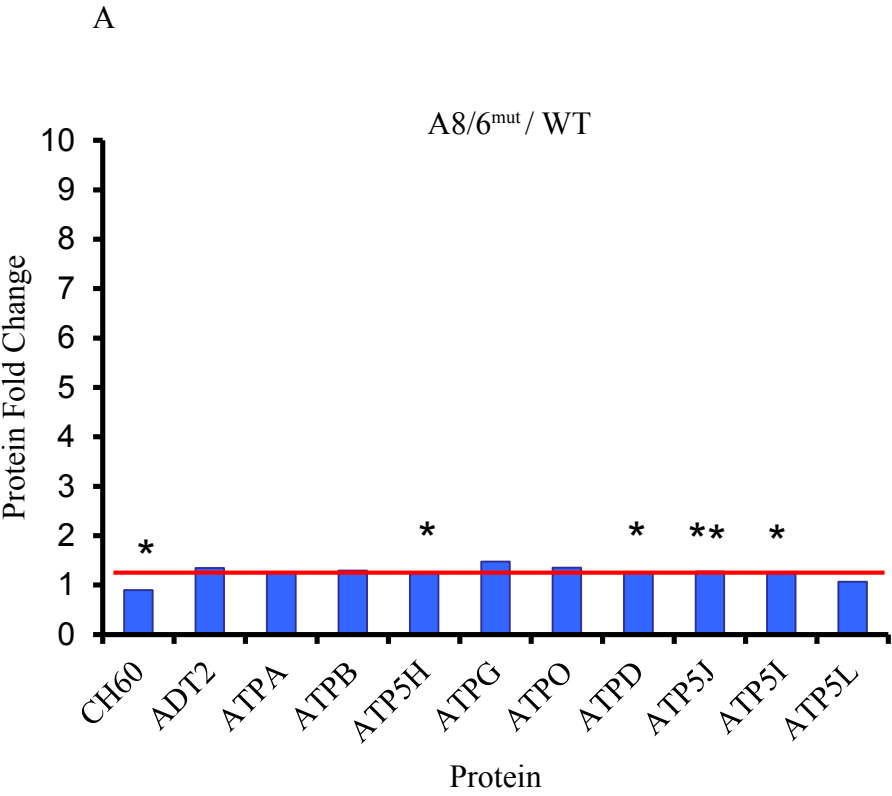
A.



B.

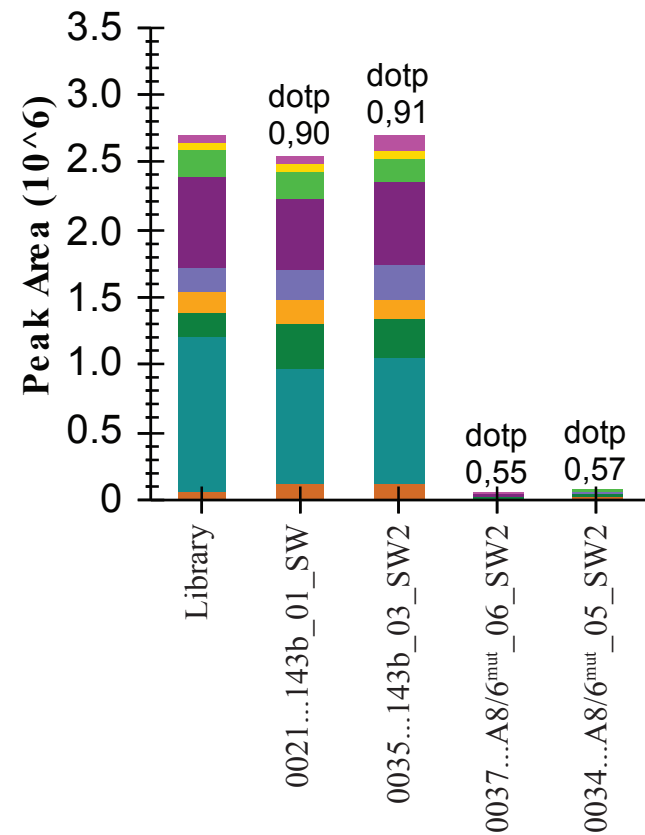


Supplementary Figure S5

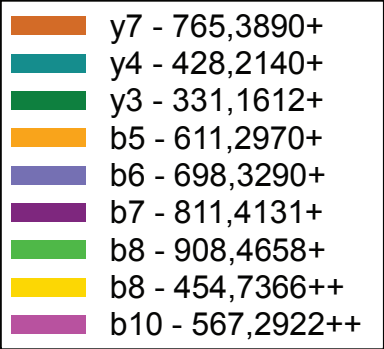
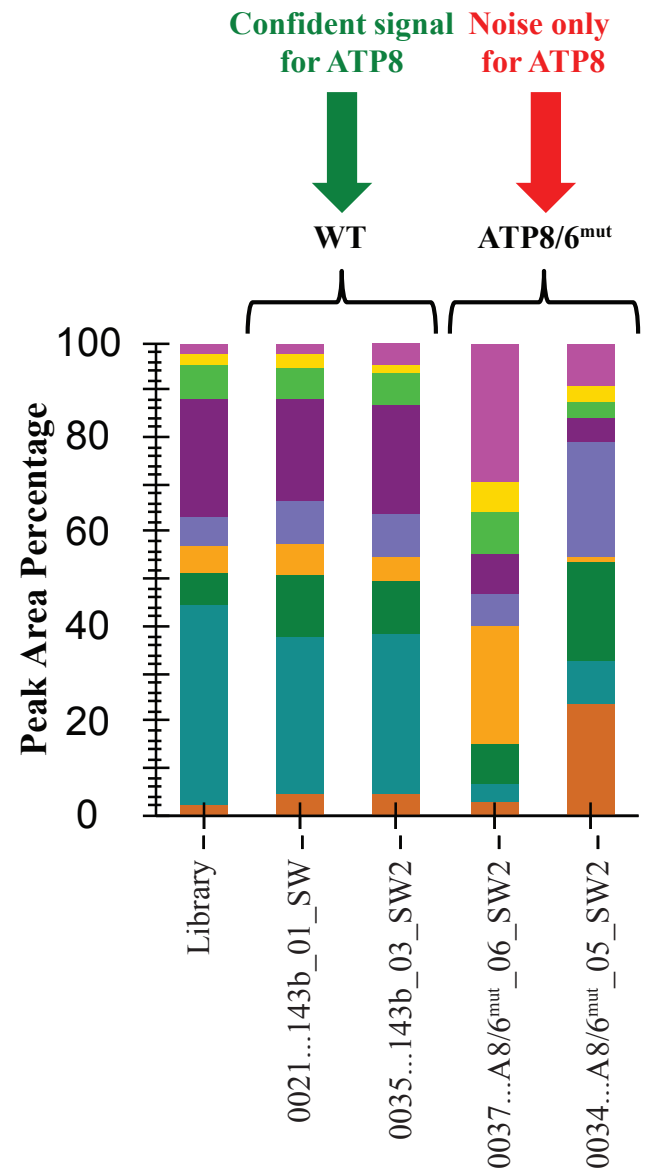


Supplementary Figure S6

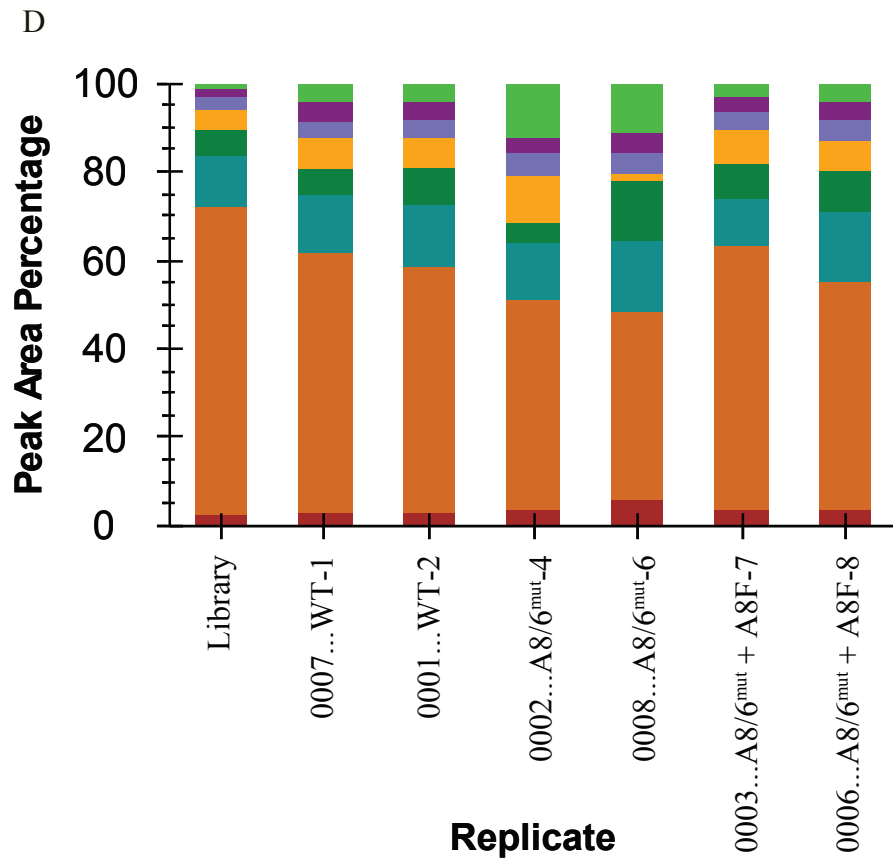
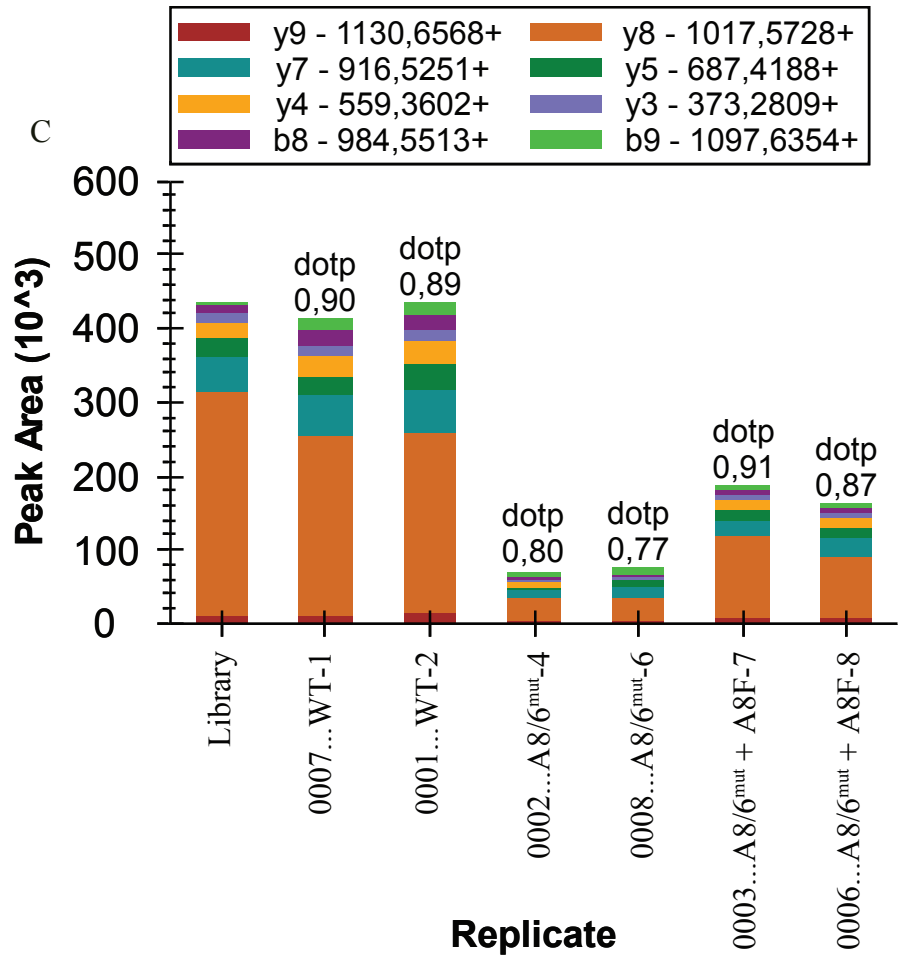
A.



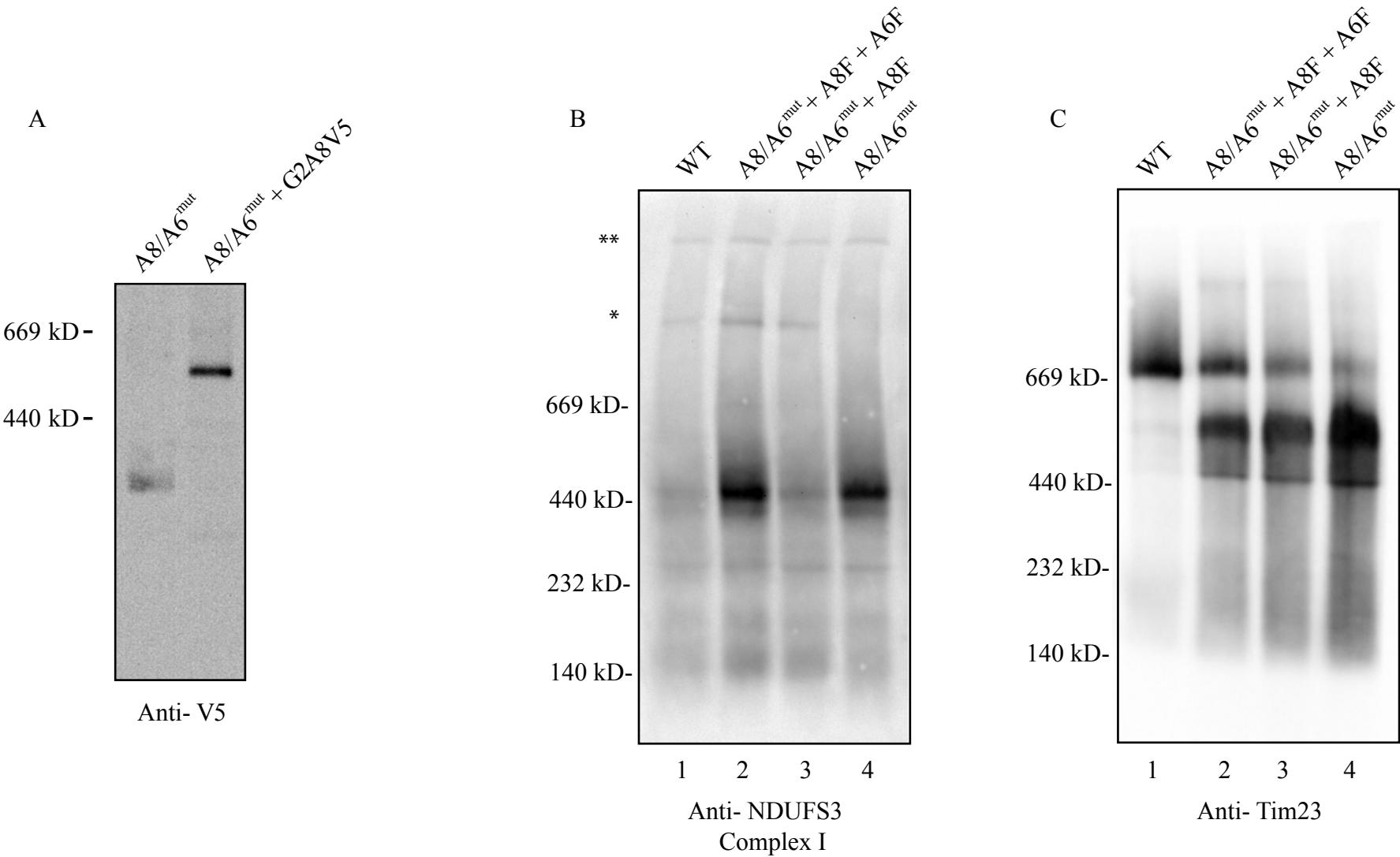
B.



Legend for fragment ions



Supplementary Figure S7



Supplementary Table S1: Mass Spectrometric Report of identified Proteins: Protein Pilot Search Results from human WT and A8/6mut cell lines

Protein Hit	Unused	Total	Seq Coverage	SwissProt Accession	Protein Name	Peptides(95%)
N	Score	Score	%Cov(95)			
1	219.8	219.8	46.0	Q09666 AHNK_HUMAN	Neuroblast differentiation-associated protein AHNK OS=Homo sapiens GN=AHNK PE=1 SV=2	129
2	159.0	159.0	47.2	P35579 MYH9_HUMAN	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	92
3	114.0	114.0	87.8	P10809 CH60_HUMAN	60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2	117
4	92.7	92.7	45.7	P42704 LPPRC_HUMAN	Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LPPRC PE=1 SV=3	65
5	90.6	90.6	67.0	P38646 GRP75_HUMAN	Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	69
6	87.7	87.7	67.4	P26038 MOES_HUMAN	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3	56
7	86.2	86.2	66.3	P40939 ECHA_HUMAN	Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2	45
8	82.0	82.0	71.4	P25705 ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1	47
9	80.5	80.5	25.1	P21333 FLNA_HUMAN	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	43
10	78.9	78.9	28.4	Q9NZM1 MYOF_HUMAN	Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1	44
11	72.1	72.1	77.6	P07355 ANXA2_HUMAN	Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	42
12	71.8	71.8	59.9	P04264 K2C1_HUMAN	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	55
13	68.0	68.0	39.5	P05023 AT1A1_HUMAN	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1	50
14	65.1	65.1	79.3	P14618 KPYM_HUMAN	Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4	37
15	63.0	63.0	81.9	P60709 ACTB_HUMAN	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	86
16	60.2	60.2	46.1	P13639 EF2_HUMAN	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	34
17	60.2	60.2	72.2	P35527 K1C9_HUMAN	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	40
18	59.6	59.6	65.3	P11021 GRP78_HUMAN	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	41
19	59.0	74.1	25.7	P35580 MYH10_HUMAN	Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3	40
20	58.9	58.9	76.6	P06576 ATPB_HUMAN	ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	45
21	58.6	58.7	69.3	P08670 VIME_HUMAN	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4	33
22	58.2	58.3	43.1	P08238 HS90B_HUMAN	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	32
23	58.0	58.0	81.7	P40926 MDHM_HUMAN	Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3	41
24	57.3	57.3	45.2	P12814 ACTN1_HUMAN	Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2	35
25	57.1	57.3	63.4	P00367 DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial OS=Homo sapiens GN=GLUD1 PE=1 SV=2	34
26	56.6	56.8	19.3	Q01082 SPTB2_HUMAN	Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2	31
27	56.3	56.3	92.5	P04406 G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	52
28	55.5	55.5	77.2	P06733 ENOA_HUMAN	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	34
29	53.4	53.4	62.1	P34897 GLYM_HUMAN	Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3	36
30	52.3	58.5	65.6	P35908 K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	41
31	52.2	56.3	48.9	P11142 HSP7C_HUMAN	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	33
32	50.7	50.7	91.2	P21796 VDAC1_HUMAN	Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	36
33	50.4	50.6	56.3	P13645 K1C10_HUMAN	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	34
34	47.8	47.8	62.4	P30101 PDIA3_HUMAN	Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4	27
35	47.3	47.3	9.5	Q14204 DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	28
36	47.2	47.2	14.4	Q13813 SPTN1_HUMAN	Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3	27
37	46.4	46.4	47.6	P14625 ENPL_HUMAN	Endoplasmic OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	26
38	45.5	45.5	43.5	O43175 SERA_HUMAN	D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4	26
39	45.2	45.3	61.0	P07437 TBB5_HUMAN	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	26
40	45.2	45.2	63.3	P49411 EFTU_HUMAN	Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2	29
41	44.7	44.8	21.0	Q02952 AKA12_HUMAN	A-kinase anchor protein 12 OS=Homo sapiens GN=AKAP12 PE=1 SV=4	22
42	44.0	44.0	77.1	P68104 EF1A1_HUMAN	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	42
43	43.6	43.7	31.0	P19367 HKK1_HUMAN	Hexokinase-1 OS=Homo sapiens GN=HK1 PE=1 SV=3	22
44	43.5	50.1	46.5	Q12931 TRAP1_HUMAN	Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3	33
45	43.0	43.0	82.4	P04075 ALDOA_HUMAN	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	27
46	40.8	40.8	77.5	P45880 VDAC2_HUMAN	Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2	29
47	40.2	40.2	65.8	P05141 ADT2_HUMAN	ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7	24
48	40.0	40.0	37.7	Q16891 MIC60_HUMAN	MICOS complex subunit MIC60 OS=Homo sapiens GN=IMMT PE=1 SV=1	22
49	39.8	39.9	12.9	Q9Y490 TLN1_HUMAN	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	24
50	39.8	39.8	43.4	P49748 ACADV_HUMAN	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1	21
51	39.3	39.3	48.3	P27824 CALX_HUMAN	Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2	22
52	36.8	36.8	58.6	P55084 ECHB_HUMAN	Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3	22
53	36.6	36.6	66.1	P04181 OAT_HUMAN	Ornithine aminotransferase, mitochondrial OS=Homo sapiens GN=OAT PE=1 SV=1	19
54	36.6	36.6	30.7	P02786 TFR1_HUMAN	Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2	20
55	36.2	36.2	70.5	Q9UJZ1 STML2_HUMAN	Stomatin-like protein 2, mitochondrial OS=Homo sapiens GN=STOML2 PE=1 SV=1	24
56	36.0	36.0	42.3	P07237 PDIA1_HUMAN	Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3	19
57	35.8	35.9	39.4	P54886 P5CS_HUMAN	Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2	23
58	35.0	35.0	48.1	Q9BQE3 TBA1C_HUMAN	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1	20
59	34.7	34.7	79.8	P35232 PHB_HUMAN	Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1	21
60	33.7	34.3	88.2	P61604 CH10_HUMAN	10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=1 SV=2	24
61	33.6	33.6	66.2	Q99623 PHB2_HUMAN	Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2	20
62	32.4	32.5	14.7	Q00610 CLH1_HUMAN	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	16
63	32.3	32.4	45.0	P04843 RPN1_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1	19
64	32.0	32.0	27.5	P36776 LONM_HUMAN	Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=1 SV=2	19
65	31.6	31.6	73.2	P54819 KAD2_HUMAN	Adenylate kinase 2, mitochondrial OS=Homo sapiens GN=AK2 PE=1 SV=2	22
66	31.1	31.1	63.5	P42765 THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2	16
67	30.9	30.9	31.7	O95831 AIFM1_HUMAN	Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1	18
68	30.8	31.0	53.8	O94826 TOM70_HUMAN	Mitochondrial import receptor subunit TOM70 OS=Homo sapiens GN=TOMM70 PE=1 SV=1	19
69	30.6	30.6	36.9	Q16822 PCKGM_HUMAN	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3	17
70	30.6	30.6	68.8	Q06830 PRDX1_HUMAN	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	17
71	30.2	30.2	55.1	P11310 ACADM_HUMAN	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=1	18
72	29.7	29.7	65.2	P30048 PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3	25
73	29.7	29.7	74.3	P27797 CALR_HUMAN	Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1	18
74	29.4	29.5	38.4	P31040 SDHA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=1 SV=1	16
75	29.1	29.2	25.6	P35221 CTNA1_HUMAN	Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1	17
76	29.1	29.2	20.9	O00159 MYO1C_HUMAN	Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4	17
77	28.9	29.0	20.2	Q7K2F4 SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens GN=SND1 PE=1 SV=1	15
78	28.7	28.7	63.9	P23284 PPIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=2	20
79	28.6	28.6	21.4	Q5JRX3 PREP_HUMAN	Presequence protease, mitochondrial OS=Homo sapiens GN=PITRM1 PE=1 SV=3	18
80	28.3	28.3	68.3	P30084 ECHM_HUMAN	Enoyl-CoA hydratase, mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4	15

81	28.2	28.3	39.1	Q10713 MPPA_HUMAN	Mitochondrial-processing peptidase subunit alpha OS=Homo sapiens GN=PMPCA PE=1 SV=2	16
82	28.2	28.3	59.0	Q9H9B4 SFXN1_HUMAN	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4	18
83	27.4	27.4	59.2	P38117 ETFB_HUMAN	Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3	16
84	26.8	26.8	55.2	P00558 PGK1_HUMAN	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	17
85	26.6	26.6	76.5	P23528 COF1_HUMAN	Cofilin-1 OS=Homo sapiens GN=COF1 PE=1 SV=3	14
86	26.5	26.5	43.8	P08754 GNAI3_HUMAN	Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3	13
87	26.1	26.1	38.3	P55809 SCOT1_HUMAN	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Homo sapiens GN=OXCT1 PE=1 SV=1	17
88	25.9	25.9	24.5	Q14697 GANAB_HUMAN	Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3	15
89	25.8	25.8	39.6	P31930 QCR1_HUMAN	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3	14
90	25.4	25.4	24.8	Q8TCS8 PNPT1_HUMAN	Polyribonucleotide nucleotidyltransferase 1, mitochondrial OS=Homo sapiens GN=PNPT1 PE=1 SV=2	14
91	25.4	25.4	33.5	P28838 AMPL_HUMAN	Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3	13
92	25.3	25.3	71.2	P13804 ETFA_HUMAN	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1	15
93	24.9	24.9	19.0	P11586 C1TC_HUMAN	C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3	14
94	24.8	24.9	64.8	O96008 TOM40_HUMAN	Mitochondrial import receptor subunit TOM40 homolog OS=Homo sapiens GN=TOMM40 PE=1 SV=1	16
95	24.7	24.8	54.9	Q15019 SEPT2_HUMAN	Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1	14
96	24.4	24.4	86.1	P62937 PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2	20
97	24.2	24.2	89.4	O75947 ATP5H_HUMAN	ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3	12
98	24.2	24.2	55.5	P32322 P5CR1_HUMAN	Pyrroline-5-carboxylate reductase 1, mitochondrial OS=Homo sapiens GN=PYCR1 PE=1 SV=2	14
99	24.0	24.1	58.6	P24752 THIL_HUMAN	Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1	17
100	24.0	24.0	63.6	Q9HAV7 GRPE1_HUMAN	GrpE protein homolog 1, mitochondrial OS=Homo sapiens GN=GRPEL1 PE=1 SV=2	12
101	24.0	24.0	59.4	P62873 GBB1_HUMAN	Guanine nucleotide-binding protein G(i)/G(s)/G(t) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3	13
102	23.2	23.2	28.7	Q99798 ACON_HUMAN	Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2	12
103	23.1	23.2	37.1	P22695 QCR2_HUMAN	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3	16
104	23.0	23.1	33.2	Q9UIS0 CMC2_HUMAN	Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13 PE=1 SV=2	15
105	23.0	23.6	21.5	Q02218 ODO1_HUMAN	2-oxoglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=OGDH PE=1 SV=3	16
106	23.0	23.0	26.2	O94925 GLSK_HUMAN	Glutaminase kidney isoform, mitochondrial OS=Homo sapiens GN=GLS PE=1 SV=1	16
107	22.9	22.9	63.5	P62258 1433E_HUMAN	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	13
108	22.8	27.6	43.6	P02533 K1C14_HUMAN	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	14
109	22.8	22.9	26.7	P28331 NDU51_HUMAN	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Homo sapiens GN=NDUFS1 PE=1 SV=3	13
110	22.7	22.9	22.2	O43491 E41L2_HUMAN	Band 4.1-like protein 2 OS=Homo sapiens GN=EPB41L2 PE=1 SV=1	11
111	22.7	22.7	71.8	P80723 BASP1_HUMAN	Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2	22
112	22.6	24.6	16.5	O43795 MYO1B_HUMAN	Unconventional myosin-1b OS=Homo sapiens GN=MYO1B PE=1 SV=3	12
113	22.5	22.6	59.0	P63244 RACK1_HUMAN	Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3	14
114	22.4	22.4	37.9	P11177 ODPB_HUMAN	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens GN=PDHB PE=1 SV=3	13
115	22.3	22.3	45.1	Q00059 TFAM_HUMAN	Transcription factor A, mitochondrial OS=Homo sapiens GN=TFAM PE=1 SV=1	13
116	22.2	22.4	12.6	Q9Y2J2 E41L3_HUMAN	Band 4.1-like protein 3 OS=Homo sapiens GN=EPB41L3 PE=1 SV=2	11
117	22.2	22.3	27.2	Q96RP9 EFGM_HUMAN	Elongation factor G, mitochondrial OS=Homo sapiens GN=GFM1 PE=1 SV=2	12
118	22.2	22.3	34.7	Q96I99 SUCB2_HUMAN	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2	12
119	22.1	22.2	20.8	Q9Y4L1 HYOU1_HUMAN	Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1	14
120	22.0	22.1	25.7	Q07065 CKAP4_HUMAN	Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2	12
121	21.9	22.0	75.4	P51149 RAB7A_HUMAN	Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1	15
122	21.8	21.9	45.6	P08559 ODPA_HUMAN	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens GN=P	15
123	21.7	21.8	23.2	Q9NV17 ATD3A_HUMAN	ATPase family AAA domain-containing protein 3A OS=Homo sapiens GN=ATAD3A PE=1 SV=2	17
124	21.7	21.8	18.8	O60716 CTND1_HUMAN	Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1	13
125	21.6	21.7	19.7	P13667 PDIA4_HUMAN	Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2	13
126	21.6	25.6	6.4	O75369 FLNB_HUMAN	Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2	14
127	21.4	21.5	35.6	P09622 DLDH_HUMAN	Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens GN=DLD PE=1 SV=2	12
128	20.9	20.9	26.4	O60488 ACSL4_HUMAN	Long-chain-fatty-acid--CoA ligase 4 OS=Homo sapiens GN=ACSL4 PE=1 SV=2	11
129	20.6	20.6	37.9	P36578 RL4_HUMAN	60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5	18
130	20.4	20.4	42.9	Q96I87 HPDL_HUMAN	4-hydroxyphenylpyruvate dioxygenase-like protein OS=Homo sapiens GN=HPDL PE=1 SV=1	13
131	20.2	20.2	52.6	P48047 ATPO_HUMAN	ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1	13
132	20.1	20.1	15.4	P17301 ITA2_HUMAN	Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	14
133	20.1	20.1	41.4	P07954 FUMH_HUMAN	Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FB PE=1 SV=3	12
134	20.0	21.5	61.2	P63104 1433Z_HUMAN	14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1	13
135	20.0	20.0	43.4	P46777 RL5_HUMAN	60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3	11
136	19.9	20.0	35.0	O75390 CISY_HUMAN	Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2	10
137	19.8	19.9	51.9	P08865 RSSA_HUMAN	40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4	12
138	19.8	19.8	82.1	P07737 PROF1_HUMAN	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2	13
139	19.6	19.7	18.9	P05566 ITB1_HUMAN	Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	11
140	19.4	42.7	33.1	P07900 HS90A_HUMAN	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	24
141	19.3	19.3	53.3	P61224 RAP1B_HUMAN	Ras-related protein Rap-1b OS=Homo sapiens GN=RAP1B PE=1 SV=1	10
142	19.3	19.3	16.8	P18206 VINC_HUMAN	Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4	11
143	19.0	19.0	33.3	P60842 IF4A1_HUMAN	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1	11
144	18.8	18.8	14.9	Q9NSE4 SIYI_HUMAN	Isoleucine--tRNA ligase, mitochondrial OS=Homo sapiens GN=IARS2 PE=1 SV=2	10
145	18.7	18.8	71.5	Q4VC31 CCD58_HUMAN	Coiled-coil domain-containing protein 58 OS=Homo sapiens GN=CCDC58 PE=1 SV=1	11
146	18.6	18.6	49.5	P62241 RS8_HUMAN	40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2	11
147	18.5	18.5	57.8	Q07021 C1QBP_HUMAN	Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Homo sapiens GN=C1QBP PE=1 SV=1	17
148	18.3	18.3	34.0	P06753 TPM3_HUMAN	Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=2	12
149	18.1	18.2	13.3	P11498 PYC_HUMAN	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2	12
150	18.0	18.0	43.9	Q15084 PDIA6_HUMAN	Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1	10
151	18.0	18.0	18.0	P43304 GPDH_HUMAN	Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Homo sapiens GN=GP2 PE=1 SV=3	9
152	17.8	17.9	31.6	Q16658 FSCN1_HUMAN	Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3	9
153	17.6	17.6	58.1	O00299 CLIC1_HUMAN	Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4	10
154	17.4	17.5	7.5	P46940 IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1	11
155	17.4	17.5	17.7	O60313 OPA1_HUMAN	Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens GN=OPA1 PE=1 SV=3	13
156	17.4	17.4	48.7	Q99714 HCD2_HUMAN	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3	18
157	17.3	17.3	39.1	P62424 RL7A_HUMAN	60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2	12
158	16.9	16.9	36.3	P05388 RLA0_HUMAN	60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	8
159	16.7	16.7	16.2	P08195 4F2_HUMAN	4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=1 SV=3	9
160	16.7	16.7	15.4	P16615 AT2A2_HUMAN	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1	9
161	16.4	16.4	43.9	P61247 RS3A_HUMAN	40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2	9
162	16.3	16.4	22.7	Q00325 MPCP_HUMAN	Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2	11
163	16.2	16.3	14.2	Q9Y4W6 AFG32_HUMAN	AFG3-like protein 2 OS=Homo sapiens GN=AFG3L2 PE=1 SV=2	9
164	16.2	16.3	59.0	P99999 CYC_HUMAN	Cytochrome c OS=Homo sapiens GN=CYCS PE=1 SV=2	8

165	16.2	16.2	20.8	P14314 GLU2B_HUMAN	Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=1 SV=2	9
166	16.2	16.2	32.9	P36542 ATPG_HUMAN	ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1	9
167	16.1	16.1	27.0	P48735 IDHP_HUMAN	Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2	8
168	16.1	16.1	55.1	P23396 RS3_HUMAN	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2	9
169	16.0	16.0	33.1	Q9UGM6 SYWM_HUMAN	Tryptophan--tRNA ligase, mitochondrial OS=Homo sapiens GN=WARS2 PE=1 SV=1	9
170	16.0	16.0	58.7	P01116 RASK_HUMAN	GTPase KRas OS=Homo sapiens GN=KRAS PE=1 SV=1	14
171	15.9	16.0	42.7	Q16836 HCDH_HUMAN	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3	8
172	15.7	15.7	37.0	Q6IS14 IF5AL_HUMAN	Eukaryotic translation initiation factor 5A-1-like OS=Homo sapiens GN=EIF5A1 PE=2 SV=2	9
173	15.5	15.6	26.9	P10412 H14_HUMAN	Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	13
174	15.4	15.5	35.7	Q9NX63 MIC19_HUMAN	MICOS complex subunit MIC19 OS=Homo sapiens GN=CHCHD3 PE=1 SV=1	11
175	15.3	15.3	51.4	P51148 RAB5C_HUMAN	Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2	9
176	15.2	15.3	32.8	P00338 LDHA_HUMAN	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	8
177	15.2	15.2	66.2	P30405 PPIF_HUMAN	Peptidyl-prolyl cis-trans isomerase F, mitochondrial OS=Homo sapiens GN=PPIF PE=1 SV=1	10
178	15.1	19.4	50.9	Q9Y277 VDAC3_HUMAN	Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1	9
179	15.0	15.1	11.1	P16070 CD44_HUMAN	CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=3	10
180	15.0	19.3	5.0	Q14315 FLNC_HUMAN	Filamin-C OS=Homo sapiens GN=FLNC PE=1 SV=3	11
181	14.9	14.9	26.0	Q12849 GRSF1_HUMAN	G-rich sequence factor 1 OS=Homo sapiens GN=GRSF1 PE=1 SV=3	9
182	14.8	29.7	22.7	Q43707 ACTN4_HUMAN	Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	19
183	14.6	15.0	23.5	P07602 SAP_HUMAN	Prosaposin OS=Homo sapiens GN=PSAP PE=1 SV=2	10
184	14.5	14.6	27.4	Q02878 RL6_HUMAN	60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3	8
185	14.5	14.6	4.9	P49327 FAS_HUMAN	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	9
186	14.5	14.5	24.4	Q96EY1 DNJA3_HUMAN	DnaJ homolog subfamily A member 3, mitochondrial OS=Homo sapiens GN=DNAJA3 PE=1 SV=2	10
187	14.5	14.5	39.9	P29692 EF1D_HUMAN	Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=5	10
188	14.4	14.4	43.0	P62753 RS6_HUMAN	40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	8
189	14.2	15.3	10.8	Q7L2E3 DHX30_HUMAN	Putative ATP-dependent RNA helicase DHX30 OS=Homo sapiens GN=DHX30 PE=1 SV=1	11
190	14.1	14.1	25.6	Q9Y6N5 SQRD_HUMAN	Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRD PE=1 SV=1	9
191	14.1	14.1	57.3	P62805 H4_HUMAN	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	8
192	14.0	14.0	21.9	O75439 MPPB_HUMAN	Mitochondrial-processing peptidase subunit beta OS=Homo sapiens GN=PMPCB PE=1 SV=2	7
193	14.0	14.2	22.7	Q8N859 TXND5_HUMAN	Thioredoxin domain-containing protein 5 OS=Homo sapiens GN=TXND5 PE=1 SV=2	7
194	14.0	22.2	52.6	P62879 GBB2_HUMAN	Guanine nucleotide-binding protein G(i)/G(s)/G(t) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3	12
195	13.9	14.0	21.7	P16401 H15_HUMAN	Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3	7
196	13.8	13.8	31.9	O43837 IDH3B_HUMAN	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial OS=Homo sapiens GN=IDH3B PE=1 SV=2	8
197	13.8	13.9	56.7	Q9H0U4 RAB1B_HUMAN	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1	8
198	13.8	13.8	28.3	P35613 BASI_HUMAN	Basigin OS=Homo sapiens GN=BSG PE=1 SV=2	10
199	13.6	13.7	22.8	P39023 RL3_HUMAN	60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2	7
200	13.6	13.6	22.0	Q6NUK1 SCMC1_HUMAN	Calcium-binding mitochondrial carrier protein SCA1 OS=Homo sapiens GN=SLC25A24 PE=1 SV=2	9
201	13.6	13.6	7.7	Q9P2E9 RRBP1_HUMAN	Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4	8
202	13.5	13.5	50.5	P52815 RM12_HUMAN	39S ribosomal protein L12, mitochondrial OS=Homo sapiens GN=MRPL12 PE=1 SV=2	8
203	13.5	13.5	25.3	P36551 HEM6_HUMAN	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial OS=Homo sapiens GN=CPOX PE=1 SV=3	8
204	13.4	23.8	25.2	P48668 K2C6C_HUMAN	Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3	14
205	13.4	13.8	19.7	Q6PI48 SYDM_HUMAN	Aspartate--tRNA ligase, mitochondrial OS=Homo sapiens GN=DARS2 PE=1 SV=1	7
206	13.2	13.3	37.7	P13995 MTDC_HUMAN	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial OS=Homo sapiens GN=	7
207	13.2	13.2	10.9	P15144 AMPN_HUMAN	Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4	7
208	13.1	13.2	13.4	Q6UB35 C1TM_HUMAN	Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1	10
209	13.1	13.1	12.2	P35222 CTNB1_HUMAN	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1	8
210	13.1	13.1	62.8	P10606 COX5B_HUMAN	Cytochrome c oxidase subunit 5B, mitochondrial OS=Homo sapiens GN=COX5B PE=1 SV=2	7
211	12.9	12.9	24.2	P22234 PUR6_HUMAN	Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3	7
212	12.9	12.9	17.2	P26641 EF1G_HUMAN	Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	7
213	12.9	12.9	31.2	Q15365 PCBP1_HUMAN	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2	7
214	12.8	32.0	52.7	P12236 ADT3_HUMAN	ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4	19
215	12.8	12.9	25.0	P07339 CATD_HUMAN	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1	10
216	12.8	12.9	14.2	P41250 SYG_HUMAN	Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3	8
217	12.7	12.8	41.1	Q96BR5 COA7_HUMAN	Cytochrome c oxidase assembly factor 7 OS=Homo sapiens GN=COA7 PE=1 SV=2	7
218	12.7	12.7	32.7	P53597 SUCA_HUMAN	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Homo sapiens GN=SUCLG1 PE=1 SV=	11
219	12.6	12.7	37.4	P60174 TPIS_HUMAN	Triosephosphate isomerase OS=Homo sapiens GN=TP1 PE=1 SV=3	8
220	12.6	12.6	55.6	P60660 MYL6_HUMAN	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	9
221	12.6	16.2	16.5	O75746 CMC1_HUMAN	Calcium-binding mitochondrial carrier protein Aralar1 OS=Homo sapiens GN=SLC25A12 PE=1 SV=2	10
222	12.6	13.7	33.8	Q9P015 RM15_HUMAN	39S ribosomal protein L15, mitochondrial OS=Homo sapiens GN=MRPL15 PE=1 SV=1	9
223	12.5	31.4	32.8	P15311 EZRI_HUMAN	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4	22
224	12.5	12.5	36.5	P26373 RL13_HUMAN	60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	8
225	12.4	12.4	26.1	P36957 ODO2_HUMAN	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitoc	8
226	12.4	12.5	30.6	P61586 RHOA_HUMAN	Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1	7
227	12.4	12.4	39.2	P37802 TAGL2_HUMAN	Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3	10
228	12.3	12.4	16.0	Q16643 DREB_HUMAN	Drebrin OS=Homo sapiens GN=DBN1 PE=1 SV=4	7
229	12.3	14.3	27.5	P07195 LDHB_HUMAN	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2	7
230	12.3	12.3	50.9	P18859 ATP5J_HUMAN	ATP synthase-coupling factor 6, mitochondrial OS=Homo sapiens GN=ATP5J PE=1 SV=1	8
231	12.2	12.3	32.8	Q02978 M2OM_HUMAN	Mitochondrial 2-oxoglutarate/malate carrier protein OS=Homo sapiens GN=SLC25A11 PE=1 SV=3	7
232	12.2	12.2	40.2	P13073 COX41_HUMAN	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens GN=COX41 PE=1 SV=1	6
233	12.2	12.2	44.4	P30044 PRDX5_HUMAN	Peroxisedoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4	7
234	12.1	12.2	20.6	P49419 AL7A1_HUMAN	Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5	8
235	12.1	12.1	17.4	P53985 MOT1_HUMAN	Monocarboxylate transporter 1 OS=Homo sapiens GN=SLC16A1 PE=1 SV=3	8
236	12.1	12.2	16.8	Q9NVA2 SEP11_HUMAN	Septin-11 OS=Homo sapiens GN=SEPT11 PE=1 SV=3	6
237	12.0	12.0	15.5	P04844 RPN2_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens GN=RPN2 PE=1 SV=	6
238	12.0	12.0	45.1	P18621 RL17_HUMAN	60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3	6
239	12.0	12.0	13.8	P39656 OST48_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOS	6
240	12.0	12.0	64.3	P30049 ATPD_HUMAN	ATP synthase subunit delta, mitochondrial OS=Homo sapiens GN=ATP5D PE=1 SV=2	7
241	11.9	11.9	41.4	Q9POLO VAPA_HUMAN	Vesicle-associated membrane protein-associated protein A OS=Homo sapiens GN=VAPA PE=1 SV=3	8
242	11.8	13.9	9.2	Q5JWF2 GNAS1_HUMAN	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Homo sapiens GN=GNAS PE=1 SV=2	10
243	11.7	18.0	36.3	P04899 GNAI2_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3	10
244	11.6	11.8	9.2	Q86UP2 KTN1_HUMAN	Kinetin OS=Homo sapiens GN=KTN1 PE=1 SV=1	9
245	11.6	11.7	64.9	Q04837 SSBP_HUMAN	Single-stranded DNA-binding protein, mitochondrial OS=Homo sapiens GN=SSBP1 PE=1 SV=1	8
246	11.6	13.2	21.7	Q9ULV4 COR1C_HUMAN	Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1	11
247	11.6	11.7	13.2	P55072 TERA_HUMAN	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	7
248	11.5	11.7	5.9	Q9NYU2 UGGG1_HUMAN	UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3	8

249	11.5	11.6	78.0	Q9GZT3 SLIRP_HUMAN	SRA stem-loop-interacting RNA-binding protein, mitochondrial OS=Homo sapiens GN=SLIRP PE=1 SV=1	7
250	11.5	11.6	20.6	P49368 TCPG_HUMAN	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4	8
251	11.3	11.5	15.3	P11940 PABP1_HUMAN	Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2	7
252	11.3	11.4	16.6	Q9HD45 TM9S3_HUMAN	Transmembrane 9 superfamily member 3 OS=Homo sapiens GN=TM9SF3 PE=1 SV=2	7
253	11.3	11.3	58.9	Q9BX68 HINT2_HUMAN	Histidine triad nucleotide-binding protein 2, mitochondrial OS=Homo sapiens GN=HINT2 PE=1 SV=1	7
254	11.2	11.4	34.9	Q16698 DECR_HUMAN	2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=1 SV=1	10
255	11.1	11.2	66.7	Q96C01 F136A_HUMAN	Protein FAM136A OS=Homo sapiens GN=FAM136A PE=1 SV=1	9
256	11.1	11.1	37.8	P62906 RL10A_HUMAN	60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	8
257	11.0	11.1	12.1	P51659 DHB4_HUMAN	Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3	6
258	11.0	11.2	11.1	Q15031 SYLM_HUMAN	Probable leucine--tRNA ligase, mitochondrial OS=Homo sapiens GN=LARS2 PE=1 SV=2	7
259	11.0	11.0	8.4	Q14974 IMB1_HUMAN	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	5
260	11.0	11.0	28.9	P43897 EFTS_HUMAN	Elongation factor Ts, mitochondrial OS=Homo sapiens GN=TSFM PE=1 SV=2	6
261	10.9	11.0	26.0	Q9BXW7 CECR5_HUMAN	Cat eye syndrome critical region protein 5 OS=Homo sapiens GN=CECR5 PE=1 SV=1	6
262	10.9	10.9	60.7	P20674 COX5A_HUMAN	Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens GN=COX5A PE=1 SV=2	7
263	10.9	11.0	18.0	P30837 AL1B1_HUMAN	Aldehyde dehydrogenase X, mitochondrial OS=Homo sapiens GN=ALDH1B1 PE=1 SV=3	6
264	10.9	11.0	55.2	P61353 RL27_HUMAN	60S ribosomal protein L27 OS=Homo sapiens GN=RPL27 PE=1 SV=2	6
265	10.8	10.9	37.3	Q99880 H2B1L_HUMAN	Histone H2B type 1-L OS=Homo sapiens GN=HIST1H2BL PE=1 SV=3	6
266	10.7	10.8	15.1	Q9NZI8 IF2B1_HUMAN	Insulin-like growth factor 2 mRNA-binding protein 1 OS=Homo sapiens GN=IGF2BP1 PE=1 SV=2	6
267	10.7	10.8	39.1	P61019 RAB2A_HUMAN	Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1	6
268	10.7	10.8	29.5	P40083 ANXA1_HUMAN	Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	6
269	10.6	10.7	13.3	Q15758 AAAT_HUMAN	Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5 PE=1 SV=2	6
270	10.6	10.6	49.2	P08574 CY1_HUMAN	Cytochrome c1, heme protein, mitochondrial OS=Homo sapiens GN=CYC1 PE=1 SV=3	9
271	10.6	10.6	13.0	P11166 GTR1_HUMAN	Solute carrier family 2, facilitated glucose transporter member 1 OS=Homo sapiens GN=SLC2A1 PE=1 SV=2	6
272	10.5	10.6	25.5	P62826 RAN_HUMAN	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3	6
273	10.5	10.6	37.3	Q9Y6C9 MTCH2_HUMAN	Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1	7
274	10.5	10.5	16.3	P78371 TCBP_HUMAN	T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4	9
275	10.4	10.5	27.6	P18669 PGAM1_HUMAN	Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2	5
276	10.4	10.4	31.2	P22626 ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPAB2B1 PE=1 SV=2	6
277	10.4	10.4	25.1	Q9UQ80 PA2G4_HUMAN	Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3	7
278	10.3	10.4	36.8	P62269 RS18_HUMAN	40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	6
279	10.3	10.3	30.7	P63000 RAC1_HUMAN	Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1	6
280	10.3	10.3	57.7	Q6FI13 H2A2A_HUMAN	Histone H2A type 2-A OS=Homo sapiens GN=HIST2H2AA3 PE=1 SV=3	7
281	10.3	18.6	21.5	P13647 K2C5_HUMAN	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	12
282	10.2	10.2	39.8	P19105 ML12A_HUMAN	Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2	5
283	10.2	10.2	28.2	Q9BPW8 NIP51_HUMAN	Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1	6
284	10.2	10.3	40.1	Q9BSH4 TACO1_HUMAN	Translational activator of cytochrome c oxidase 1 OS=Homo sapiens GN=TACO1 PE=1 SV=1	6
285	10.1	10.3	25.7	Q14745 NHRF1_HUMAN	Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Homo sapiens GN=SLC9A3R1 PE=1 SV=4	6
286	10.1	10.2	19.5	P50914 RL14_HUMAN	60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4	7
287	10.1	12.1	13.4	Q8IX11 MIRO2_HUMAN	Mitochondrial Rho GTPase 2 OS=Homo sapiens GN=RHOT2 PE=1 SV=2	6
288	10.0	10.1	36.3	P09429 HMG81_HUMAN	High mobility group protein B1 OS=Homo sapiens GN=HMG81 PE=1 SV=3	5
289	10.0	10.1	23.4	Q9BYD6 RM01_HUMAN	39S ribosomal protein L1, mitochondrial OS=Homo sapiens GN=MRPL1 PE=1 SV=2	6
290	10.0	10.0	35.8	Q9Y6H1 CHCH2_HUMAN	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2 OS=Homo sapiens GN=CHCHD2 PE=1 SV=1	16
291	10.0	10.0	39.0	P62249 RS16_HUMAN	40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2	6
292	10.0	10.1	10.2	Q13423 NNTM_HUMAN	NAD(P) transhydrogenase, mitochondrial OS=Homo sapiens GN=NNT PE=1 SV=3	6
293	9.9	10.0	34.8	P54709 AT1B3_HUMAN	Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens GN=ATP1B3 PE=1 SV=1	7
294	9.9	10.0	11.9	Q96TA2 YME1L1_HUMAN	ATP-dependent zinc metalloprotease YME1L1 OS=Homo sapiens GN=YME1L1 PE=1 SV=2	5
295	9.9	10.0	30.5	Q9NYK5 RM39_HUMAN	39S ribosomal protein L39, mitochondrial OS=Homo sapiens GN=MRPL39 PE=1 SV=3	7
296	9.9	10.0	54.4	P21291 CSR1_HUMAN	Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSR1 PE=1 SV=3	6
297	9.8	9.9	8.0	P50416 CPT1A_HUMAN	Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A PE=1 SV=2	5
298	9.8	9.9	29.1	Q9BRJ2 RM45_HUMAN	39S ribosomal protein L45, mitochondrial OS=Homo sapiens GN=MRPL45 PE=1 SV=2	5
299	9.8	9.9	23.6	P09001 RM03_HUMAN	39S ribosomal protein L3, mitochondrial OS=Homo sapiens GN=MRPL3 PE=1 SV=1	5
300	9.8	9.9	23.5	P15880 RS2_HUMAN	40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2	6
301	9.8	9.9	66.2	Q9NS69 TOM22_HUMAN	Mitochondrial import receptor subunit TOM22 homolog OS=Homo sapiens GN=TOMM22 PE=1 SV=3	9
302	9.7	10.0	17.2	Q8NBX0 SCPD1_HUMAN	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1	6
303	9.7	10.0	26.1	Q7LOY3 MRRP1_HUMAN	Mitochondrial ribonuclease P protein 1 OS=Homo sapiens GN=TRMT10C PE=1 SV=2	8
304	9.7	9.9	25.4	P50395 GDI8_HUMAN	Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2	7
305	9.7	9.9	20.7	Q96CS3 FAF2_HUMAN	FAS-associated factor 2 OS=Homo sapiens GN=FAF2 PE=1 SV=2	6
306	9.6	9.7	10.3	O00116 ADAS_HUMAN	Alkyl-dihydroxyacetonephosphate synthase, peroxisomal OS=Homo sapiens GN=AGPS PE=1 SV=1	5
307	9.6	12.0	16.7	Q16181 SEPT7_HUMAN	Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2	6
308	9.6	9.7	49.2	P25398 RS12_HUMAN	40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	7
309	9.5	9.6	41.7	P27144 KAD4_HUMAN	Adenylate kinase 4, mitochondrial OS=Homo sapiens GN=AK4 PE=1 SV=1	6
310	9.5	9.7	8.2	P23634 AT2B4_HUMAN	Plasma membrane calcium-transporting ATPase 4 OS=Homo sapiens GN=ATP2B4 PE=1 SV=2	7
311	9.4	9.5	23.2	Q9H9J2 RM44_HUMAN	39S ribosomal protein L44, mitochondrial OS=Homo sapiens GN=MRPL44 PE=1 SV=1	6
312	9.4	9.5	24.3	P62701 RS4X_HUMAN	40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	5
313	9.3	9.4	14.0	P13797 PLST_HUMAN	Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4	5
314	9.3	9.3	34.5	P60866 RS20_HUMAN	40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1	5
315	9.2	9.4	19.7	P82650 RT22_HUMAN	28S ribosomal protein S22, mitochondrial OS=Homo sapiens GN=MRPS22 PE=1 SV=1	5
316	9.2	9.3	53.6	Q96EL3 RM53_HUMAN	39S ribosomal protein L53, mitochondrial OS=Homo sapiens GN=MRPL53 PE=1 SV=1	7
317	9.2	9.3	11.1	Q9H845 ACAD9_HUMAN	Acyl-CoA dehydrogenase family member 9, mitochondrial OS=Homo sapiens GN=ACAD9 PE=1 SV=1	5
318	9.2	9.3	23.5	P61313 RL15_HUMAN	60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2	5
319	9.2	9.3	12.6	Q9NQC3 RTN4_HUMAN	Reticulon-4 OS=Homo sapiens GN=RTN4 PE=1 SV=2	7
320	9.1	9.2	13.2	Q9NZW5 MPP6_HUMAN	MAGUK p55 subfamily member 6 OS=Homo sapiens GN=MPP6 PE=1 SV=2	7
321	9.1	9.2	25.3	Q96DV4 RM38_HUMAN	39S ribosomal protein L38, mitochondrial OS=Homo sapiens GN=MRPL38 PE=1 SV=2	7
322	9.1	9.2	13.2	Q9Y2D5 AKAP2_HUMAN	A-kinase anchor protein 2 OS=Homo sapiens GN=AKAP2 PE=1 SV=3	5
323	9.0	9.1	48.6	P09211 GSTP1_HUMAN	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2	7
324	9.0	9.0	47.8	Q86SX6 GLRX5_HUMAN	Glutaredoxin-related protein 5, mitochondrial OS=Homo sapiens GN=GLRX5 PE=1 SV=2	6
325	8.9	9.0	25.3	Q9BYD1 RM13_HUMAN	39S ribosomal protein L13, mitochondrial OS=Homo sapiens GN=MRPL13 PE=1 SV=1	7
326	8.9	9.0	34.0	P50897 PPT1_HUMAN	Palmitoyl-protein thioesterase 1 OS=Homo sapiens GN=PPT1 PE=1 SV=1	7
327	8.9	9.0	18.7	Q96ER9 CCD51_HUMAN	Coiled-coil domain-containing protein 51 OS=Homo sapiens GN=CCDC51 PE=1 SV=2	5
328	8.9	9.0	10.9	Q9H223 EHD4_HUMAN	EH domain-containing protein 4 OS=Homo sapiens GN=EHD4 PE=1 SV=1	6
329	8.8	8.9	12.2	O95202 LETM1_HUMAN	LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=Homo sapiens GN=LETM1 PE=1 SV=1	6
330	8.8	8.9	21.9	O00151 PDLIM1_HUMAN	PDZ and LIM domain protein 1 OS=Homo sapiens GN=PDLIM1 PE=1 SV=4	5
331	8.7	8.8	48.8	P67809 YBOX1_HUMAN	Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3	5
332	8.7	8.9	23.3	P62136 PP1A_HUMAN	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1	7

333	8.6	9.2	20.9	P07858 CATB_HUMAN	Cathepsin B OS=Homo sapiens GN=CTSB PE=1 SV=3	5
334	8.6	8.7	29.9	P83731 RL24_HUMAN	60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1	7
335	8.6	8.7	25.8	P24539 AT5F1_HUMAN	ATP synthase F(0) complex subunit B1, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2	6
336	8.6	8.6	27.1	P47756 CAPZB_HUMAN	F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4	5
337	8.5	8.6	46.7	P09382 LEG1_HUMAN	Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2	5
338	8.5	8.5	12.4	Q9HCC0 MCCB_HUMAN	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCCB PE=1 SV=1	5
339	8.5	8.6	23.9	Q07020 RL18_HUMAN	60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2	5
340	8.4	9.1	22.1	P12277 KCRB_HUMAN	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1	5
341	8.4	8.6	18.2	Q9Y676 RT18B_HUMAN	28S ribosomal protein S18b, mitochondrial OS=Homo sapiens GN=MRPS18B PE=1 SV=1	6
342	8.4	8.6	9.1	Q9H078 CLPB_HUMAN	Caseinolytic peptidase B protein homolog OS=Homo sapiens GN=CLPB PE=1 SV=1	5
343	8.3	12.5	38.4	Q96C36 P5CR2_HUMAN	Pyrroline-5-carboxylate reductase 2 OS=Homo sapiens GN=PYCR2 PE=1 SV=1	9
344	8.3	8.3	22.6	P18124 RL7_HUMAN	60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1	5
345	8.2	8.3	15.4	Q9BZE1 RM37_HUMAN	39S ribosomal protein L37, mitochondrial OS=Homo sapiens GN=MRPL37 PE=1 SV=2	5
346	8.2	8.3	27.9	Q5T653 RM02_HUMAN	39S ribosomal protein L2, mitochondrial OS=Homo sapiens GN=MRPL2 PE=1 SV=2	5
347	8.2	8.2	38.6	Q13405 RM49_HUMAN	39S ribosomal protein L49, mitochondrial OS=Homo sapiens GN=MRPL49 PE=1 SV=1	5
348	8.1	8.2	14.0	P61978 HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPKE PE=1 SV=1	5
349	8.1	8.2	33.1	P62917 RL8_HUMAN	60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2	4
350	8.1	8.1	30.2	O96000 NDUBA_HUMAN	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 OS=Homo sapiens GN=NDUFB10 PE=1 SV=1	4
351	8.1	8.1	17.5	P10316 1A69_HUMAN	HLA class I histocompatibility antigen, A-69 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=2	5
352	8.0	8.0	21.6	O75880 SCO1_HUMAN	Protein SCO1 homolog, mitochondrial OS=Homo sapiens GN=SCO1 PE=1 SV=1	4
353	8.0	8.0	57.7	P60903 S10AA_HUMAN	Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2	4
354	8.0	9.3	32.5	P31946 1433B_HUMAN	14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3	5
355	8.0	8.3	23.9	Q12907 LMAN2_HUMAN	Vesicular integral-membrane protein VIP36 OS=Homo sapiens GN=LMAN2 PE=1 SV=1	4
356	8.0	8.0	28.5	Q9Y696 CLIC4_HUMAN	Chloride intracellular channel protein 4 OS=Homo sapiens GN=CLIC4 PE=1 SV=4	5
357	8.0	8.0	15.1	Q9NR28 DBLOH_HUMAN	Diablo homolog, mitochondrial OS=Homo sapiens GN=DIABLO PE=1 SV=1	6
358	8.0	8.0	75.6	P14854 CX6B1_HUMAN	Cytochrome c oxidase subunit 6B1 OS=Homo sapiens GN=COX6B1 PE=1 SV=2	5
359	8.0	8.0	84.2	P05386 RLA1_HUMAN	60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1	4
360	8.0	8.0	53.7	Q9Y5L4 TIM13_HUMAN	Mitochondrial import inner membrane translocase subunit Tim13 OS=Homo sapiens GN=TIMM13 PE=1 SV=1	6
361	8.0	8.0	85.7	Q14061 COX17_HUMAN	Cytochrome c oxidase copper chaperone OS=Homo sapiens GN=COX17 PE=1 SV=2	4
362	8.0	8.0	25.2	P27635 RL10_HUMAN	60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4	5
363	8.0	8.0	37.5	P22392 NDKB_HUMAN	Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1	5
364	7.9	8.1	5.7	O95782 AP2A1_HUMAN	AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3	5
365	7.9	8.0	15.3	P02768 ALBU_HUMAN	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	15
366	7.9	8.0	14.3	Q96HE7 ERO1A_HUMAN	ERO1-like protein alpha OS=Homo sapiens GN=ERO1A PE=1 SV=2	5
367	7.9	7.9	21.3	O75323 NIPS2_HUMAN	Protein NipSnap homolog 2 OS=Homo sapiens GN=GBAS PE=1 SV=1	4
368	7.9	8.0	50.9	P30050 RL12_HUMAN	60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1	6
369	7.8	7.9	9.9	Q96AC1 FERM2_HUMAN	Fermitin family homolog 2 OS=Homo sapiens GN=FERMT2 PE=1 SV=1	4
370	7.8	10.1	27.4	P20340 RAB6A_HUMAN	Ras-related protein Rab-6A OS=Homo sapiens GN=RAB6A PE=1 SV=3	6
371	7.8	7.9	19.9	P11233 RALA_HUMAN	Ras-related protein Ral-A OS=Homo sapiens GN=RALA PE=1 SV=1	7
372	7.8	7.9	18.9	Q9H936 GHC1_HUMAN	Mitochondrial glutamate carrier 1 OS=Homo sapiens GN=SLC25A22 PE=1 SV=1	4
373	7.8	7.8	11.8	P38606 VATA_HUMAN	V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2	5
374	7.8	7.8	51.5	O75964 ATP5L_HUMAN	ATP synthase subunit g, mitochondrial OS=Homo sapiens GN=ATP5L PE=1 SV=3	6
375	7.7	7.8	37.2	Q6P1L8 RM14_HUMAN	39S ribosomal protein L14, mitochondrial OS=Homo sapiens GN=MRPL14 PE=1 SV=1	5
376	7.7	7.8	55.9	P49006 MRP_HUMAN	MARCKS-related protein OS=Homo sapiens GN=MARCKSL1 PE=1 SV=2	9
377	7.7	7.8	15.2	Q13283 G3BP1_HUMAN	Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1	5
378	7.7	7.8	26.5	P62263 RS14_HUMAN	40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3	5
379	7.7	7.7	9.9	Q9P2R7 SUCB1_HUMAN	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLA2 PE=1 SV=3	5
380	7.6	7.7	20.1	O75489 NDUS3_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Homo sapiens GN=NDUFS3 PE=1	4
381	7.6	7.7	17.7	P32969 RL9_HUMAN	60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1	5
382	7.6	7.6	51.3	P62888 RL30_HUMAN	60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2	5
383	7.5	7.6	9.9	P50990 TCPQ_HUMAN	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4	5
384	7.5	7.7	17.3	Q01518 CAP1_HUMAN	Adenyllyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=5	5
385	7.5	7.6	12.7	P31943 HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNP1 PE=1 SV=4	5
386	7.4	7.6	15.1	Q9BR76 COR1B_HUMAN	Coronin-1B OS=Homo sapiens GN=CORO1B PE=1 SV=1	4
387	7.4	7.6	27.7	O00264 PGRMC1_HUMAN	Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=1 SV=3	5
388	7.4	7.5	34.4	Q96A26 F162A_HUMAN	Protein FAM162A OS=Homo sapiens GN=FAM162A PE=1 SV=2	5
389	7.4	7.7	15.3	P50213 IDH3A_HUMAN	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Homo sapiens GN=IDH3A PE=1 SV=1	4
390	7.4	7.5	12.6	Q9Y512 SAM50_HUMAN	Sorting and assembly machinery component 50 homolog OS=Homo sapiens GN=SAMM50 PE=1 SV=3	5
391	7.4	7.5	22.9	Q9Y5M8 SRPRB_HUMAN	Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3	5
392	7.4	7.4	14.9	O43852 CALU_HUMAN	Calumenin OS=Homo sapiens GN=CALU PE=1 SV=2	4
393	7.3	7.5	24.6	P21912 SDHB_HUMAN	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Homo sapiens GN=SDHB PE=1	6
394	7.3	7.4	26.7	O95881 TXD12_HUMAN	Thioredoxin domain-containing protein 12 OS=Homo sapiens GN=TXNDC12 PE=1 SV=1	5
395	7.2	7.3	12.7	P23368 MAOM_HUMAN	NAD-dependent malic enzyme, mitochondrial OS=Homo sapiens GN=ME2 PE=1 SV=1	7
396	7.1	8.5	27.3	P27348 14337_HUMAN	14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1	5
397	7.1	7.9	10.4	Q13308 PTK7_HUMAN	Inactive tyrosine-protein kinase 7 OS=Homo sapiens GN=PTK7 PE=1 SV=2	6
398	7.0	7.1	21.7	O95299 NDUAA_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Homo sapiens GN=ND	5
399	6.9	7.1	55.7	P62158 CALM_HUMAN	Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2	8
400	6.9	7.1	33.0	P07203 GPX1_HUMAN	Glutathione peroxidase 1 OS=Homo sapiens GN=GPX1 PE=1 SV=4	4
401	6.9	7.0	24.3	O95292 VAPB_HUMAN	Vesicle-associated membrane protein-associated protein B/C OS=Homo sapiens GN=VAPB PE=1 SV=3	5
402	6.9	6.9	15.9	P40925 MDHC_HUMAN	Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4	4
403	6.9	6.9	36.9	P30042 ES1_HUMAN	ES1 protein homolog, mitochondrial OS=Homo sapiens GN=C21orf33 PE=1 SV=3	4
404	6.8	7.0	10.3	Q96920 TBGR4_HUMAN	Protein TBGR4 OS=Homo sapiens GN=TBGR4 PE=1 SV=1	6
405	6.8	6.9	8.2	P00390 GSHR_HUMAN	Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR PE=1 SV=2	4
406	6.8	7.0	59.1	P00441 SODC_HUMAN	Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2	4
407	6.8	6.9	11.7	P49189 AL9A1_HUMAN	4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3	4
408	6.8	6.9	4.7	P19022 CADH2_HUMAN	Cadherin-2 OS=Homo sapiens GN=CDH2 PE=1 SV=4	4
409	6.8	7.0	22.8	Q96CW1 AP2M1_HUMAN	AP-2 complex subunit mu OS=Homo sapiens GN=AP2M1 PE=1 SV=2	6
410	6.7	6.8	36.8	P09936 UCHL1_HUMAN	Ubiquitin carboxyl-terminal hydrolase isozyme L1 OS=Homo sapiens GN=UCHL1 PE=1 SV=2	6
411	6.7	6.8	6.0	O76031 CLPX_HUMAN	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial OS=Homo sapiens GN=CLPX PE=1	3
412	6.7	6.8	14.6	Q9Y617 SERC_HUMAN	Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2	4
413	6.7	6.8	12.0	P23526 SAHH_HUMAN	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4	5
414	6.7	6.8	11.6	Q9NP81 SYSM_HUMAN	Serine--tRNA ligase, mitochondrial OS=Homo sapiens GN=SARS2 PE=1 SV=1	4
415	6.6	6.7	16.9	P13693 TCTP_HUMAN	Translationally-controlled tumor protein OS=Homo sapiens GN=TPT1 PE=1 SV=1	3
416	6.6	6.7	36.9	P62244 RS15A_HUMAN	40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=2	4

417	6.6	6.8	10.1	P13674 P4HA1_HUMAN	Prolyl 4-hydroxylase subunit alpha-1 OS=Homo sapiens GN=P4HA1 PE=1 SV=2	4
418	6.6	6.8	28.9	P62750 RL23A_HUMAN	60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	6
419	6.6	6.7	30.4	P46776 RL27A_HUMAN	60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2	4
420	6.5	6.6	26.5	O75396 SEC22B_HUMAN	Vesicle-trafficking protein SEC22b OS=Homo sapiens GN=SEC22B PE=1 SV=4	3
421	6.5	6.5	41.4	Q96DA6 TIM14_HUMAN	Mitochondrial import inner membrane translocase subunit TIM14 OS=Homo sapiens GN=DNAJC19 PE=1 SV=1	3
422	6.5	6.5	44.4	P08708 RS17_HUMAN	40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2	3
423	6.5	6.6	31.0	P47985 UCR1_HUMAN	Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Homo sapiens GN=UQCRCF1 PE=1 SV=2	6
424	6.4	6.5	14.8	Q16762 THTR_HUMAN	Thiosulfate sulfurtransferase OS=Homo sapiens GN=TST PE=1 SV=4	4
425	6.4	18.0	40.7	P67936 TPM4_HUMAN	Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3	13
426	6.4	6.5	37.9	P55145 MANF_HUMAN	Mesencephalic astrocyte-derived neurotrophic factor OS=Homo sapiens GN=MANF PE=1 SV=3	4
427	6.4	6.8	6.8	O75534 CSDE1_HUMAN	Cold shock domain-containing protein E1 OS=Homo sapiens GN=CSDE1 PE=1 SV=2	6
428	6.4	6.4	32.2	P62072 TIM10_HUMAN	Mitochondrial import inner membrane translocase subunit Tim10 OS=Homo sapiens GN=TIMM10 PE=1 SV=1	3
429	6.4	6.5	11.2	P49821 NDUV1_HUMAN	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=Homo sapiens GN=NDUVF1 PE=1 SV=4	4
430	6.4	6.5	18.1	Q96A35 RM24_HUMAN	39S ribosomal protein L24, mitochondrial OS=Homo sapiens GN=MRPL24 PE=1 SV=1	3
431	6.4	6.4	41.2	P62081 RS7_HUMAN	40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1	4
432	6.3	6.4	12.5	Q3ZCQ8 TIM50_HUMAN	Mitochondrial import inner membrane translocase subunit TIM50 OS=Homo sapiens GN=TIMM50 PE=1 SV=2	5
433	6.3	6.5	44.6	Q9Y2R5 RT17_HUMAN	28S ribosomal protein S17, mitochondrial OS=Homo sapiens GN=MRPS17 PE=1 SV=1	3
434	6.3	6.4	22.5	P62913 RL11_HUMAN	60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2	4
435	6.3	6.3	11.7	O75521 ECI2_HUMAN	Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4	3
436	6.3	6.4	20.2	Q15907 RB11B_HUMAN	Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1 SV=4	4
437	6.3	6.3	30.5	Q9H2W6 RM46_HUMAN	39S ribosomal protein L46, mitochondrial OS=Homo sapiens GN=MRPL46 PE=1 SV=1	5
438	6.3	6.3	13.5	P51553 IDH3G_HUMAN	Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial OS=Homo sapiens GN=IDH3G PE=1 SV=1	3
439	6.3	6.3	12.0	Q96EY7 PTCD3_HUMAN	Pentatricopeptide repeat domain-containing protein 3, mitochondrial OS=Homo sapiens GN=PTCD3 PE=1 SV=1	5
440	6.2	6.2	5.6	Q92896 GSLG1_HUMAN	Golgi apparatus protein 1 OS=Homo sapiens GN=GSLG1 PE=1 SV=2	4
441	6.2	6.2	17.2	P42126 ECI1_HUMAN	Enoyl-CoA delta isomerase 1, mitochondrial OS=Homo sapiens GN=ECI1 PE=1 SV=1	3
442	6.2	6.2	10.8	Q15043 S39AE_HUMAN	Zinc transporter ZIP14 OS=Homo sapiens GN=SLC39A14 PE=1 SV=3	3
443	6.2	6.2	22.8	Q9NWU5 RM22_HUMAN	39S ribosomal protein L22, mitochondrial OS=Homo sapiens GN=MRPL22 PE=1 SV=1	3
444	6.1	10.3	21.9	Q9BWM7 SFXN3_HUMAN	Sideroflexin-3 OS=Homo sapiens GN=SFXN3 PE=1 SV=2	5
445	6.1	6.4	9.1	Q9H9P8 L2HDH_HUMAN	L-2-hydroxyglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=L2HGDH PE=1 SV=3	3
446	6.1	6.3	34.6	Q7Z2W9 RM21_HUMAN	39S ribosomal protein L21, mitochondrial OS=Homo sapiens GN=MRPL21 PE=1 SV=2	5
447	6.1	6.1	21.6	Q5JTJ3 COA6_HUMAN	Cytochrome c oxidase assembly factor 6 homolog OS=Homo sapiens GN=COA6 PE=1 SV=1	4
448	6.1	6.1	41.4	Q5U5X0 LYRM7_HUMAN	Complex III assembly factor LYRM7 OS=Homo sapiens GN=LYRM7 PE=1 SV=1	4
449	6.1	6.2	7.7	Q05682 CALD1_HUMAN	Caldesmon OS=Homo sapiens GN=CALD1 PE=1 SV=3	4
450	6.1	6.1	3.9	Q8NCN5 PDPR_HUMAN	Pyruvate dehydrogenase phosphatase regulatory subunit, mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=1	3
451	6.1	6.1	22.4	P49755 TMEDA_HUMAN	Transmembrane emp24 domain-containing protein 10 OS=Homo sapiens GN=TMED10 PE=1 SV=2	3
452	6.1	6.1	44.6	P63220 RS21_HUMAN	40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1	3
453	6.1	6.2	17.5	O00161 SNP23_HUMAN	Synaptosomal-associated protein 23 OS=Homo sapiens GN=SNAP23 PE=1 SV=1	3
454	6.1	6.1	28.9	O60220 TIM8A_HUMAN	Mitochondrial import inner membrane translocase subunit Tim8 A OS=Homo sapiens GN=TIMM8A PE=1 SV=1	3
455	6.1	6.1	13.7	P05198 IF2A_HUMAN	Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF251 PE=1 SV=3	3
456	6.1	6.1	24.4	P04792 HSPB1_HUMAN	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	4
457	6.0	6.1	11.2	P49257 LMAN1_HUMAN	Protein ERGIC-53 OS=Homo sapiens GN=LMAN1 PE=1 SV=2	4
458	6.0	6.1	24.9	P60981 DEST_HUMAN	Dextrin OS=Homo sapiens GN=DSTN PE=1 SV=3	3
459	6.0	6.0	34.8	P62910 RL32_HUMAN	60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2	3
460	6.0	6.0	12.2	Q13011 ECH1_HUMAN	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Homo sapiens GN=ECH1 PE=1 SV=2	3
461	6.0	6.0	10.7	P12268 IMDH2_HUMAN	Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2	3
462	6.0	8.0	9.7	O00425 IF2B3_HUMAN	Insulin-like growth factor 2 mRNA-binding protein 3 OS=Homo sapiens GN=IGF2BP3 PE=1 SV=2	4
463	6.0	6.0	12.0	P55209 NP1L1_HUMAN	Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1	4
464	6.0	6.0	10.3	Q6YN16 HSDL2_HUMAN	Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1	3
465	6.0	6.0	8.4	Q13740 CD166_HUMAN	CD166 antigen OS=Homo sapiens GN=ALCAM PE=1 SV=2	3
466	6.0	6.1	18.8	P17931 LEG3_HUMAN	Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5	5
467	6.0	6.0	35.6	P62633 CNBP_HUMAN	Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP PE=1 SV=1	3
468	6.0	6.0	15.0	P52907 CAZA1_HUMAN	F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3	3
469	6.0	6.0	5.8	P22102 PUR2_HUMAN	Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1	4
470	6.0	6.0	15.6	Q9HD33 RM47_HUMAN	39S ribosomal protein L47, mitochondrial OS=Homo sapiens GN=MRPL47 PE=1 SV=2	3
471	6.0	6.0	8.7	Q14103 HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1	3
472	6.0	6.0	18.6	P78540 ARGI2_HUMAN	Arginase-2, mitochondrial OS=Homo sapiens GN=ARG2 PE=1 SV=1	5
473	6.0	6.0	18.1	P62847 RS24_HUMAN	40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=1 SV=1	3
474	6.0	6.0	36.2	P56385 ATP5I_HUMAN	ATP synthase subunit e, mitochondrial OS=Homo sapiens GN=ATP5I PE=1 SV=2	3
475	6.0	6.0	41.1	P17096 HMG1_HUMAN	High mobility group protein HMG-I/HMG-Y OS=Homo sapiens GN=HMG1 PE=1 SV=3	3
476	6.0	6.0	46.8	O75380 NDUS6_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial OS=Homo sapiens GN=NDUFS6 PE=1 SV=1	3
477	6.0	6.0	3.8	Q02241 KIF23_HUMAN	Kinesin-like protein KIF23 OS=Homo sapiens GN=KIF23 PE=1 SV=3	3
478	6.0	6.1	15.7	Q8NC51 PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	3
479	6.0	6.0	42.6	P56134 ATPK_HUMAN	ATP synthase subunit f, mitochondrial OS=Homo sapiens GN=ATP5J2 PE=1 SV=3	3
480	5.9	6.0	32.8	P13987 CD59_HUMAN	CD59 glycoprotein OS=Homo sapiens GN=CD59 PE=1 SV=1	4
481	5.9	6.3	20.4	Q9NX40 OCAD1_HUMAN	OCIA domain-containing protein 1 OS=Homo sapiens GN=OCAD1 PE=1 SV=1	4
482	5.9	6.2	10.5	P49590 SYHM_HUMAN	Probable histidine--tRNA ligase, mitochondrial OS=Homo sapiens GN=HARS2 PE=1 SV=1	5
483	5.9	6.0	12.0	Q9Y2S7 PDIP2_HUMAN	Polymerase delta-interacting protein 2 OS=Homo sapiens GN=POLDIP2 PE=1 SV=1	3
484	5.9	6.0	39.8	P35268 RL22_HUMAN	60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2	3
485	5.8	6.0	11.8	Q13409 DC1I2_HUMAN	Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=1 SV=3	3
486	5.8	5.9	16.8	P50454 SERPH_HUMAN	Serpin H1 OS=Homo sapiens GN=SERP1H1 PE=1 SV=2	4
487	5.8	6.0	5.7	P29317 EPA2_HUMAN	Ephrin type-A receptor 2 OS=Homo sapiens GN=EPA2 PE=1 SV=2	5
488	5.8	5.8	18.5	Q969H8 MYDGF_HUMAN	Myeloid-derived growth factor OS=Homo sapiens GN=MYDGF PE=1 SV=1	3
489	5.7	6.0	8.0	Q00839 HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	4
490	5.7	5.8	16.9	Q9Y2R9 RT07_HUMAN	28S ribosomal protein S7, mitochondrial OS=Homo sapiens GN=MRPS7 PE=1 SV=2	3
491	5.7	5.7	30.8	P62979 RS27A_HUMAN	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2	3
492	5.7	5.7	5.2	P55884 EIF3B_HUMAN	Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3	3
493	5.6	5.8	12.6	P17987 TCPA_HUMAN	T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1	5
494	5.6	5.9	29.1	Q9NUJ1 ABHDA_HUMAN	Mycophenolic acid acyl-glucuronide esterase, mitochondrial OS=Homo sapiens GN=ABHD10 PE=1 SV=1	5
495	5.6	5.8	28.0	Q14847 LASP1_HUMAN	LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1 PE=1 SV=2	6
496	5.5	5.6	9.6	Q92947 GCDH_HUMAN	Glutaryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=GCDH PE=1 SV=1	3
497	5.5	5.6	14.7	P26440 IVD_HUMAN	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=IVD PE=1 SV=1	4
498	5.5	5.6	20.3	Q9POM9 RM27_HUMAN	39S ribosomal protein L27, mitochondrial OS=Homo sapiens GN=MRPL27 PE=1 SV=1	3
499	5.5	5.8	5.3	O95140 MFN2_HUMAN	Mitofusin-2 OS=Homo sapiens GN=MFN2 PE=1 SV=3	4
500	5.4	5.6	13.1	Q6P4A7 SFXN4_HUMAN	Sideroflexin-4 OS=Homo sapiens GN=SFXN4 PE=1 SV=1	4

501	5.4	5.5	43.4	Q71DI3 H32_HUMAN	Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3	4
502	5.4	5.4	22.8	P42766 RL35_HUMAN	60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2	3
503	5.3	5.4	20.4	P24534 EF1B_HUMAN	Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3	3
504	5.3	13.0	55.6	P62820 RAB1A_HUMAN	Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3	8
505	5.3	5.4	34.9	P51970 NDUA8_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 OS=Homo sapiens GN=NDUFA8 PE=1 SV=3	3
506	5.3	5.4	60.9	P62857 RS28_HUMAN	40S ribosomal protein S28 OS=Homo sapiens GN=RPS28 PE=1 SV=1	3
507	5.3	6.5	6.5	O95819 M4K4_HUMAN	Mitogen-activated protein kinase kinase kinase 4 OS=Homo sapiens GN=MAP4K4 PE=1 SV=2	6
508	5.3	5.4	40.9	P05387 RLA2_HUMAN	60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1	3
509	5.3	5.4	18.8	QZ72H8 RM10_HUMAN	39S ribosomal protein L10, mitochondrial OS=Homo sapiens GN=MRPL10 PE=1 SV=3	5
510	5.3	5.3	21.9	Q9Y3U8 RL36_HUMAN	60S ribosomal protein L36 OS=Homo sapiens GN=RPL36 PE=1 SV=3	3
511	5.2	5.3	21.2	P62277 RS13_HUMAN	40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2	3
512	5.2	5.4	22.2	P30040 ERP29_HUMAN	Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=1 SV=4	4
513	5.2	5.3	7.1	O14672 ADA10_HUMAN	Disintegrin and metalloproteinase domain-containing protein 10 OS=Homo sapiens GN=ADAM10 PE=1 SV=1	3
514	5.2	5.4	22.1	P62280 RS11_HUMAN	40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3	3
515	5.2	5.3	46.4	P62829 RL23_HUMAN	60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1	4
516	5.2	9.4	24.4	Q15366 PCBP2_HUMAN	Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1	5
517	5.1	5.2	34.2	O14880 MGST3_HUMAN	Microsomal glutathione S-transferase 3 OS=Homo sapiens GN=MGST3 PE=1 SV=1	6
518	5.1	5.2	11.2	P05091 ALDH2_HUMAN	Aldehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH2 PE=1 SV=2	4
519	5.1	5.2	4.5	P27816 MAP4_HUMAN	Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3	3
520	5.1	5.3	10.6	P06744 G6PI_HUMAN	Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4	3
521	5.1	5.1	42.6	Q9N245 CISD1_HUMAN	CDGSH iron-sulfur domain-containing protein 1 OS=Homo sapiens GN=CISD1 PE=1 SV=1	3
522	5.0	5.1	20.7	P00403 COX2_HUMAN	Cytochrome c oxidase subunit 2 OS=Homo sapiens GN=MT-CO2 PE=1 SV=1	3
523	5.0	5.2	10.7	Q14444 CAPR1_HUMAN	Caprin-1 OS=Homo sapiens GN=CAPRIN1 PE=1 SV=2	4
524	5.0	7.4	31.2	P61106 RAB14_HUMAN	Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4	4
525	5.0	5.7	27.6	P39019 RS19_HUMAN	40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2	4
526	5.0	5.2	11.7	O75083 WDR1_HUMAN	WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4	4
527	5.0	5.2	81.6	Q9NVJ1 COA4_HUMAN	Cytochrome c oxidase assembly factor 4 homolog, mitochondrial OS=Homo sapiens GN=COA4 PE=1 SV=2	5
528	5.0	5.1	21.7	Q15785 TOM34_HUMAN	Mitochondrial import receptor subunit TOM34 OS=Homo sapiens GN=TOMM34 PE=1 SV=2	4
529	4.9	5.2	7.7	Q6L8Q7 PDE12_HUMAN	2',5'-phosphodiesterase 12 OS=Homo sapiens GN=PDE12 PE=1 SV=2	4
530	4.9	5.0	8.1	Q9Y3I0 RTCB_HUMAN	tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=RTCB PE=1 SV=1	3
531	4.9	5.0	16.0	Q6UXV4 MIC27_HUMAN	MICOS complex subunit MIC27 OS=Homo sapiens GN=APOOL PE=1 SV=1	3
532	4.9	5.0	38.1	P31949 S10A8_HUMAN	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2	3
533	4.9	5.3	8.7	P40227 TCPZ_HUMAN	T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3	3
534	4.9	5.0	21.5	Q9BYD3 RM04_HUMAN	39S ribosomal protein L4, mitochondrial OS=Homo sapiens GN=MRPL4 PE=1 SV=1	4
535	4.8	5.1	21.2	P40429 RL13A_HUMAN	60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2	4
536	4.8	5.0	20.7	P51572 BAP31_HUMAN	B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31 PE=1 SV=3	3
537	4.8	4.9	8.3	P41091 IF2G_HUMAN	Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF253 PE=1 SV=3	3
538	4.8	4.9	11.8	O00165 HAX1_HUMAN	HCLS1-associated protein X-1 OS=Homo sapiens GN=HAX1 PE=1 SV=2	3
539	4.8	4.8	36.1	O75347 TBCA_HUMAN	Tubulin-specific chaperone A OS=Homo sapiens GN=TBCA PE=1 SV=3	3
540	4.8	4.9	14.6	P51991 ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2	3
541	4.7	4.8	31.7	Q8N5N7 RM50_HUMAN	39S ribosomal protein L50, mitochondrial OS=Homo sapiens GN=MRPL50 PE=1 SV=2	3
542	4.7	4.8	5.3	Q92667 AKAP1_HUMAN	A-kinase anchor protein 1, mitochondrial OS=Homo sapiens GN=AKAP1 PE=1 SV=1	3
543	4.7	4.8	7.4	P49757 NUMB_HUMAN	Protein numb homolog OS=Homo sapiens GN=NUMB PE=1 SV=2	3
544	4.7	4.8	9.6	P21281 VATB2_HUMAN	V-type proton ATPase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3	3
545	4.7	4.8	33.9	P62854 RS26_HUMAN	40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3	3
546	4.7	4.8	9.3	Q16850 CP51A_HUMAN	Lanosterol 14-alpha demethylase OS=Homo sapiens GN=CYP51A1 PE=1 SV=3	3
547	4.7	4.8	8.3	Q15599 NHRF2_HUMAN	Na(+)/H(+) exchange regulatory cofactor NHE-RF2 OS=Homo sapiens GN=SLC9A3R2 PE=1 SV=2	2
548	4.7	8.8	23.2	Q9HAV0 GBB4_HUMAN	Guanine nucleotide-binding protein subunit beta-4 OS=Homo sapiens GN=GNB4 PE=1 SV=3	6
549	4.6	4.7	15.2	Q5SRD1 TI23B_HUMAN	Putative mitochondrial import inner membrane translocase subunit Tim23B OS=Homo sapiens GN=TIMM23E	2
550	4.6	4.7	18.4	P82932 RT06_HUMAN	28S ribosomal protein S6, mitochondrial OS=Homo sapiens GN=MRPS6 PE=1 SV=3	2
551	4.6	4.7	18.5	Q99497 PARK7_HUMAN	Protein deglycase DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2	3
552	4.6	4.6	8.8	Q658P3 STEAP3_HUMAN	Metalloreductase STEAP3 OS=Homo sapiens GN=STEAP3 PE=1 SV=2	3
553	4.6	4.6	8.6	Q5T749 KPRP_HUMAN	Keratinocyte proline-rich protein OS=Homo sapiens GN=KPRP PE=1 SV=1	3
554	4.6	4.9	9.3	P26639 SYTC_HUMAN	Threonine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3	4
555	4.6	4.9	4.2	P10515 ODP2_HUMAN	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondria	3
556	4.5	4.6	0.7	P46939 UTRO_HUMAN	Utrrophin OS=Homo sapiens GN=UTRN PE=1 SV=2	2
557	4.5	4.8	33.0	P84095 RHOG_HUMAN	Rho-related GTP-binding protein RhoG OS=Homo sapiens GN=RHOG PE=1 SV=1	5
558	4.5	4.6	10.6	P78406 RAE1L_HUMAN	mRNA export factor OS=Homo sapiens GN=RAE1 PE=1 SV=1	3
559	4.5	4.5	32.4	Q8WYQ3 CHC10_HUMAN	Coiled-coil-helix-coiled-coil-helix domain-containing protein 10, mitochondrial OS=Homo sapiens GN=CHCHD	4
560	4.5	4.6	5.7	P48643 TCPE_HUMAN	T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1	3
561	4.5	4.5	16.7	P28799 GRN_HUMAN	Granulins OS=Homo sapiens GN=GRN PE=1 SV=2	4
562	4.4	33.9	45.0	P68363 TBA1B_HUMAN	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1	21
563	4.4	4.6	0.7	Q9UPN3 MACF1_HUMAN	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 OS=Homo sapiens GN=MACF1 PE=1 SV=4	4
564	4.4	4.6	4.1	Q99613 EIF3C_HUMAN	Eukaryotic translation initiation factor 3 subunit C OS=Homo sapiens GN=EIF3C PE=1 SV=1	3
565	4.4	4.5	17.6	Q9NUQ9 FA49B_HUMAN	Protein FAM49B OS=Homo sapiens GN=FAM49B PE=1 SV=1	3
566	4.4	4.5	16.5	Q02543 RL18A_HUMAN	60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2	2
567	4.4	6.2	16.4	Q9NR12 PDLI7_HUMAN	PDZ and LIM domain protein 7 OS=Homo sapiens GN=PDLIM7 PE=1 SV=1	6
568	4.4	4.5	11.0	Q5RI15 COX20_HUMAN	Cytochrome c oxidase protein 20 homolog OS=Homo sapiens GN=COX20 PE=1 SV=2	2
569	4.4	4.5	3.1	P30530 UFO_HUMAN	Tyrosine-protein kinase receptor UFO OS=Homo sapiens GN=AXL PE=1 SV=3	2
570	4.3	4.4	4.9	O00410 IPO5_HUMAN	Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4	4
571	4.3	4.6	19.3	Q9Y387 RM11_HUMAN	39S ribosomal protein L11, mitochondrial OS=Homo sapiens GN=MRPL11 PE=1 SV=1	3
572	4.3	4.4	6.3	O75306 NDUS2_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial OS=Homo sapiens GN=NDUFS2 PE=1	2
573	4.3	8.4	11.0	O95573 ACSL3_HUMAN	Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3	5
574	4.3	4.5	11.6	P04040 CATA_HUMAN	Catalase OS=Homo sapiens GN=CAT PE=1 SV=3	3
575	4.3	4.4	13.9	Q9NX20 RM16_HUMAN	39S ribosomal protein L16, mitochondrial OS=Homo sapiens GN=MRPL16 PE=1 SV=1	3
576	4.3	4.4	3.8	P22307 NLTP_HUMAN	Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2	2
577	4.2	27.5	22.6	P35241 RADI_HUMAN	Radixin OS=Homo sapiens GN=RDX PE=1 SV=1	18
578	4.2	4.4	16.9	Q6NZI2 PTRF_HUMAN	Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1	4
579	4.2	4.2	17.7	Q16740 CLPP_HUMAN	ATP-dependent Clp protease proteolytic subunit, mitochondrial OS=Homo sapiens GN=CLPP PE=1 SV=1	2
580	4.2	4.3	6.9	Q16795 NDUA9_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Homo sapiens GN=NDL	3
581	4.2	4.2	16.2	P46778 RL21_HUMAN	60S ribosomal protein L21 OS=Homo sapiens GN=RPL21 PE=1 SV=2	2
582	4.1	4.2	1.6	Q07157 ZO1_HUMAN	Tight junction protein ZO-1 OS=Homo sapiens GN=TJP1 PE=1 SV=3	2
583	4.1	4.2	23.2	Q96HS1 PGAM5_HUMAN	Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Homo sapiens GN=PGAM5 PE=1 SV=2	3
584	4.1	41.4	54.2	P68371 TBB4B_HUMAN	Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	24

585	4.1	4.1	6.5	Q6NYC8 PPR18_HUMAN	Phostensin OS=Homo sapiens GN=PPP1R18 PE=1 SV=1	2
586	4.1	4.1	5.9	Q9NSD9 SYFB_HUMAN	Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FAR5B PE=1 SV=3	2
587	4.1	4.5	3.2	Q9NQW6 ANLN_HUMAN	Actin-binding protein anillin OS=Homo sapiens GN=ANLN PE=1 SV=2	3
588	4.1	4.3	10.0	P19404 NDUV2_HUMAN	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Homo sapiens GN=NDUFV2 PE=1 SV=2	2
589	4.1	4.1	24.2	Q16540 RM23_HUMAN	39S ribosomal protein L23, mitochondrial OS=Homo sapiens GN=MRPL23 PE=1 SV=1	2
590	4.1	4.3	3.8	Q5JTZ9 SYAM_HUMAN	Alanine--tRNA ligase, mitochondrial OS=Homo sapiens GN=AARS2 PE=1 SV=1	3
591	4.1	4.1	51.6	P07919 QCR6_HUMAN	Cytochrome b-c1 complex subunit 6, mitochondrial OS=Homo sapiens GN=UQCRH PE=1 SV=2	3
592	4.1	4.2	5.5	Q8IY88 SUV3_HUMAN	ATP-dependent RNA helicase SUPV3L1, mitochondrial OS=Homo sapiens GN=SUPV3L1 PE=1 SV=1	3
593	4.1	4.1	6.4	P52209 6PGD_HUMAN	6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3	2
594	4.0	4.2	28.4	P43487 RANG_HUMAN	Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1	3
595	4.0	4.1	8.2	Q9HDC9 APMAP_HUMAN	Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP PE=1 SV=2	2
596	4.0	4.1	5.7	Q99805 TM9S2_HUMAN	Transmembrane 9 superfamily member 2 OS=Homo sapiens GN=TM9SF2 PE=1 SV=1	2
597	4.0	4.1	9.2	P84098 RL19_HUMAN	60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1	2
598	4.0	4.0	8.6	P11279 LAMP1_HUMAN	Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3	3
599	4.0	4.1	9.4	P08758 ANXA5_HUMAN	Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2	2
600	4.0	4.0	7.9	P61160 ARP2_HUMAN	Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1	2
601	4.0	4.3	1.6	O75970 MPDZ_HUMAN	Multiple PDZ domain protein OS=Homo sapiens GN=MPDZ PE=1 SV=2	2
602	4.0	4.1	8.3	Q10469 MGAT2_HUMAN	Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase OS=Homo sapiens GN=MGAT2 PE=	3
603	4.0	4.0	5.5	O15371 EIF3D_HUMAN	Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1	4
604	4.0	4.0	6.7	P48426 PI42A_HUMAN	Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha OS=Homo sapiens GN=PIP4K2A PE=1 SV=2	2
605	4.0	4.0	34.8	Q9Y5J7 TIM9_HUMAN	Mitochondrial import inner membrane translocase subunit Tim9 OS=Homo sapiens GN=TIMM9 PE=1 SV=1	2
606	4.0	4.0	7.7	Q15942 ZYX_HUMAN	Zyxin OS=Homo sapiens GN=ZYX PE=1 SV=1	2
607	4.0	4.0	11.6	Q03405 UPAR_HUMAN	Urokinase plasminogen activator surface receptor OS=Homo sapiens GN=PLAUR PE=1 SV=1	2
608	4.0	4.0	19.6	Q99536 VAT1_HUMAN	Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2	3
609	4.0	4.0	9.7	Q9NX47 MARCH5_HUMAN	E3 ubiquitin-protein ligase MARCH5 OS=Homo sapiens GN=MARCH5 PE=1 SV=1	2
610	4.0	4.0	4.2	Q96HC4 PDLI5_HUMAN	PDZ and LIM domain protein 5 OS=Homo sapiens GN=PDLIM5 PE=1 SV=5	2
611	4.0	8.0	21.5	P61026 RAB10_HUMAN	Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1	5
612	4.0	8.0	10.5	Q9Y6M1 IF2B2_HUMAN	Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens GN=IGF2BP2 PE=1 SV=2	4
613	4.0	4.0	8.0	Q13418 ILK_HUMAN	Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=2	3
614	4.0	4.0	56.4	P81605 DCD_HUMAN	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	4
615	4.0	4.0	45.8	Q9UBI6 GBG12_HUMAN	Guanine nucleotide-binding protein G(i)/G(s)/G(o) subunit gamma-12 OS=Homo sapiens GN=GNG12 PE=1 SV=	2
616	4.0	4.0	3.3	Q96QK1 VPS35_HUMAN	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2	2
617	4.0	4.0	4.3	Q96QD8 S38A2_HUMAN	Sodium-coupled neutral amino acid transporter 2 OS=Homo sapiens GN=SLC38A2 PE=1 SV=2	2
618	4.0	4.0	11.7	Q13084 RM28_HUMAN	39S ribosomal protein L28, mitochondrial OS=Homo sapiens GN=MRPL28 PE=1 SV=4	2
619	4.0	4.0	28.0	P62899 RL31_HUMAN	60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1	2
620	4.0	4.0	16.4	P61225 RAP2B_HUMAN	Ras-related protein Rap-2b OS=Homo sapiens GN=RAP2B PE=1 SV=1	2
621	4.0	4.0	13.3	P28066 PSA5_HUMAN	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	3
622	4.0	4.0	2.1	O15118 NPC1_HUMAN	Niemann-Pick C1 protein OS=Homo sapiens GN=NPC1 PE=1 SV=2	2
623	4.0	4.0	11.4	Q9BQ69 MACD1_HUMAN	O-acetyl-ADP-ribose deacetylase MACROD1 OS=Homo sapiens GN=MACROD1 PE=1 SV=2	2
624	4.0	4.0	7.7	Q8NE86 MCU_HUMAN	Calcium uniporter protein, mitochondrial OS=Homo sapiens GN=MCU PE=1 SV=1	2
625	4.0	4.0	8.3	Q8NBJ7 SUMF2_HUMAN	Sulfatase-modifying factor 2 OS=Homo sapiens GN=SUMF2 PE=1 SV=2	3
626	4.0	4.0	1.7	Q15075 EEA1_HUMAN	Early endosome antigen 1 OS=Homo sapiens GN=EEA1 PE=1 SV=2	2
627	4.0	4.0	4.5	Q14699 RFTN1_HUMAN	Raftlin OS=Homo sapiens GN=RFTN1 PE=1 SV=4	2
628	4.0	4.0	18.2	P60033 CD81_HUMAN	CD81 antigen OS=Homo sapiens GN=CD81 PE=1 SV=1	2
629	4.0	4.0	10.1	P47914 RL29_HUMAN	60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2	2
630	4.0	4.0	17.3	P23434 GCSH_HUMAN	Glycine cleavage system H protein, mitochondrial OS=Homo sapiens GN=GCSH PE=1 SV=2	2
631	4.0	4.0	17.4	P14174 MIF_HUMAN	Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4	3
632	4.0	4.0	6.8	P11182 ODB2_HUMAN	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochon	2
633	4.0	4.0	14.1	P10109 ADX_HUMAN	Adrenodoxin, mitochondrial OS=Homo sapiens GN=FDX1 PE=1 SV=1	2
634	4.0	4.0	17.3	P09669 COX6C_HUMAN	Cytochrome c oxidase subunit 6C OS=Homo sapiens GN=COX6C PE=1 SV=2	2
635	4.0	4.0	16.7	P06748 NPM_HUMAN	Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	2
636	3.9	4.1	33.1	O43716 GATC_HUMAN	Glutamyl-tRNA(Gln) amidotransferase subunit C, mitochondrial OS=Homo sapiens GN=GATC PE=1 SV=1	3
637	3.9	4.0	9.3	Q8WZ82 OVCA2_HUMAN	Esterase OVCA2 OS=Homo sapiens GN=OVCA2 PE=1 SV=1	2
638	3.9	4.0	15.4	Q13765 NACA_HUMAN	Nascent polypeptide-associated complex subunit alpha OS=Homo sapiens GN=NACA PE=1 SV=1	2
639	3.9	4.1	5.9	O60506 HNRPQ_HUMAN	Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2	4
640	3.9	4.0	11.4	P00505 AATM_HUMAN	Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=3	3
641	3.9	4.0	13.0	Q9Y3B3 TMED7_HUMAN	Transmembrane emp24 domain-containing protein 7 OS=Homo sapiens GN=TMED7 PE=1 SV=2	2
642	3.8	4.3	7.1	P00533 EGFR_HUMAN	Epidermal growth factor receptor OS=Homo sapiens GN=EGFR PE=1 SV=2	5
643	3.8	4.1	5.5	P06756 ITAV_HUMAN	Integrin alpha-V OS=Homo sapiens GN=ITGAV PE=1 SV=2	5
644	3.8	4.0	5.8	Q9UDR5 AASS_HUMAN	Alpha-aminoadipic semialdehyde synthase, mitochondrial OS=Homo sapiens GN=AASS PE=1 SV=1	4
645	3.8	4.1	14.9	Q02252 MMSA_HUMAN	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Homo sapiens GN=ALDH6A1 PI	6
646	3.8	4.0	4.3	Q96A33 CCD47_HUMAN	Coiled-coil domain-containing protein 47 OS=Homo sapiens GN=CCDC47 PE=1 SV=1	2
647	3.8	4.1	5.0	P47897 SYQ_HUMAN	Glutamine--tRNA ligase OS=Homo sapiens GN=QARS PE=1 SV=1	3
648	3.8	4.0	2.7	P07814 SYEP_HUMAN	Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	3
649	3.8	4.0	9.5	Q14195 DPYL3_HUMAN	Dihydropyrimidinase-related protein 3 OS=Homo sapiens GN=DPYSL3 PE=1 SV=1	3
650	3.8	3.9	16.9	Q9H4G4 GAPR1_HUMAN	Golgi-associated plant pathogenesis-related protein 1 OS=Homo sapiens GN=GLIPR2 PE=1 SV=3	2
651	3.8	4.0	9.0	Q9H7Z7 PGES2_HUMAN	Prostaglandin E synthase 2 OS=Homo sapiens GN=PTGES2 PE=1 SV=1	3
652	3.7	3.9	10.5	Q9NVV4 PAPD1_HUMAN	Poly(A) RNA polymerase, mitochondrial OS=Homo sapiens GN=MTPAP PE=1 SV=1	3
653	3.7	3.9	50.6	O75531 BAF_HUMAN	Barrier-to-autointegration factor OS=Homo sapiens GN=BANF1 PE=1 SV=1	2
654	3.7	3.9	15.0	Q9NQ50 RM40_HUMAN	39S ribosomal protein L40, mitochondrial OS=Homo sapiens GN=MRPL40 PE=1 SV=1	2
655	3.7	3.8	14.9	Q15056 IF4H_HUMAN	Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H PE=1 SV=5	2
656	3.7	3.8	5.6	Q9H3Q1 BORG4_HUMAN	Cdc42 effector protein 4 OS=Homo sapiens GN=CDC42EP4 PE=1 SV=1	2
657	3.7	3.9	7.0	Q99832 TCPH_HUMAN	T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2	3
658	3.7	3.8	8.9	Q9H3N1 TMX1_HUMAN	Thioredoxin-related transmembrane protein 1 OS=Homo sapiens GN=TMX1 PE=1 SV=1	3
659	3.7	4.0	8.1	Q86UE4 LYRIC_HUMAN	Protein LYRIC OS=Homo sapiens GN=MTDH PE=1 SV=2	3
660	3.7	3.8	8.1	P26599 PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1	3
661	3.7	4.1	12.4	O43615 TIM44_HUMAN	Mitochondrial import inner membrane translocase subunit TIM44 OS=Homo sapiens GN=TIMM44 PE=1 SV=2	5
662	3.7	3.9	4.2	P26006 ITA3_HUMAN	Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5	2
663	3.7	3.8	9.5	Q6IBS0 TWF2_HUMAN	Twinfilin-2 OS=Homo sapiens GN=TWF2 PE=1 SV=2	2
664	3.7	3.8	7.7	Q15006 EMC2_HUMAN	ER membrane protein complex subunit 2 OS=Homo sapiens GN=EMC2 PE=1 SV=1	2
665	3.6	3.9	6.0	Q13505 MTX1_HUMAN	Metaxin-1 OS=Homo sapiens GN=MTX1 PE=1 SV=2	2
666	3.6	3.8	23.4	Q9NYL4 FKBP11_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP11 OS=Homo sapiens GN=FKBP11 PE=1 SV=1	3
667	3.6	3.7	4.3	P05362 ICAM1_HUMAN	Intercellular adhesion molecule 1 OS=Homo sapiens GN=ICAM1 PE=1 SV=2	2
668	3.6	3.8	28.0	Q15691 MARE1_HUMAN	Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens GN=MAPRE1 PE=1 SV=3	4

669	3.6	3.8	4.3	P15586 GNS_HUMAN	N-acetylglucosamine-6-sulfatase OS=Homo sapiens GN=GNS PE=1 SV=3	2
670	3.6	3.9	7.5	Q9H3K2 GHITM_HUMAN	Growth hormone-inducible transmembrane protein OS=Homo sapiens GN=GHITM PE=1 SV=2	3
671	3.6	3.7	17.9	O75208 COQ9_HUMAN	Ubiquinone biosynthesis protein COQ9, mitochondrial OS=Homo sapiens GN=COQ9 PE=1 SV=1	6
672	3.6	3.7	13.1	Q16270 IBP7_HUMAN	Insulin-like growth factor-binding protein 7 OS=Homo sapiens GN=IGFBP7 PE=1 SV=1	2
673	3.6	3.9	9.8	P50991 TCPD_HUMAN	T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	3
674	3.5	3.7	1.6	P55196 AFAD_HUMAN	Afadin OS=Homo sapiens GN=MLLT4 PE=1 SV=3	2
675	3.5	3.6	6.1	Q9Y697 NFS1_HUMAN	Cysteine desulfurase, mitochondrial OS=Homo sapiens GN=NFS1 PE=1 SV=3	2
676	3.5	3.6	13.6	Q56VL3 OCAD2_HUMAN	OCIA domain-containing protein 2 OS=Homo sapiens GN=OCIA2 PE=1 SV=1	2
677	3.5	3.6	4.3	Q12959 DLG1_HUMAN	Disks large homolog 1 OS=Homo sapiens GN=DLG1 PE=1 SV=2	2
678	3.5	3.7	13.8	Q9NV52 RT18A_HUMAN	28S ribosomal protein S18a, mitochondrial OS=Homo sapiens GN=MRPS18A PE=1 SV=1	2
679	3.5	3.8	11.9	Q15417 CNN3_HUMAN	Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1	2
680	3.5	3.6	8.3	P05026 AT1B1_HUMAN	Sodium/potassium-transporting ATPase subunit beta-1 OS=Homo sapiens GN=ATP1B1 PE=1 SV=1	2
681	3.5	3.6	9.6	P31689 DNJA1_HUMAN	DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2	2
682	3.5	3.6	2.6	P53992 SC24C_HUMAN	Protein transport protein Sec24C OS=Homo sapiens GN=SEC24C PE=1 SV=3	2
683	3.5	3.6	31.4	P82912 RT11_HUMAN	28S ribosomal protein S11, mitochondrial OS=Homo sapiens GN=MRPS11 PE=1 SV=2	3
684	3.4	3.5	14.2	P16989 YBOX3_HUMAN	Y-box-binding protein 3 OS=Homo sapiens GN=YBX3 PE=1 SV=4	2
685	3.4	3.6	10.5	Q9H2U2 IPYR2_HUMAN	Inorganic pyrophosphatase 2, mitochondrial OS=Homo sapiens GN=PPA2 PE=1 SV=2	2
686	3.4	3.5	34.5	P63027 VAMP2_HUMAN	Vesicle-associated membrane protein 2 OS=Homo sapiens GN=VAMP2 PE=1 SV=3	2
687	3.4	3.5	4.4	Q9UBM7 DHCR7_HUMAN	7-dehydrocholesterol reductase OS=Homo sapiens GN=DHCR7 PE=1 SV=1	2
688	3.4	3.5	19.1	Q9NVR9 HEBP1_HUMAN	Heme-binding protein 1 OS=Homo sapiens GN=HEBP1 PE=1 SV=1	2
689	3.4	18.9	26.9	P08779 K1C16_HUMAN	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	9
690	3.4	3.4	13.9	Q9UBX3 DIC_HUMAN	Mitochondrial dicarboxylate carrier OS=Homo sapiens GN=SLC25A10 PE=1 SV=2	2
691	3.3	3.5	7.3	Q9NVH1 DJC11_HUMAN	DnaJ homolog subfamily C member 11 OS=Homo sapiens GN=DNAJC11 PE=1 SV=2	3
692	3.3	3.5	14.0	Q8TAE8 G45IP_HUMAN	Growth arrest and DNA damage-inducible proteins-interacting protein 1 OS=Homo sapiens GN=GADD45GIP1	2
693	3.3	3.5	7.4	Q7Z4W1 DCXR_HUMAN	L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2	2
694	3.3	3.4	11.3	Q13636 RAB31_HUMAN	Ras-related protein Rab-31 OS=Homo sapiens GN=RAB31 PE=1 SV=1	2
695	3.3	3.4	24.0	O95168 NDUB4_HUMAN	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4 OS=Homo sapiens GN=NDUFB4 PE=1 SV=3	2
696	3.2	3.5	11.9	P46781 RS9_HUMAN	40S ribosomal protein S9 OS=Homo sapiens GN=RP59 PE=1 SV=3	2
697	3.2	3.4	2.5	P13010 XRCC5_HUMAN	X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3	2
698	3.2	3.4	4.2	P22413 ENPP1_HUMAN	Ectonucleotide pyrophosphatase/phosphodiesterase family member 1 OS=Homo sapiens GN=ENPP1 PE=1 SV=2	2
699	3.2	3.3	22.4	Q16718 NDUA5_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5 OS=Homo sapiens GN=NDUFA5 PE=1 SV=3	2
700	3.2	3.3	4.2	P08240 SRPRA_HUMAN	Signal recognition particle receptor subunit alpha OS=Homo sapiens GN=SRPRA PE=1 SV=2	2
701	3.2	3.3	7.5	P78417 GSTO1_HUMAN	Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2	2
702	3.2	3.4	8.2	P49406 RM19_HUMAN	39S ribosomal protein L19, mitochondrial OS=Homo sapiens GN=MRPL19 PE=1 SV=2	3
703	3.2	3.2	10.7	P33316 DUT_HUMAN	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial OS=Homo sapiens GN=DUT PE=1 SV=4	2
704	3.1	3.2	5.9	O43464 HTRA2_HUMAN	Serine protease HTRA2, mitochondrial OS=Homo sapiens GN=HTRA2 PE=1 SV=2	2
705	3.1	3.3	25.7	P60953 CDC42_HUMAN	Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2	3
706	3.1	3.2	4.4	Q9H3G5 CPVL_HUMAN	Probable serine carboxypeptidase CPVL OS=Homo sapiens GN=CPVL PE=1 SV=2	2
707	3.1	17.0	21.3	Q5T9A4 ATD3B_HUMAN	ATPase family AAA domain-containing protein 3B OS=Homo sapiens GN=ATAD3B PE=1 SV=1	14
708	3.1	3.4	3.8	Q7L576 CYFP1_HUMAN	Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1	4
709	3.1	3.3	2.3	P26640 SYVC_HUMAN	Valine--tRNA ligase OS=Homo sapiens GN=VAR5 PE=1 SV=4	2
710	3.1	3.2	6.8	Q9BTV4 TMM43_HUMAN	Transmembrane protein 43 OS=Homo sapiens GN=TMEM43 PE=1 SV=1	2
711	3.1	3.3	6.5	Q9NZ01 TECR_HUMAN	Very-long-chain enoyl-CoA reductase OS=Homo sapiens GN=TECR PE=1 SV=1	2
712	3.1	3.3	4.3	P60228 EIF3E_HUMAN	Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1	2
713	3.0	3.2	12.4	Q13642 FHL1_HUMAN	Four and a half LIM domains protein 1 OS=Homo sapiens GN=FHL1 PE=1 SV=4	3
714	3.0	3.1	14.3	O43674 NDUB5_HUMAN	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial OS=Homo sapiens GN=NDUI1	2
715	3.0	3.1	6.8	Q13838 DX39B_HUMAN	Spliceosome RNA helicase DDX39B OS=Homo sapiens GN=DDX39B PE=1 SV=1	2
716	3.0	3.3	7.7	Q9Y3F4 STRAP_HUMAN	Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1	2
717	3.0	3.3	5.5	Q9UJ83 HACL1_HUMAN	2-hydroxyacyl-CoA lyase 1 OS=Homo sapiens GN=HACL1 PE=1 SV=2	2
718	3.0	3.1	9.7	Q8WW59 SPRY4_HUMAN	SPRY domain-containing protein 4 OS=Homo sapiens GN=SPRYD4 PE=1 SV=2	2
719	3.0	3.1	3.3	P98194 AT2C1_HUMAN	Calcium-transporting ATPase type 2C member 1 OS=Homo sapiens GN=ATP2C1 PE=1 SV=3	2
720	3.0	3.2	4.1	Q96AY3 FKBP10_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP10 OS=Homo sapiens GN=FKBP10 PE=1 SV=1	2
721	3.0	3.1	31.3	O43678 NDUA2_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 OS=Homo sapiens GN=NDUFA2 PE=1 SV=3	3
722	3.0	3.1	8.8	P82675 RT05_HUMAN	28S ribosomal protein S5, mitochondrial OS=Homo sapiens GN=MRPS5 PE=1 SV=2	2
723	3.0	12.6	29.9	P07951 TPM2_HUMAN	Tropomyosin beta chain OS=Homo sapiens GN=TPM2 PE=1 SV=1	7
724	3.0	3.1	6.1	P22570 ADRO_HUMAN	NADPH:adenodoxin oxidoreductase, mitochondrial OS=Homo sapiens GN=FDXR PE=1 SV=3	2
725	2.9	3.0	7.8	P18031 PTN1_HUMAN	Tyrosine-protein phosphatase non-receptor type 1 OS=Homo sapiens GN=PTPN1 PE=1 SV=1	2
726	2.9	3.0	20.0	P46783 RS10_HUMAN	40S ribosomal protein S10 OS=Homo sapiens GN=RP510 PE=1 SV=1	2
727	2.9	3.0	4.2	Q9H857 NT5D2_HUMAN	5'-nucleotidase domain-containing protein 2 OS=Homo sapiens GN=NT5DC2 PE=1 SV=1	2
728	2.9	3.3	7.9	P07947 YES_HUMAN	Tyrosine-protein kinase Yes OS=Homo sapiens GN=YES1 PE=1 SV=3	2
729	2.9	3.0	5.3	P61221 ABCE1_HUMAN	ATP-binding cassette sub-family E member 1 OS=Homo sapiens GN=ABCE1 PE=1 SV=1	2
730	2.9	3.0	4.4	O60476 MA1A2_HUMAN	Mannosyl-oligosaccharide 1,2-alpha-mannosidase IB OS=Homo sapiens GN=MAN1A2 PE=1 SV=1	2
731	2.9	3.2	7.5	Q16555 DPYL2_HUMAN	Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1	3
732	2.9	3.1	6.2	Q9NYY8 FAKD2_HUMAN	FAST kinase domain-containing protein 2, mitochondrial OS=Homo sapiens GN=FASTKD2 PE=1 SV=1	3
733	2.9	3.0	7.9	Q96G23 CERS2_HUMAN	Ceramide synthase 2 OS=Homo sapiens GN=CERS2 PE=1 SV=1	2
734	2.9	3.0	6.5	Q9UKU7 ACAD8_HUMAN	Isobutyryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACAD8 PE=1 SV=1	2
735	2.9	3.0	19.8	P09496 CLCA_HUMAN	Clathrin light chain A OS=Homo sapiens GN=CLTA PE=1 SV=1	3
736	2.9	2.9	3.0	Q14644 RASA3_HUMAN	Ras GTPase-activating protein 3 OS=Homo sapiens GN=RASA3 PE=1 SV=3	2
737	2.8	3.0	3.8	P16278 BGAL_HUMAN	Beta-galactosidase OS=Homo sapiens GN=GLB1 PE=1 SV=2	2
738	2.8	3.1	6.7	P46459 NSF_HUMAN	Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=3	4
739	2.8	2.9	30.1	P14406 CX7A2_HUMAN	Cytochrome c oxidase subunit 7A2, mitochondrial OS=Homo sapiens GN=COX7A2 PE=1 SV=1	2
740	2.8	3.1	3.0	A3KMH1 VWA8_HUMAN	von Willebrand factor A domain-containing protein 8 OS=Homo sapiens GN=VWA8 PE=1 SV=2	4
741	2.8	2.9	4.6	P17813 EGLN_HUMAN	Endoglin OS=Homo sapiens GN=ENG PE=1 SV=2	2
742	2.8	2.9	3.6	Q8IVF2 AHNK2_HUMAN	Protein AHNAK2 OS=Homo sapiens GN=AHNAK2 PE=1 SV=2	2
743	2.8	2.9	4.6	Q15334 L2GL1_HUMAN	Lethal(2) giant larvae protein homolog 1 OS=Homo sapiens GN=LLGL1 PE=1 SV=3	3
744	2.8	26.4	46.2	Q05639 EF1A2_HUMAN	Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1	28
745	2.8	3.0	5.0	Q96RQ3 MCCA_HUMAN	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Homo sapiens GN=MCCC1 PE=1 SV=3	3
746	2.7	3.0	3.7	P08133 ANXA6_HUMAN	Annexin A6 OS=Homo sapiens GN=ANXA6 PE=1 SV=3	2
747	2.7	2.8	6.7	Q9BY44 EIF2A_HUMAN	Eukaryotic translation initiation factor 2A OS=Homo sapiens GN=EIF2A PE=1 SV=3	2
748	2.7	2.8	40.0	O75394 RM33_HUMAN	39S ribosomal protein L33, mitochondrial OS=Homo sapiens GN=MRPL33 PE=1 SV=1	2
749	2.7	2.9	3.5	P11387 TOP1_HUMAN	DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2	2
750	2.7	2.8	20.4	O43676 NDUB3_HUMAN	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3 OS=Homo sapiens GN=NDUFB3 PE=1 SV=3	2
751	2.7	2.8	2.7	P53396 ACLY_HUMAN	ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3	3
752	2.7	2.8	28.9	P52565 GDRI1_HUMAN	Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDI1 PE=1 SV=3	3

753	2.7	2.9	10.5	P31948 STIP1_HUMAN	Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1	3
754	2.7	2.9	3.6	P33121 ACSL1_HUMAN	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1	2
755	2.7	2.7	37.3	P56381 ATP5E_HUMAN	ATP synthase subunit epsilon, mitochondrial OS=Homo sapiens GN=ATP5E PE=1 SV=2	2
756	2.7	2.7	1.6	P56199 ITA1_HUMAN	Integrin alpha-1 OS=Homo sapiens GN=ITA1 PE=1 SV=2	2
757	2.7	2.7	19.7	O75251 NDU57_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial OS=Homo sapiens GN=NDU57 PE=1	5
758	2.6	2.7	8.0	Q9BRK5 CAB45_HUMAN	45 kDa calcium-binding protein OS=Homo sapiens GN=SDF4 PE=1 SV=1	2
759	2.6	2.9	14.3	O00217 NDUS8_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial OS=Homo sapiens GN=NDUFS8 PE=1	2
760	2.6	2.7	8.2	Q15293 RCN1_HUMAN	Reticulocalbin-1 OS=Homo sapiens GN=RCN1 PE=1 SV=1	2
761	2.6	2.7	6.9	O75477 ERLN1_HUMAN	Erlin-1 OS=Homo sapiens GN=ERLN1 PE=1 SV=1	2
762	2.6	2.9	0.5	P78527 PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3	2
763	2.6	2.7	18.4	Q04941 PLP2_HUMAN	Proteolipid protein 2 OS=Homo sapiens GN=PLP2 PE=1 SV=1	3
764	2.6	2.9	14.7	O75955 FLOT1_HUMAN	Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3	4
765	2.6	2.7	20.1	Q9Y6M9 NDUB9_HUMAN	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9 OS=Homo sapiens GN=NDUF89 PE=1 SV=3	2
766	2.6	2.7	7.5	P31942 HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens GN=HNRNPH3 PE=1 SV=2	2
767	2.6	2.7	15.9	Q9UIU7 KAD3_HUMAN	GTP:AMP phosphotransferase AK3, mitochondrial OS=Homo sapiens GN=AK3 PE=1 SV=4	3
768	2.6	2.9	11.0	P61158 ARP3_HUMAN	Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3	5
769	2.6	2.6	7.6	Q9BQP7 MGME1_HUMAN	Mitochondrial genome maintenance exonuclease 1 OS=Homo sapiens GN=MGME1 PE=1 SV=1	2
770	2.5	2.8	11.5	P82930 RT34_HUMAN	28S ribosomal protein S34, mitochondrial OS=Homo sapiens GN=MRPS34 PE=1 SV=2	4
771	2.5	2.8	5.5	Q969V3 NCLN_HUMAN	Nicalin OS=Homo sapiens GN=NCLN PE=1 SV=2	2
772	2.5	2.7	4.7	P13196 HEM1_HUMAN	5-aminolevulinate synthase, nonspecific, mitochondrial OS=Homo sapiens GN=ALAS1 PE=1 SV=2	2
774	2.5	2.6	14.3	P62330 ARF6_HUMAN	ADP-ribosylation factor 6 OS=Homo sapiens GN=ARF6 PE=1 SV=2	2
775	2.5	2.6	24.3	P82909 RT36_HUMAN	28S ribosomal protein S36, mitochondrial OS=Homo sapiens GN=MRPS36 PE=1 SV=2	2
776	2.5	2.6	20.4	P46779 RL28_HUMAN	60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3	2
777	2.5	2.7	1.9	Q8WW11 LMO7_HUMAN	LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=3	2
779	2.5	2.6	3.3	P22033 MUTA_HUMAN	Methylmalonyl-CoA mutase, mitochondrial OS=Homo sapiens GN=MUT PE=1 SV=4	2
780	2.5	2.6	31.7	Q9Y6G3 RM42_HUMAN	39S ribosomal protein L42, mitochondrial OS=Homo sapiens GN=MRPL42 PE=1 SV=1	4
784	2.5	2.5	3.9	Q13425 SNTB2_HUMAN	Beta-2-syntrophin OS=Homo sapiens GN=SNTB2 PE=1 SV=1	2
785	2.4	2.6	4.3	P12956 XRCC6_HUMAN	X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2	2
786	2.4	6.0	14.8	P09972 ALDOC_HUMAN	Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2	5
787	2.4	2.7	11.1	P50552 VASP_HUMAN	Vasodilator-stimulated phosphoprotein OS=Homo sapiens GN=VASP PE=1 SV=3	4
788	2.4	2.6	3.9	Q9P2B2 FPRP_HUMAN	Prostaglandin F2 receptor negative regulator OS=Homo sapiens GN=PTGFRN PE=1 SV=2	2
789	2.4	2.5	15.2	P62841 RS15_HUMAN	40S ribosomal protein S15 OS=Homo sapiens GN=RPS15 PE=1 SV=2	2
790	2.4	2.6	9.4	P21953 ODDB_HUMAN	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial OS=Homo sapiens GN=BCKDHB PE=1 SV=2	3
792	2.4	2.5	3.0	Q3SY69 AL1L2_HUMAN	Mitochondrial 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L2 PE=1 SV=2	2
793	2.4	2.4	3.3	Q92598 HS105_HUMAN	Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1	2
794	2.4	2.4	50.6	Q9NRP2 COXM2_HUMAN	COX assembly mitochondrial protein 2 homolog OS=Homo sapiens GN=CMC2 PE=1 SV=1	2
795	2.4	2.4	12.9	Q01629 IFM2_HUMAN	Interferon-induced transmembrane protein 2 OS=Homo sapiens GN=IFITM2 PE=1 SV=2	3
799	2.3	2.4	6.9	Q70UQ0 IKIP_HUMAN	Inhibitor of nuclear factor kappa-B kinase-interacting protein OS=Homo sapiens GN=IKBIP PE=1 SV=1	2
800	2.3	2.4	13.1	P56537 IF6_HUMAN	Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1	3
801	2.3	2.5	12.0	Q9Y3D7 TIM16_HUMAN	Mitochondrial import inner membrane translocase subunit TIM16 OS=Homo sapiens GN=PAM16 PE=1 SV=2	2
803	2.3	11.6	30.6	P08134 RHOC_HUMAN	Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOC PE=1 SV=1	7
804	2.3	2.3	3.2	Q8TCT9 HM13_HUMAN	Minor histocompatibility antigen H13 OS=Homo sapiens GN=HM13 PE=1 SV=1	2
805	2.3	2.4	5.9	Q8IVS2 FABD_HUMAN	Malonyl-CoA-acyl carrier protein transacylase, mitochondrial OS=Homo sapiens GN=MCAT PE=1 SV=2	2
808	2.2	2.5	6.3	Q14108 SCRB2_HUMAN	Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2	2
809	2.2	2.4	24.2	Q03135 CAV1_HUMAN	Caveolin-1 OS=Homo sapiens GN=CAV1 PE=1 SV=4	2
814	2.2	2.3	8.8	Q9Y2B0 CNPY2_HUMAN	Protein canopy homolog 2 OS=Homo sapiens GN=CNPY2 PE=1 SV=1	2
817	2.2	2.4	4.6	P14868 SYDC_HUMAN	Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2	2
818	2.2	2.3	12.9	Q9HBL7 PLRKT_HUMAN	Plasminogen receptor (KT) OS=Homo sapiens GN=PLGRKT PE=1 SV=1	2
821	2.2	2.2	11.5	P82673 RT35_HUMAN	28S ribosomal protein S35, mitochondrial OS=Homo sapiens GN=MRPS35 PE=1 SV=1	2
822	2.1	2.2	24.4	Q86TS9 RM52_HUMAN	39S ribosomal protein L52, mitochondrial OS=Homo sapiens GN=MRPL52 PE=1 SV=2	3
825	2.1	6.1	9.5	Q13310 PABP4_HUMAN	Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 PE=1 SV=1	4
827	2.1	2.2	1.7	Q9BYT8 NEUL_HUMAN	Neurolysin, mitochondrial OS=Homo sapiens GN=NLN PE=1 SV=1	2
830	2.1	2.1	24.6	Q99622 C10_HUMAN	Protein C10 OS=Homo sapiens GN=C12orf57 PE=1 SV=1	2
834	2.1	2.7	6.6	Q9P0V9 SEP10_HUMAN	Septin-10 OS=Homo sapiens GN=SEPT10 PE=1 SV=2	2
838	2.1	4.4	17.7	P51153 RAB13_HUMAN	Ras-related protein Rab-13 OS=Homo sapiens GN=RAB13 PE=1 SV=1	4
840	2.1	2.2	35.7	P63173 RL38_HUMAN	60S ribosomal protein L38 OS=Homo sapiens GN=RPL38 PE=1 SV=2	2
841	2.1	2.1	17.6	Q9Y2Q9 RT28_HUMAN	28S ribosomal protein S28, mitochondrial OS=Homo sapiens GN=MRPS28 PE=1 SV=1	2
842	2.1	2.1	7.4	Q86TX2 ACOT1_HUMAN	Acyl-coenzyme A thioesterase 1 OS=Homo sapiens GN=ACOT1 PE=1 SV=1	2
843	2.1	2.1	9.2	P20290 BTF3_HUMAN	Transcription factor BTF3 OS=Homo sapiens GN=BTF3 PE=1 SV=1	2
846	2.0	6.0	4.8	Q9UKE5 TNIK_HUMAN	TRAF2 and NCK-interacting protein kinase OS=Homo sapiens GN=TNIK PE=1 SV=1	5
847	2.0	4.4	0.7	Q15149 PLEC_HUMAN	Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3	2
855	2.0	2.0	20.5	O14561 ACPM_HUMAN	Acyl carrier protein, mitochondrial OS=Homo sapiens GN=NDUFAB1 PE=1 SV=3	2
858	2.0	11.5	27.2	P16403 H12_HUMAN	Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2	12
863	2.0	2.0	12.2	Q9UM50 NFU1_HUMAN	NFU1 iron-sulfur cluster scaffold homolog, mitochondrial OS=Homo sapiens GN=NFU1 PE=1 SV=2	2
865	2.0	2.5	4.9	Q01650 LAT1_HUMAN	Large neutral amino acids transporter small subunit 1 OS=Homo sapiens GN=SLC7A5 PE=1 SV=2	2
866	2.0	2.1	3.7	P17844 DDX5_HUMAN	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1	2
879	2.0	63.0	81.6	P63261 ACTG_HUMAN	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1	84
880	2.0	10.2	30.7	P15153 RAC2_HUMAN	Ras-related C3 botulinum toxin substrate 2 OS=Homo sapiens GN=RAC2 PE=1 SV=1	6
881	2.0	7.2	42.3	P01111 RASN_HUMAN	GTPase NRas OS=Homo sapiens GN=NRAS PE=1 SV=1	8
882	2.0	6.2	35.4	Q93077 H2A1C_HUMAN	Histone H2A type 1-C OS=Homo sapiens GN=HIST1H2AC PE=1 SV=3	4
883	2.0	6.0	17.4	P61006 RAB8A_HUMAN	Ras-related protein Rab-8A OS=Homo sapiens GN=RAB8A PE=1 SV=1	4
887	2.0	2.0	8.9	P61803 DAD1_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 OS=Homo sapiens GN=DAD1 P	2
889	2.0	2.0	6.9	P53634 CATC_HUMAN	Dipeptidyl peptidase 1 OS=Homo sapiens GN=CTSC PE=1 SV=2	2
927	2.0	2.0	17.4	Q8N8J7 CD032_HUMAN	Uncharacterized protein C4orf32 OS=Homo sapiens GN=C4orf32 PE=2 SV=2	2
929	2.0	2.0	15.5	Q71UM5 RS27L_HUMAN	40S ribosomal protein S27-like OS=Homo sapiens GN=RPS27L PE=1 SV=3	2
961	2.0	2.0	5.6	P04632 CPNS1_HUMAN	Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1	2
964	2	2.0	16.2	P03928 ATP8_HUMAN	ATP synthase protein 8 OS=Homo sapiens GN=MT-ATP8 PE=1 SV=1	1

Supplementary Table S2

3-4 biological replicates for each strain												
		precursor [M] - 622.37++	precursor [M+1] - 622.88++	y9 - 1130.66+	y8 - 1017.57+	y7 - 916.53+	y5 - 687.42+	y4 - 559.36+	y3 - 373.28+	b8 - 984.55+	b9 - 1097.64+	Sum all transitions
Replicate	Strain	Peak Area normalized to Stds	Peak Area normalized to Stds	Peak Area normalized to Stds	Peak Area normalized to Stds	Peak Area normalized to Stds	Peak Area normalized to Stds	Peak Area normalized to Stds	Peak Area normalized to Stds	Peak Area normalized to Stds	Peak Area normalized to Stds	Peak Area normalized to Stds
0007_MBS_WT_1	WT	0.00121	0.00102	2.84E-05	0.00062	0.00014	6.10E-05	7.16E-05	3.79E-05	4.57E-05	4.83E-05	0.00328
0001_MBS_WT_2	WT	0.00174	0.00131	4.92E-05	0.00087	0.00022	0.00013	0.00011	6.11E-05	6.46E-05	6.75E-05	0.00462
0004_MBS_WT_3	WT	0.00152	0.00099	3.38E-05	0.00080	0.00015	7.66E-05	9.40E-05	5.01E-05	5.09E-05	4.26E-05	0.00380
0002_MBS_A8MUT_4	A8/6mut	0.00030	0.00014	6.23E-06	8.28E-05	2.27E-05	7.61E-06	1.83E-05	9.08E-06	6.47E-06	2.18E-05	0.00061
0005_MBS_A8MUT_5	A8/6mut	4.55E-05	1.63E-05	8.92E-06	8.74E-05	2.77E-05	8.90E-05	6.18E-06	8.92E-06	2.23E-05	1.39E-05	0.00033
0008_MBS_A8MUT_6	A8/6mut	0.00018	0.00016	1.67E-05	0.00013	4.83E-05	4.02E-05	4.03E-06	1.49E-05	1.28E-05	3.39E-05	0.00063
0003_MBS_nuA8_7	A8/6mut + A8F	0.00048	0.00040	1.50E-05	0.00024	4.28E-05	3.20E-05	3.05E-05	1.79E-05	1.21E-05	1.37E-05	0.00129
0006_MBS_nuA8_8	A8/6mut + A8F	0.00066	0.00045	2.16E-05	0.00030	9.45E-05	5.36E-05	4.19E-05	2.79E-05	2.42E-05	2.39E-05	0.00170
0009_MBS_nuA8_9	A8/6mut + A8F	0.00070	0.00031	8.01E-06	0.00017	4.29E-05	6.27E-05	3.27E-05	1.86E-05	7.67E-05	1.34E-05	0.00143
0010_MBS_nuA8_10	A8/6mut + A8F	0.00031	0.00045	1.83E-05	0.00020	7.24E-05	9.19E-06	3.27E-05	2.02E-05	5.40E-05	2.91E-05	0.00120
ATP6 levels (all transitions)												
				WT	A8/6mut	A8/6mut + A8F					pvalue	
average (normalized Peak Area)				0.00390	0.00052	0.00140		A8/6mut vs WT			0.00965	
stdev (normalized Peak Area)				0.00068	0.00017	0.00022		A8/6mut+A8F vs WT			0.01768	
								A8/6mut+A8F vs A8/6mut			0.00190	
strain comparisons				Protein Ratio ATP6		p-value						
A8/6mut vs WT				0.13		0.00965						
A8/6mut + A8F vs WT				0.36		0.01768						
A8/6mut + A8F vs A8/6mut				2.69		0.00190						

Supplementary Table S3

Primer	Wild type	Mutant
Fwd 0	5'ttataacaaaccctgagaaccaaagt <b>g</b> 3'	5'ttataacaaaccctgagaaccaaata <b>a</b> 3'
Fwd 1	5'ttataacaaaccctgagaaccaaag <b>g</b> 3'	5'ttataacaaaccctgagaaccaaaca <b>a</b> 3'
Fwd 2	5'ttataacaaaccctgagaaccaaag <b>tcg</b> 3'	5'ttataacaaaccctgagaaccaaag <b>ca</b> 3'
Reverse	5'gtactgatcattctatttcc3'	5'gtactgatcattctatttcc3'

Supplementary Table S4

Strain/clone	$\Delta C_T$ (Mut1bp-WT1bp)	Strain/clone	$\Delta C_T$ (Mut1bp-WT1bp)
WT(143 B)	14.87	R2 $\Delta$ A8#1	5.8
$\Delta$ A8 parental	-7.75	R2 $\Delta$ A8#2	7.42
R1 $\Delta$ A8#1	13.885	R2 $\Delta$ A8#3	13.23
R1 $\Delta$ A8#2	-1.66	R2 $\Delta$ A8#4	10.4
R1 $\Delta$ A8#3	13.005	R2 $\Delta$ A8#5	14.51
R1 $\Delta$ A8#5	14.82	R2 $\Delta$ A8#8	14.52
R1 $\Delta$ A8#7	-8.25	R2 $\Delta$ A8#9	13.05
R1 $\Delta$ A8#11	3.32	R2 $\Delta$ A8#10	13.31
R1 $\Delta$ A8#12	-8.54	R2 $\Delta$ A8#16	13.92
R1 $\Delta$ A8#13	-11.08*	R2 $\Delta$ A8#18	14.12
R1 $\Delta$ A8#14	-7.92	R2 $\Delta$ A8#19	12.85
R1 $\Delta$ A8#16	14.32	R2 $\Delta$ A8#20	14.21
R1 $\Delta$ A8#17	8.3	R2 $\Delta$ A8#22	15.58
R1 $\Delta$ A8#22	13.82		
R1 $\Delta$ A8#23	14.24		

\*had very slow growth.

Supplementary Table S5

Cell line	G1- <i>ATP8</i> - $\Delta C_T$ <sub>(test-parental)</sub>	G1- <i>ATP6</i> - $\Delta C_T$ <sub>(test-parental)</sub>
A8/6 <sup>mut</sup> + A8F	10.84 ± 0.56	0.77 ± 0.44
A8/6 <sup>mut</sup> + A8F + A6F	12.74 ± 1.15	8.58 ± 0.79
A8/6 <sup>mut</sup> + A6F	0.84 ± 1.13	8.36 ± 1.25

Supplementary Table S6

Cell line	15 Days Glucose		28 Days Glucose		11 Days Galactose	
	WT	Mutant	WT	Mutant	WT	Mutant
WT	$0.37 \pm 0.04$	$0.84 \pm 0.23$	$0.17 \pm 0.16$	$0.30 \pm 0.03$	$0.21 \pm 0.24$	$0.46 \pm 0.09$
A8/6 <sup>mut</sup>	$0.12 \pm 0.15$	$0.08 \pm 0.11$	$0.06 \pm 0.64$	$0.18 \pm 0.93$	N/A*	
A8/6 <sup>mut</sup> + A6F	$-0.47 \pm 0.16$	$-0.10 \pm 0.27$	$0.38 \pm 0.39$	$2.51 \pm 0.58$	N/A*	
A8/6 <sup>mut</sup> + A8F	$-1.10 \pm 0.19$	$0.01 \pm 0.09$	$-0.45 \pm 0.01$	$-0.20 \pm 0.42$	$-0.72 \pm 0.07$	$-0.23 \pm 0.55$
A8/6 <sup>mut</sup> + A8F + A6F	$0.57 \pm 0.16$	$-0.06 \pm 0.09$	$-0.15 \pm 0.06$	$0.05 \pm 0.16$	$0.31 \pm 0.26$	$-0.03 \pm 0.16$

 $\Delta\Delta C_r$  Values