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 TGCTGCTGACACTGTTCCTGATTACTCAGCTGAAGATGCTGAACACCAAT    300

mtATP8           97 TACCACCTACCTCCCTCACCAAAGCCCATAAAAATAAAAAATTATAACAA    146
                    ||||||||.||.||.||.||||||.||||||.||.||.||||||.||||||.||
oATP8           301 TACCACCTGCCCCCTTCCCCAAAACCCATGAAGATGAAAAACTATAATAA    350

mtATP8          147 ACCCTGAGAACCAAAATGAACGAAAATCTGTTCGCTTCATTCATTGCCCC    196
                    .||||||.||||||.||.||.||.||||||||||...||.|||....|||||.|
oATP8           351 GCCCTGGGAACCTAAGTGGACCAAAATCTGTAGCCTGCATAGCCTGCCAC    400

mtATP8          197 CACAATCC-----------------------------------------    204
                    |.||.||.
oATP8           401 CTCAGTCACTCGAGCAGAAACTCATCTCAGAAGAGGATCTGGCAGCAAAT    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           MQTAGALFISPALIRCCTRGLIRPVSASFLNSPVNSSKQPSYSNFPLQVARREFQTSVVS 60
mtATP8          ------------------------------------------------------------ 0

                ______
oATP8           RDIDTATRMPQLNTTVWPTMITPMLLTLFLITQLKMLNTNYHLPPSPKPMKMKNYNKPWE 120
mtATP8          --------MPQLNTTVWPTMITPMLLTLFLITQLKMLNTNYHLPPSPKPMKMKNYNKPWE 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 ATGCAGACCGCCGGGGCATTATTCATTTCTCCAGCTCTGATCCGCTGTTG     50

mtATP6            1 --------------------------------------------------      0

rATP6            51 TACCAGGGGTCTAATCAGGCCTGTGTCTGCCTCCTTCTTGAATAGCCCAG    100

mtATP6            1 --------------------------------------------------      0

rATP6           101 TGAATTCATCTAAACAGCCTTCCTACAGCAACTTCCCACTCCAGGTGGCC    150

mtATP6            1 --------------------------------------------------      0

rATP6           151 AGACGGGAGTTCCAGACCAGTGTTGTCTCCCGGGACATTGACACGGCGAC    200

mtATP6            1 -----ACGAAAATCTGTTCGCTTCATTCATTGCCCCCACAATCCTAGGCC     45
                        |||||||||||||||||||||||||||||||||||||||||||||
rATP6           201 GCGTAACGAAAATCTGTTCGCTTCATTCATTGCCCCCACAATCCTAGGCC    250

mtATP6           46 TACCCGCCGCAGTACTGATCATTCTATTTCCCCCTCTATTGATCCCCACC     95
                    ||||||||||||||||||||||||||||||||||||||||||||||||||
rATP6           251 TACCCGCCGCAGTACTGATCATTCTATTTCCCCCTCTATTGATCCCCACC    300

mtATP6           96 TCCAAATATCTCATCAACAACCGACTAATCACCACCCAACAATGACTAAT    145
                    ||||||||||||||||||||||||||||||||||||||||||.|||||
rATP6           301 TCCAAATATCTCATCAACAACCGACTAATCACCACCCAACAATGGCTAAT    350

mtATP6          146 CAAACTAACCTCAAAACAAATGATAACCATACACAACACTAAAGGACGAA    195
                    |||||||||||||||||||||||.|||||.||||||||||||||||||||
rATP6           351 CAAACTAACCTCAAAACAAATGATGACCATGCACAACACTAAAGGACGAA    400

mtATP6          196 CCTGATCTCTTATACTAGTATCCTTAATCATTTTTATTGCCACAACTAAC    245
                    ||||.||||||||.||||||||||||||||||||||||||||||||||||
rATP6           401 CCTGGTCTCTTATGCTAGTATCCTTAATCATTTTTATTGCCACAACTAAC    450

mtATP6          246 CTCCTCGGACTCCTGCCTCACTCATTTACACCAACCACCCAACTATCTAT    295
```

```
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
rATP6            451 CTCCTCGGACTCCTGCCTCACTCATTTACACCAACCACCCAACTATCTAT    500

mtATP6           296 AAACCTAGCCATGGCCATCCCCTTATGAGCGGGCACAGTGATTATAGGCT    345
                     .|||||||||||||||||||||||||||.||||||||||||||||||.||||
rATP6            501 GAACCTAGCCATGGCCATCCCCTTATGGGCGGGCACAGTGATTATGGGCT    550

mtATP6           346 TTCGCTCTAAGATTAAAAATGCCCTAGCCCACTTCTTACCACAAGGCACA    395
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
 rATP6            551 TTCGCTCTAAGATTAAAAATGCCCTAGCCCACTTCTTACCACAAGGCACA    600

mtATP6           396 CCTACACCCCTTATCCCCATACTAGTTATTATCGAAACCATCAGCCTACT    445
                     |||||||||||||||||||||.||||||||||||||||||||||||||||||
rATP6            601 CCTACACCCCTTATCCCCATGCTAGTTATTATCGAAACCATCAGCCTACT    650

mtATP6           446 CATTCAACCAATAGCCCTGGCCGTACGCCTAACCGCTAACATTACTGCAG    495
                     ||||||||||||.||||||||||||||||||||||||||||||||||||||
rATP6            651 CATTCAACCAATGGCCCTGGCCGTACGCCTAACCGCTAACATTACTGCAG    700

mtATP6           496 GCCACCTACTCATGCACCTAATTGGAAGCGCCACCCTAGCAATATCAACC    545
                     ||||||||||||||||||||||||||||||||||||||||||||.||||||
rATP6            701 GCCACCTACTCATGCACCTAATTGGAAGCGCCACCCTAGCAATGTCAACC    750

mtATP6           546 ATTAACCTTCCCTCTACACTTATCATCTTCACAATTCTAATTCTACTGAC    595
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
rATP6            751 ATTAACCTTCCCTCTACACTTATCATCTTCACAATTCTAATTCTACTGAC    800

mtATP6           596 TATCCTAGAAATCGCTGTCGCCTTAATCCAAGCCTACGTTTTCACACTTC    645
                     ||||||||||||||||||||||||||||||||||||||||||||||||||
rATP6            801 TATCCTAGAAATCGCTGTCGCCTTAATCCAAGCCTACGTTTTCACACTTC    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*.

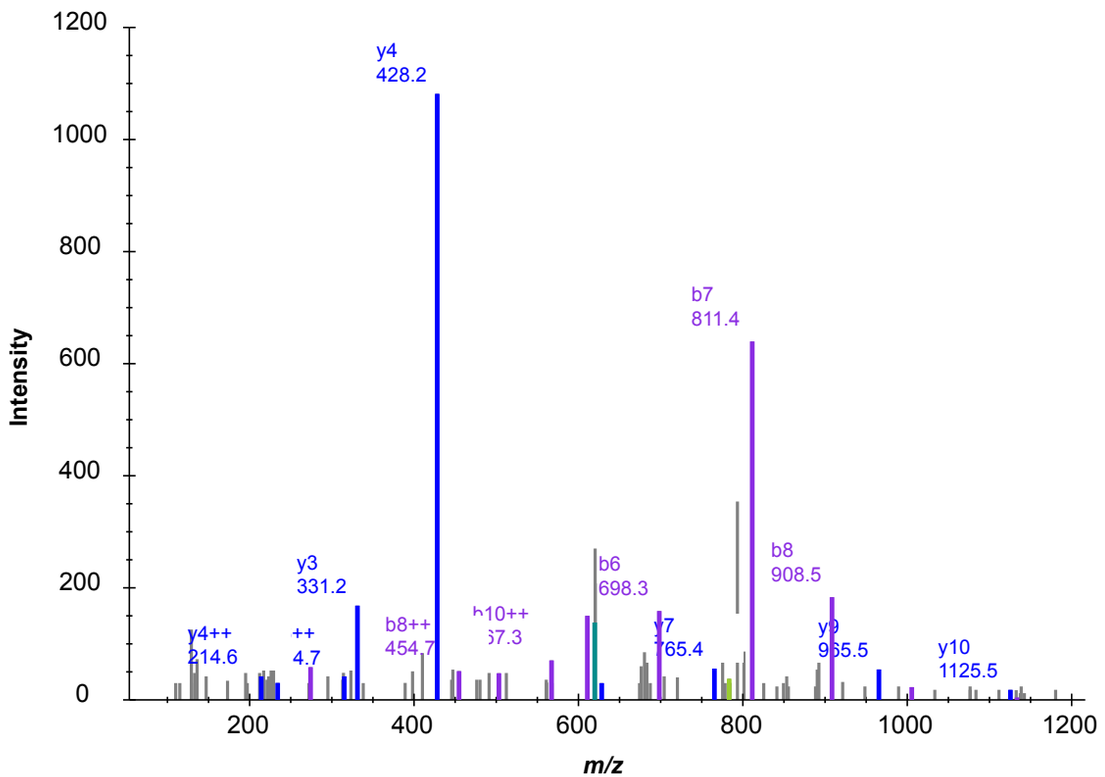
```
                                   ATP5G1 MTS
                 ____________________________________________________________
rATP6        MQTAGALFISPALIRCCTRGLIRPVSASFLNSPVNSSKQPSYSNFPLQVARREFQTSVVS   60
mtATP6       ------------------------------------------------------------   0

             ______
rATP6        RDIDTATRNENLFASFIAPTILGLPAAVLIILFPPLLIPTSKYLINNRLITTQQWLIKLT   120
mtATP6       -------MNENLFASFIAPTILGLPAAVLIILFPPLLIPTSKYLINNRLITTQQWLIKLT   53

rATP6        SKQMMTMHNTKGRTWSLMLVSLIIFIATTNLLGLLPHSFTPTTQLSMNLAMAIPLWAGTV   180
mtATP6       SKQMMTMHNTKGRTWSLMLVSLIIFIATTNLLGLLPHSFTPTTQLSMNLAMAIPLWAGTV   113
```

```
rATP6       IMGFRSKIKNALAHFLPQGTPTPLIPMLVIIETISLLIQPMALAVRLTANITAGHLLMHL   240
mtATP6      IMGFRSKIKNALAHFLPQGTPTPLIPMLVIIETISLLIQPMALAVRLTANITAGHLLMHL   173

                                                                Myc tag

rATP6       IGSATLAMSTINLPSTLIIFTILILLTILEIAVALIQAYVFTLLVSLYLHDNTLEQKLIS   300
mtATP6      IGSATLAMSTINLPSTLIIFTILILLTILEIAVALIQAYVFTLLVSLYLHDNT-------   226

                     FLAG tag

rATP6       EEDLAANDILDYKDDDDKV  319
mtATP6      -------------------  226
```

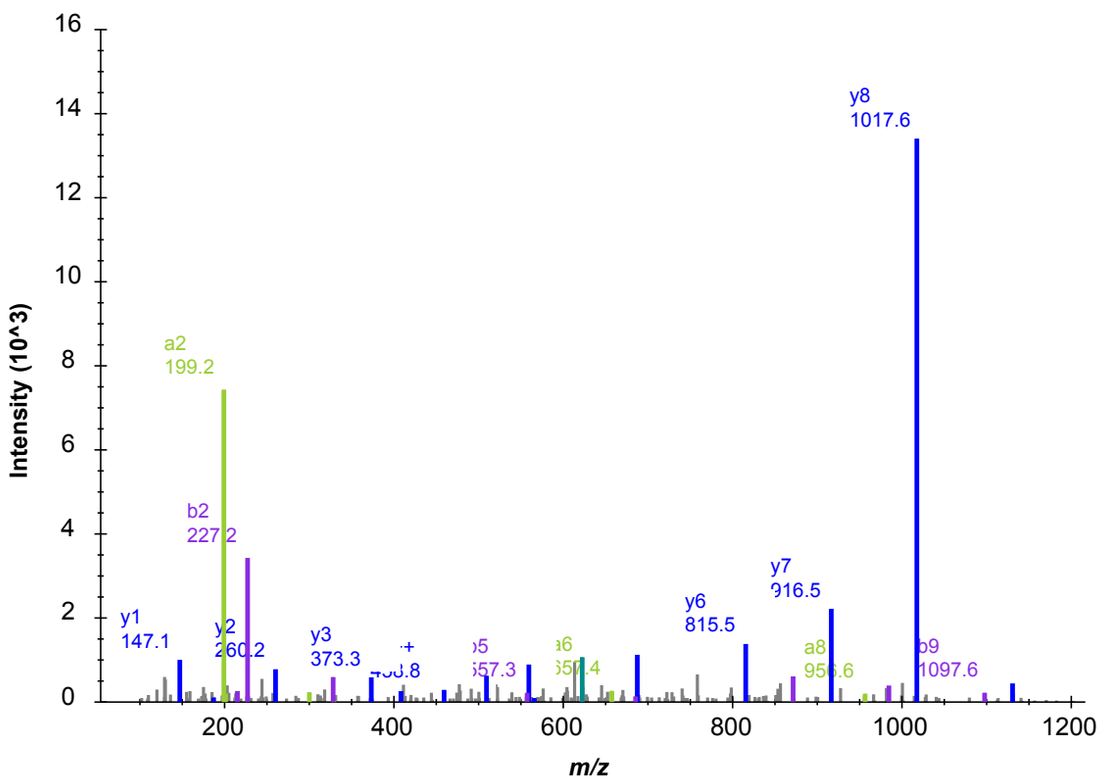
*Nucleotides labelled in red indicate required coding for productive nuclear translation.

Supplementary Figure S2

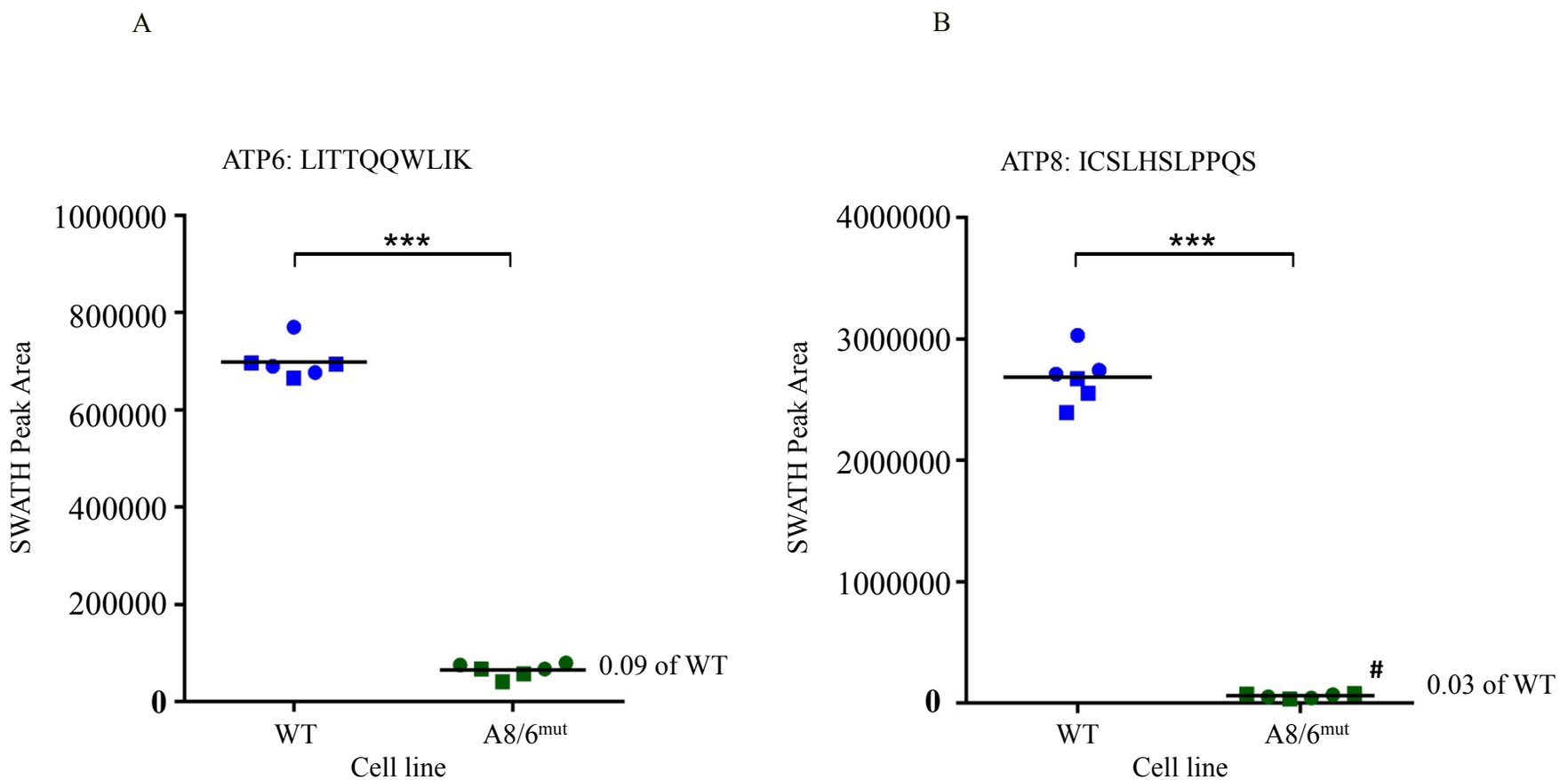
A



B

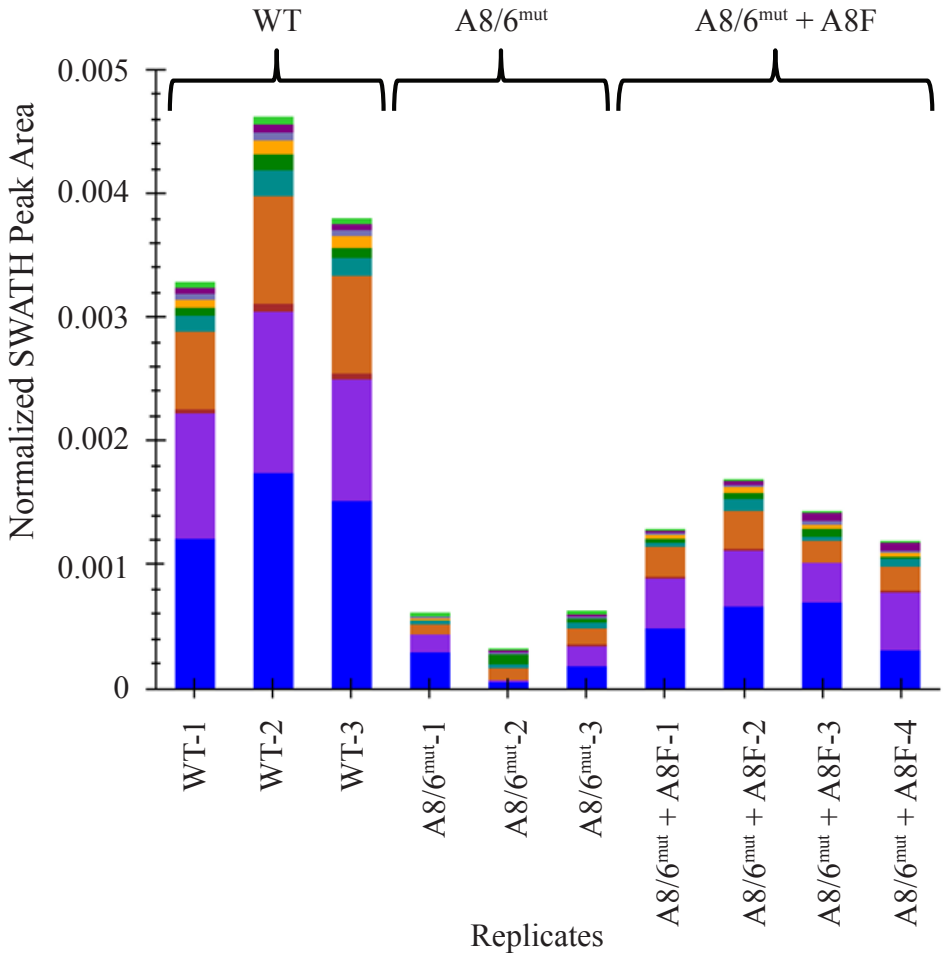


Supplementary Figure S3

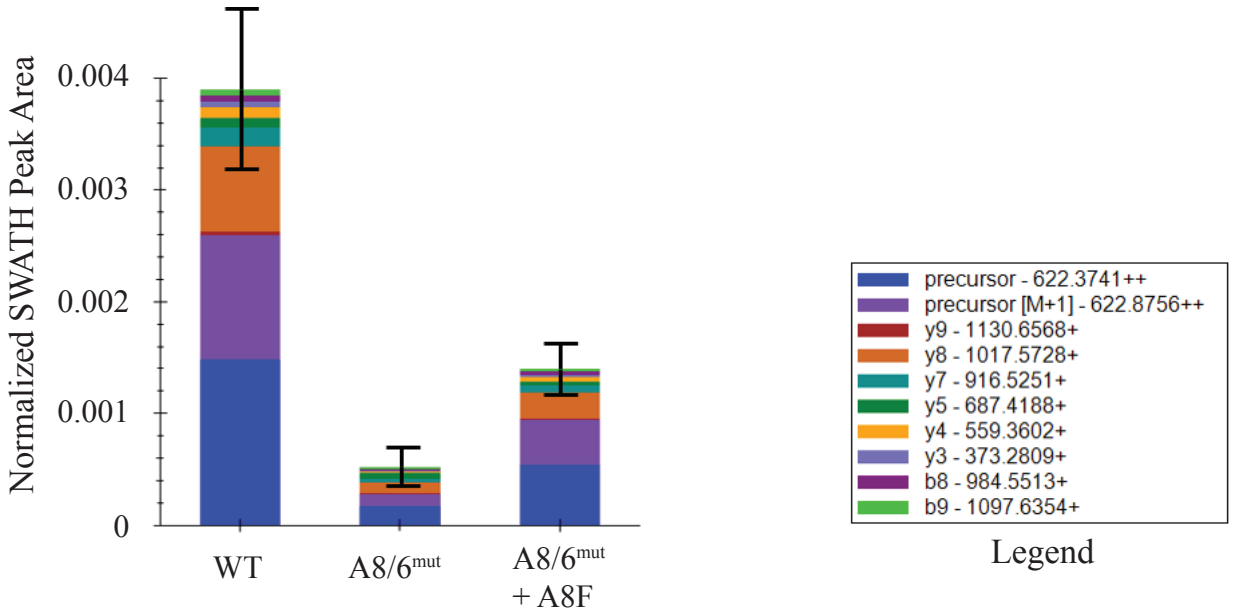


Supplementary Figure S4

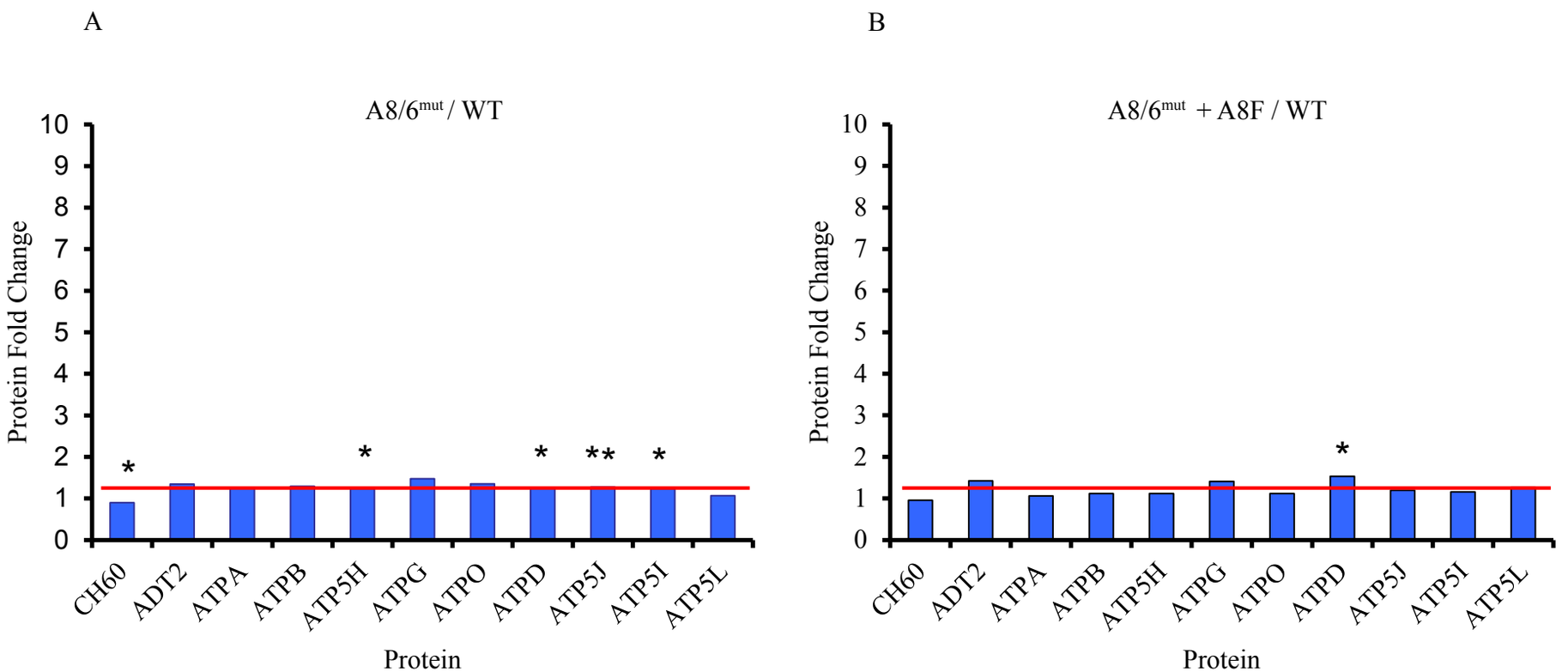
A.



B.

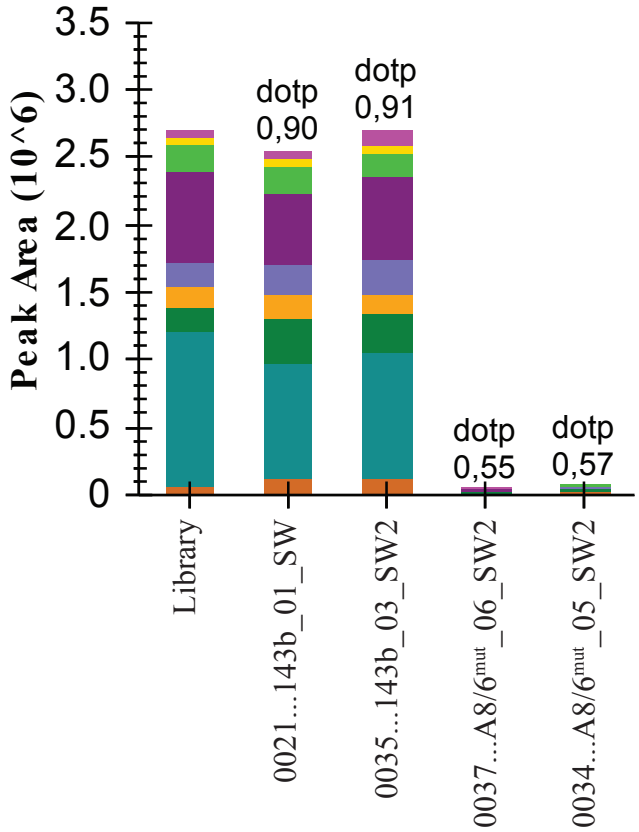


Supplementary Figure S5



Supplementary Figure S6

A.



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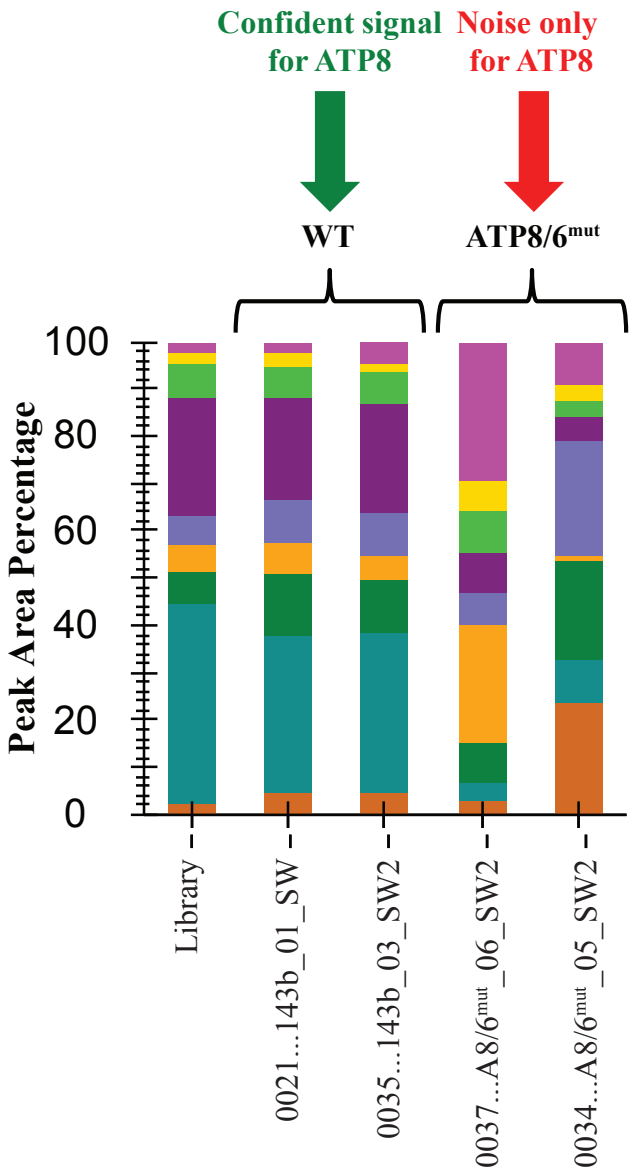
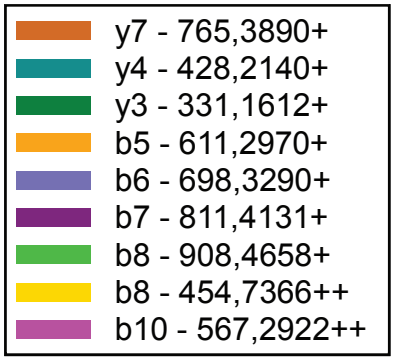
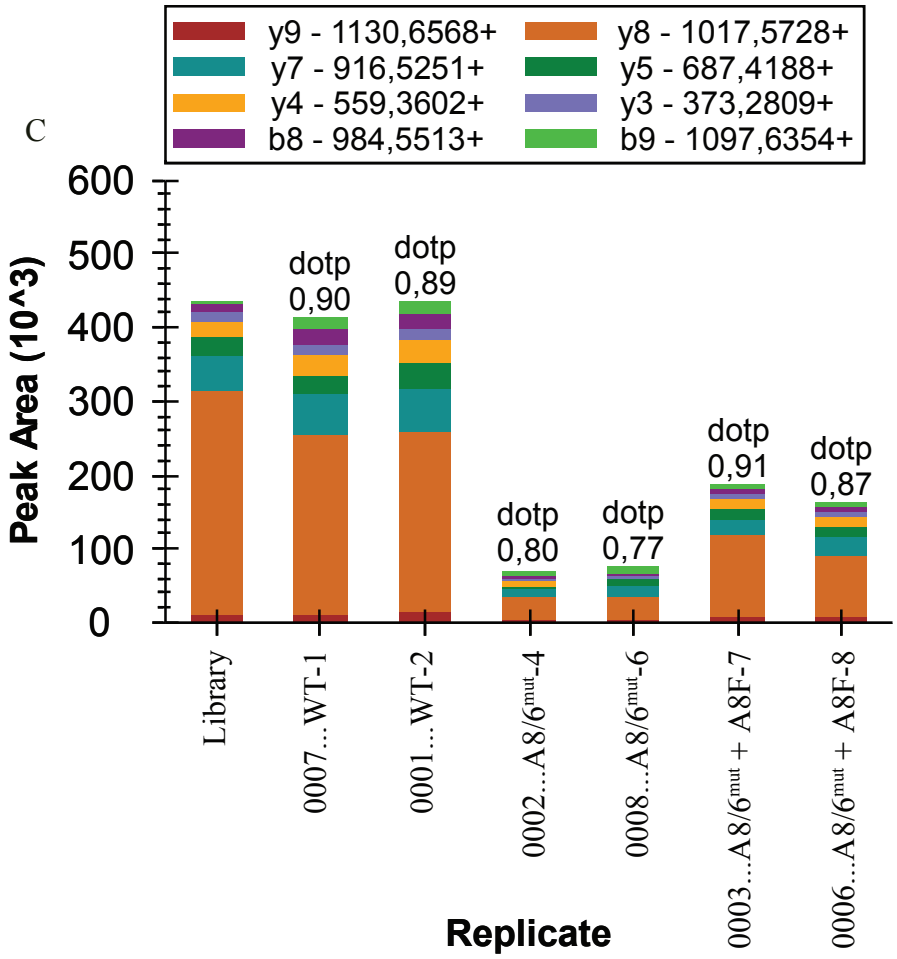




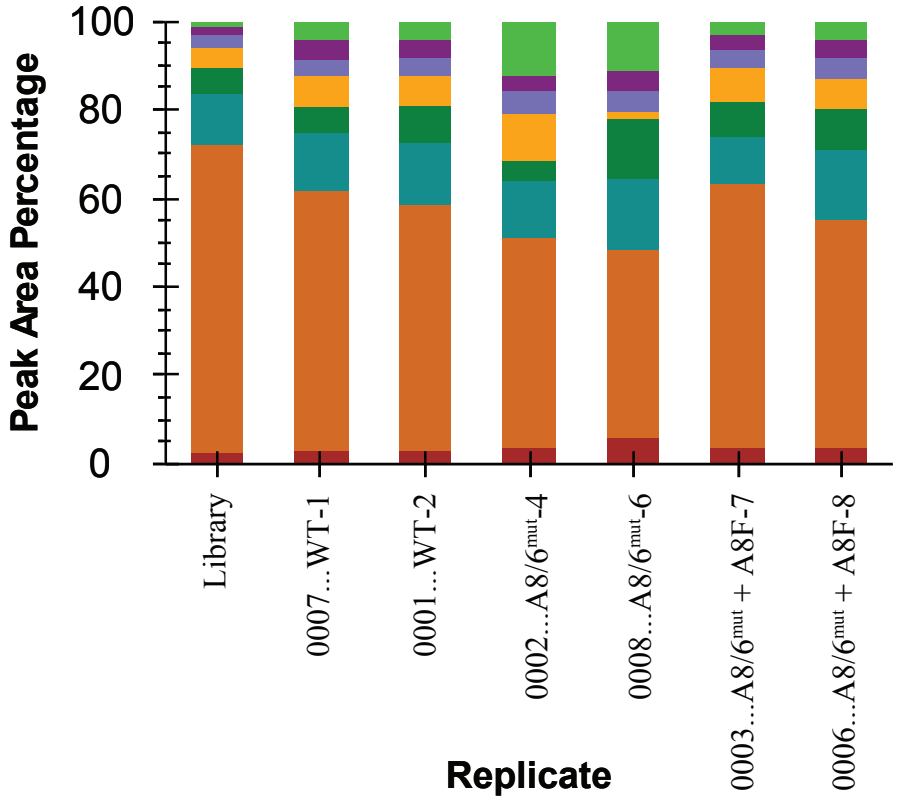
Legend for fragment ions

Supplementary Figure S6

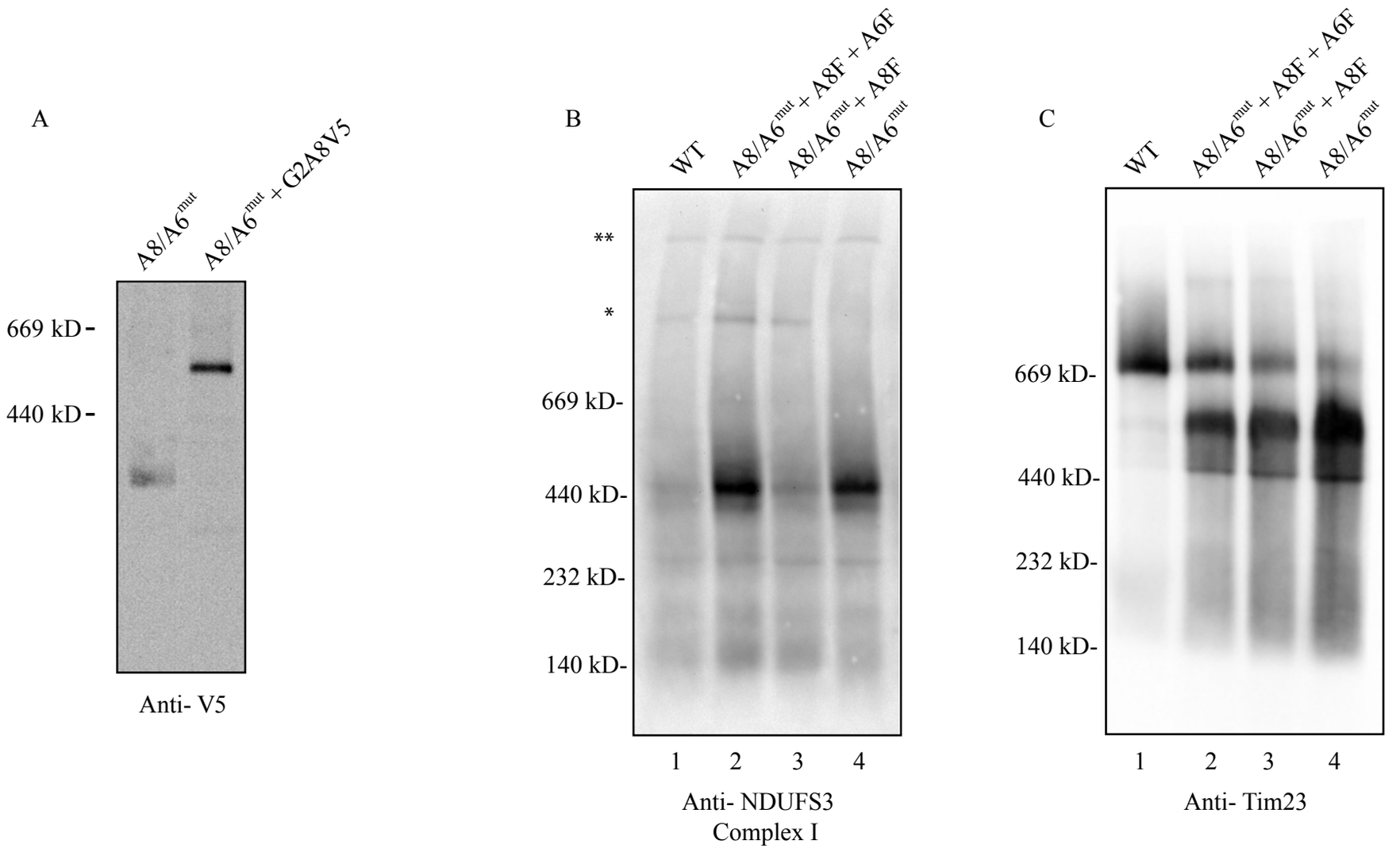
C



D



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 N	Unused Score	Total Score	Seq Coverage %Cov(95)	SwissProt Accession	Protein Name	Peptides(95%)
1	219.8	219.8	46.0	Q09666|AHNK_HUMAN	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK 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=LRPPRC 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	Endoplasmin 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|HXK1_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 S	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=	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	Q7KZF4|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=CFL1 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	Q9UJS0|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|NDUS1_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-Ib 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	Q9NVI7|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	Q96IR7|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=FH 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	P05556|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|SYIM_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 PI	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|GPDM_HUMAN	Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Homo sapiens GN=GPD2 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	10
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=EIF5AL1 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	O43707|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=SQRDL 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	Q8NBS9|TXND5_HUMAN	Thioredoxin domain-containing protein 5 OS=Homo sapiens GN=TXNDC5 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 SCaMC-1 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=TPI1 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=COX4I1 PE=1 SV=1	6
233	12.2	12.2	44.4	P30044|PRDX5_HUMAN	Peroxiredoxin-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 S	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=DDOST	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	Q9P0L0|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	Kinectin 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	P04083|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|TCPB_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=HNRNPA2B1 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|NIPS1_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	O14745|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	Q8IXI1|MIRO2_HUMAN	Mitochondrial Rho GTPase 2 OS=Homo sapiens GN=RHOT2 PE=1 SV=2	6
288	10.0	10.1	36.3	P09429|HMGB1_HUMAN	High mobility group protein B1 OS=Homo sapiens GN=HMGB1 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|YMEL1_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|CSRP1_HUMAN	Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSRP1 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|SCPDL_HUMAN	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1	6
303	9.7	10.0	26.1	Q7L0Y3|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|GDIB_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	Alkyldihydroxyacetonephosphate 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	5
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	5
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|PDLI1_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=MCCC2 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=HNRNPK 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=	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	4
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	Adenylyl 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=HNRNPH1 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|PGRC1_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	4
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	4
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|1433T_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	4
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	Q969Z0|TBRG4_HUMAN	Protein TBRG4 OS=Homo sapiens GN=TBRG4 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|SC22B_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=	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|UCRI_HUMAN	Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Homo sapiens GN=UQCRFS1 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=NDUFV1 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=	5
440	6.2	6.2	5.6	Q92896|GSLG1_HUMAN	Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 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 S	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=	3
455	6.1	6.1	13.7	P05198|IF2A_HUMAN	Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 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	Destrin 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|HMGA1_HUMAN	High mobility group protein HMG-I/HMG-Y OS=Homo sapiens GN=HMGA1 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	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=OCIAD1 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	4
486	5.8	5.9	16.8	P50454|SERPH_HUMAN	Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2	4
487	5.8	6.0	5.7	P29317|EPHA2_HUMAN	Ephrin type-A receptor 2 OS=Homo sapiens GN=EPHA2 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	Q9P0M9|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 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	Q7Z7H8|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	Q9NZ45|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	Q9NYJ1|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|S10AB_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=EIF2S3 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=TIMM23B	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|STEA3_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	Utrophin 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	Q9Y3B7|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=NDU	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=FARSB 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	Q8IYB8|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|MARH5_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 S\	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	3
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|FKB11_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=OCIAD2 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	Q9NVS2|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	Q9NRV9|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=RPS9 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
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=VARS 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=NDUI	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|FKB10_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:adrenodoxin 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=RPS10 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|GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1 OS=Homo sapiens GN=ARHGDIA 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=ITGA1 PE=1 SV=2	2
757	2.7	2.7	19.7	O75251|NDUS7_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial OS=Homo sapiens GN=NDUFS7 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=ERLIN1 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=NDUFB9 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	Q9UIJ7|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	Q8WWI1|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|ODBB_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	3
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	Q9UMS0|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

Replicate	Strain	precursor [M] - 622.37++ Peak Area normalized to Stds	precursor [M+1] - 622.88++ Peak Area normalized to Stds	y9 - 1130.66+ Peak Area normalized to Stds	y8 - 1017.57+ Peak Area normalized to Stds	y7 - 916.53+ Peak Area normalized to Stds	y5 - 687.42+ Peak Area normalized to Stds	y4 - 559.36+ Peak Area normalized to Stds	y3 - 373.28+ Peak Area normalized to Stds	b8 - 984.55+ Peak Area normalized to Stds	b9 - 1097.64+ Peak Area normalized to Stds	**Sum all transitions Peak Area normalized to Stds**
0007_MB5_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_MB5_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_MB5_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_MB5_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_MB5_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_MB5_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_MB5_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_MB5_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_MB5_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_MB5_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
average (normalized Peak Area	0.00390	0.00052	0.00140
stdev (normalized Peak Area)	0.00068	0.00017	0.00022

	pvalue
A8/6mut vs WT	0.00965
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’ttataacaaaccctgagaaccaaaat**g3’**	5’ttataacaaaccctgagaaccaaaat**a3’**
Fwd 1	5’ttataacaaaccctgagaaccaaaa**cg**3’	5’ttataacaaaccctgagaaccaaaa**ca3’**
Fwd 2	5’ttataacaaaccctgagaaccaaa**tcg3’**	5’ttataacaaaccctgagaaccaaa**tca3’**
Reverse	5’gtactgatcattctatttcc3’	5’gtactgatcattctatttcc3’

Supplementary Table S4

Strain/clone	**ΔC_T (Mut1bp-WT1bp)**	**Strain/clone**	**ΔCT (Mut1bp-WT1bp)**
WT(143 B)	14.87	R2ΔA8#1	5.8
ΔA8 parental	-7.75	R2ΔA8#2	7.42
R1ΔA8#1	13.885	R2ΔA8#3	13.23
R1ΔA8#2	-1.66	R2ΔA8#4	10.4
R1ΔA8#3	13.005	R2ΔA8#5	14.51
R1ΔA8#5	14.82	R2ΔA8#8	14.52
R1ΔA8#7	-8.25	R2ΔA8#9	13.05
R1ΔA8#11	3.32	R2ΔA8#10	13.31
R1ΔA8#12	-8.54	R2ΔA8#16	13.92
R1ΔA8#13	-11.08*	R2ΔA8#18	14.12
R1ΔA8#14	-7.92	R2ΔA8#19	12.85
R1ΔA8#16	14.32	R2ΔA8#20	14.21
R1ΔA8#17	8.3	R2ΔA8#22	15.58
R1ΔA8#22	13.82		
R1ΔA8#23	14.24		

*had very slow growth.

Supplementary Table S5

Cell line	**G1-*ATP8* -$\Delta C_{T(test-parental)}$**	**G1-*ATP6* -$\Delta C_{T(test-parental)}$**
A8/6^{mut} + A8F	10.84 ± 0.56	0.77 ± 0.44
A8/6^{mut} + A8F + A6F	12.74 ± 1.15	8.58 ± 0.79
A8/6^{mut} + 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 ± 0.04	0.84 ± 0.23	0.17 ± 0.16	0.30 ± 0.03	0.21 ± 0.24	0.46 ± 0.09
A8/6^{mut}	0.12 ± 0.15	0.08 ± 0.11	0.06 ± 0.64	0.18 ± 0.93	N/A*	
A8/6^{mut} +A6F	-0.47 ± 0.16	-0.10 ± 0.27	0.38 ± 0.39	2.51 ± 0.58	N/A*	
A8/6^{mut} +A8F	-1.10 ± 0.19	0.01 ± 0.09	-0.45 ± 0.01	-0.20 ± 0.42	-0.72 ± 0.07	-0.23 ± 0.55
A8/6^{mut} + A8F + A6F	0.57 ± 0.16	-0.06 ± 0.09	-0.15 ± 0.06	0.05 ± 0.16	0.31 ± 0.26	-0.03 ± 0.16

$\Delta\Delta C_T$ Values