Supplemental Table 1. MRM transitions for targeted peptides.

Peptide	Sequence	Precursor m/z (charge)	Transitions (ions, m/z)						
NCC	SGGTYFLISR	550.8 (2+)	y_9 1013.5	$y_9^{(2+)}$ 507.3	y_8 956.5	y_7 899.5	y_6 798.5	y_5 635.4	y_4 488.3
αENaC	AEQNDFIPLLSTVTGAR	916.5 (2+)	y_{12} 1274.7	y_{11} 1127.7	y_{10} 1014.6	y_8 804.5	y_7 691.4	y_6 604.3	
γENaC	HLLADLEQETR	662.8 (2+)	y_{10} 1187.6	y_9 1074.5	y_8 961.5	y_7 890.4	y_6 775.4	y_4 533.3	

Supplemental Table 2. Significantly altered proteins

	Protein Annotation	Protein Name/Description	Ratio LS/HS	Adjusted *p* -value
1	sp|Q7L3S4|ZN771_HUMAN	Zinc finger protein 771 OS=Homo sapiens GN=ZNF771 PE=1 SV=1	2.56	0.00000
2	sp|Q5SSJ5|HP1B3_HUMAN	Heterochromatin protein 1-binding protein 3 OS=Homo sapiens GN=HP1BP3 PE=1 SV=1	0.37	0.00000
3	sp|O00187|MASP2_HUMAN	Mannan-binding lectin serine protease 2 OS=Homo sapiens GN=MASP2 PE=1 SV=4	5.44	0.00005
4	sp|Q6NT55|CP4FN_HUMAN	Cytochrome P450 4F22 OS=Homo sapiens GN=CYP4F22 PE=2 SV=1	0.43	0.00005
5	sp|Q92556|ELMO1_HUMAN	Engulfment and cell motility protein 1 OS=Homo sapiens GN=ELMO1 PE=1 SV=2	0.51	0.00005
6	sp|P40394|ADH7_HUMAN	Alcohol dehydrogenase class 4 mu/sigma chain OS=Homo sapiens GN=ADH7 PE=1 SV=2	0.45	0.00005
7	sp|Q9C075|K1C23_HUMAN	Keratin, type I cytoskeletal 23 OS=Homo sapiens GN=KRT23 PE=1 SV=2	0.16	0.00005
8	sp|Q9BXJ7|AMNLS_HUMAN	Protein amnionless OS=Homo sapiens GN=AMN PE=1 SV=2	1.29	0.00008
9	sp|Q92619|HMHA1_HUMAN	Minor histocompatibility protein HA-1 OS=Homo sapiens GN=HMHA1 PE=1 SV=2	0.43	0.00008
10	sp|P49411|EFTU_HUMAN	Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2	0.37	0.00014
11	sp|Q9ULG6|CCPG1_HUMAN	Cell cycle progression protein 1 OS=Homo sapiens GN=CCPG1 PE=1 SV=3	0.08	0.00021
12	sp|P52272|HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3	0.23	0.00030
13	sp|K1HA_HUMAN|	sp|K1HA_HUMAN|	0.19	0.00030
14	sp|Q15274|NADC_HUMAN	Nicotinate-nucleotide pyrophosphorylase [carboxylating] OS=Homo sapiens GN=QPRT PE=1 SV=3	3.06	0.00031
15	sp|P13639|EF2_HUMAN	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	0.47	0.00039
16	sp|Q9H2M9|RBGPR_HUMAN	Rab3 GTPase-activating protein non-catalytic subunit OS=Homo sapiens GN=RAB3GAP2 PE=1 SV=1	0.48	0.00041
17	sp|Q8NI99|ANGL6_HUMAN	Angiopoietin-related protein 6 OS=Homo sapiens GN=ANGPTL6 PE=1 SV=1	4.42	0.00043
18	sp|P19878|NCF2_HUMAN	Neutrophil cytosol factor 2 OS=Homo sapiens GN=NCF2 PE=1 SV=2	0.38	0.00047
19	sp|Q9BRT3|MIEN1_HUMAN	Migration and invasion enhancer 1 OS=Homo sapiens GN=MIEN1 PE=1 SV=1	2.15	0.00050
20	sp|Q5VVQ6|OTU1_HUMAN	Ubiquitin thioesterase OTU1 OS=Homo sapiens GN=YOD1 PE=1 SV=1	0.35	0.00050
21	sp|Q9H0P0|5NT3_HUMAN	Cytosolic 5'-nucleotidase 3 OS=Homo sapiens GN=NT5C3 PE=1 SV=3	0.50	0.00050
22	sp|Q13508|NAR3_HUMAN	Ecto-ADP-ribosyltransferase 3 OS=Homo sapiens GN=ART3 PE=1 SV=2	0.52	0.00050
23	sp|P15880|RS2_HUMAN	40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2	0.30	0.00055
24	sp|P30519|HMOX2_HUMAN	Heme oxygenase 2 OS=Homo sapiens GN=HMOX2 PE=1 SV=2	0.49	0.00055
25	sp|O95171|SCEL_HUMAN	Sciellin OS=Homo sapiens GN=SCEL PE=1 SV=2	0.26	0.00061
26	sp|O43149|ZZEF1_HUMAN	Zinc finger ZZ-type and EF-hand domain-containing protein 1 OS=Homo sapiens GN=ZZEF1 PE=1 SV=6	0.19	0.00061
27	sp|Q9Y446|PKP3_HUMAN	Plakophilin-3 OS=Homo sapiens GN=PKP3 PE=1 SV=1	0.29	0.00087
28	sp|P02545|LMNA_HUMAN	Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	0.31	0.00088
29	sp|O75594|PGRP1_HUMAN	Peptidoglycan recognition protein 1 OS=Homo sapiens GN=PGLYRP1 PE=1 SV=1	3.33	0.00101
30	sp|P49327|FAS_HUMAN	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	0.44	0.00130
31	sp|P35232|PHB_HUMAN	Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1	0.41	0.00130
32	sp|Q14515|SPRL1_HUMAN	SPARC-like protein 1 OS=Homo sapiens GN=SPARCL1 PE=1 SV=2	3.28	0.00134
33	sp|Q14116|IL18_HUMAN	Interleukin-18 OS=Homo sapiens GN=IL18 PE=1 SV=1	0.37	0.00134
34	sp|O75487|GPC4_HUMAN	Glypican-4 OS=Homo sapiens GN=GPC4 PE=1 SV=4	4.41	0.00143
35	sp|O43175|SERA_HUMAN	D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4	0.61	0.00144
36	sp|P00749|UROK_HUMAN	Urokinase-type plasminogen activator OS=Homo sapiens GN=PLAU PE=1 SV=2	2.78	0.00148
37	sp|P01033|TIMP1_HUMAN	Metalloproteinase inhibitor 1 OS=Homo sapiens GN=TIMP1 PE=1 SV=1	1.12	0.00148
38	sp|P24158|PRTN3_HUMAN	Myeloblastin OS=Homo sapiens GN=PRTN3 PE=1 SV=3	2.91	0.00156
39	sp|Q86XP0|PA24D_HUMAN	Cytosolic phospholipase A2 delta OS=Homo sapiens GN=PLA2G4D PE=2 SV=2	0.37	0.00156
40	sp|Q9H159|CAD19_HUMAN	Cadherin-19 OS=Homo sapiens GN=CDH19 PE=2 SV=1	1.96	0.00171
41	sp|Q9HAT2|SIAE_HUMAN	Sialate O-acetylesterase OS=Homo sapiens GN=SIAE PE=1 SV=1	2.79	0.00171
42	sp|Q96FV2|SCRN2_HUMAN	Secernin-2 OS=Homo sapiens GN=SCRN2 PE=2 SV=3	1.60	0.00178
43	sp|P14923|PLAK_HUMAN	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	0.33	0.00180
44	sp|P20700|LMNB1_HUMAN	Lamin-B1 OS=Homo sapiens GN=LMNB1 PE=1 SV=2	0.54	0.00205
45	sp|P18827|SDC1_HUMAN	Syndecan-1 OS=Homo sapiens GN=SDC1 PE=1 SV=3	2.80	0.00223
46	sp|Q8N1N4|K2C78_HUMAN	Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=2 SV=2	0.49	0.00223
47	sp|P51572|BAP31_HUMAN	B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31 PE=1 SV=3	0.46	0.00223
48	sp|P61254|RL26_HUMAN	60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1	0.35	0.00258
49	sp|P55083|MFAP4_HUMAN	Microfibril-associated glycoprotein 4 OS=Homo sapiens GN=MFAP4 PE=1 SV=2	2.07	0.00316
50	sp|Q6W4X9|MUC6_HUMAN	Mucin-6 OS=Homo sapiens GN=MUC6 PE=1 SV=3	9.31	0.00330
51	sp|Q92817|EVPL_HUMAN	Envoplakin OS=Homo sapiens GN=EVPL PE=1 SV=3	0.42	0.00336
52	sp|P55290|CAD13_HUMAN	Cadherin-13 OS=Homo sapiens GN=CDH13 PE=1 SV=1	1.46	0.00348
53	sp|Q7Z406|MYH14_HUMAN	Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2	0.39	0.00348
54	sp|A1L0T0|ILVBL_HUMAN	Acetolactate synthase-like protein OS=Homo sapiens GN=ILVBL PE=1 SV=2	0.45	0.00348
55	sp|Q6B0K9|HBM_HUMAN	Hemoglobin subunit mu OS=Homo sapiens GN=HBM PE=2 SV=1	1.72	0.00351
56	sp|P33121|ACSL1_HUMAN	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1	0.37	0.00351
57	sp|P62280|RS11_HUMAN	40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3	0.25	0.00351
58	sp|O15372|EIF3H_HUMAN	Eukaryotic translation initiation factor 3 subunit H OS=Homo sapiens GN=EIF3H PE=1 SV=1	0.45	0.00351
59	sp|P07305|H10_HUMAN	Histone H1.0 OS=Homo sapiens GN=H1F0 PE=1 SV=3	0.36	0.00351
60	sp|Q96NR8|RDH12_HUMAN	Retinol dehydrogenase 12 OS=Homo sapiens GN=RDH12 PE=1 SV=3	0.64	0.00400
61	sp|Q6ZUI0|TPRG1_HUMAN	Tumor protein p63-regulated gene 1 protein OS=Homo sapiens GN=TPRG1 PE=2 SV=1	0.44	0.00400
62	sp|P30101|PDIA3_HUMAN	Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4	0.30	0.00406
63	sp|Q02083|NAAA_HUMAN	N-acylethanolamine-hydrolyzing acid amidase OS=Homo sapiens GN=NAAA PE=1 SV=3	2.27	0.00426
64	sp|P30046|DOPD_HUMAN	D-dopachrome decarboxylase OS=Homo sapiens GN=DDT PE=1 SV=3	1.63	0.00459
65	sp|Q9BTV4|TMM43_HUMAN	Transmembrane protein 43 OS=Homo sapiens GN=TMEM43 PE=1 SV=1	0.43	0.00459
66	sp|P01611|KV119_HUMAN	Ig kappa chain V-I region Wes OS=Homo sapiens PE=1 SV=1	2.12	0.00462
67	sp|Q96DA0|ZG16B_HUMAN	Zymogen granule protein 16 homolog B OS=Homo sapiens GN=ZG16B PE=1 SV=3	4.13	0.00462
68	sp|P01833|PIGR_HUMAN	Polymeric immunoglobulin receptor OS=Homo sapiens GN=PIGR PE=1 SV=4	2.57	0.00462
69	sp|P00367|DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial OS=Homo sapiens GN=GLUD1 PE=1 SV=2	0.39	0.00462
70	sp|P06576|ATPB_HUMAN	ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	0.29	0.00462
71	sp|Q3ZCV2|CA177_HUMAN	Uncharacterized protein C1orf177 OS=Homo sapiens GN=C1orf177 PE=2 SV=3	0.40	0.00462
72	sp|Q07065|CKAP4_HUMAN	Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2	0.42	0.00473
73	sp|Q9UMR5|PPT2_HUMAN	Lysosomal thioesterase PPT2 OS=Homo sapiens GN=PPT2 PE=1 SV=4	0.31	0.00473
74	sp|Q13835|PKP1_HUMAN	Plakophilin-1 OS=Homo sapiens GN=PKP1 PE=1 SV=2	0.35	0.00518
75	sp|Q13332|PTPRS_HUMAN	Receptor-type tyrosine-protein phosphatase S OS=Homo sapiens GN=PTPRS PE=1 SV=3	2.08	0.00519
76	sp|P15924|DESP_HUMAN	Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	0.36	0.00519
77	sp|P46776|RL27A_HUMAN	60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2	0.40	0.00531
78	sp|P12273|PIP_HUMAN	Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1	5.85	0.00586
79	sp|Q92614|MY18A_HUMAN	Unconventional myosin-XVIIIa OS=Homo sapiens GN=MYO18A PE=1 SV=3	0.49	0.00586
80	sp|P25705|ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1	0.31	0.00616

	Protein Annotation	Protein Name/Description	Ratio LS/HS	Adjusted *p* -value
81	sp|P12956|XRCC6_HUMAN	X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2	0.38	0.00633
82	sp|P05109|S10A8_HUMAN	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	2.27	0.00653
83	sp|Q00839|HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	0.28	0.00654
84	sp|P36639|8ODP_HUMAN	7,8-dihydro-8-oxoguanine triphosphatase OS=Homo sapiens GN=NUDT1 PE=1 SV=3	1.52	0.00666
85	sp|P04843|RPN1_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1	0.39	0.00674
86	sp|P46781|RS9_HUMAN	40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3	0.49	0.00750
87	sp|Q02818|NUCB1_HUMAN	Nucleobindin-1 OS=Homo sapiens GN=NUCB1 PE=1 SV=4	1.96	0.00756
88	sp|O14964|HGS_HUMAN	Hepatocyte growth factor-regulated tyrosine kinase substrate OS=Homo sapiens GN=HGS PE=1 SV=1	0.48	0.00789
89	sp|Q07507|DERM_HUMAN	Dermatopontin OS=Homo sapiens GN=DPT PE=2 SV=2	1.35	0.00794
90	sp|P49755|TMEDA_HUMAN	Transmembrane emp24 domain-containing protein 10 OS=Homo sapiens GN=TMED10 PE=1 SV=2	0.44	0.00858
91	sp|P07942|LAMB1_HUMAN	Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=1 SV=2	1.43	0.00859
92	sp|O75015|FCG3B_HUMAN	Low affinity immunoglobulin gamma Fc region receptor III-B OS=Homo sapiens GN=FCGR3B PE=1 SV=2	0.38	0.00859
93	sp|P09871|C1S_HUMAN	Complement C1s subcomponent OS=Homo sapiens GN=C1S PE=1 SV=1	1.15	0.00893
94	sp|P45381|ACY2_HUMAN	Aspartoacylase OS=Homo sapiens GN=ASPA PE=1 SV=1	1.36	0.00948
95	sp|P16615|AT2A2_HUMAN	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1	0.46	0.00948
96	sp|P42766|RL35_HUMAN	60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2	0.46	0.00948
97	sp|P83731|RL24_HUMAN	60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1	0.33	0.00948
98	sp|P61970|NTF2_HUMAN	Nuclear transport factor 2 OS=Homo sapiens GN=NUTF2 PE=1 SV=1	2.42	0.00974
99	sp|P60842|IF4A1_HUMAN	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1	0.57	0.01009
100	sp|Q8WVV4|POF1B_HUMAN	Protein POF1B OS=Homo sapiens GN=POF1B PE=1 SV=3	0.28	0.01025
101	sp|Q9H8H3|MET7A_HUMAN	Methyltransferase-like protein 7A OS=Homo sapiens GN=METTL7A PE=1 SV=1	0.49	0.01035
102	sp|Q9NZ01|TECR_HUMAN	Trans-2,3-enoyl-CoA reductase OS=Homo sapiens GN=TECR PE=1 SV=1	0.56	0.01035
103	sp|Q71DI3|H32_HUMAN	Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3	0.34	0.01044
104	sp|O60613|SEP15_HUMAN	15 kDa selenoprotein OS=Homo sapiens GN=SEP15 PE=1 SV=3	1.43	0.01054
105	sp|Q9Y287|ITM2B_HUMAN	Integral membrane protein 2B OS=Homo sapiens GN=ITM2B PE=1 SV=1	2.87	0.01054
106	sp|P18124|RL7_HUMAN	60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1	0.50	0.01054
107	sp|K1C15_SHEEP|	sp|K1C15_SHEEP|	0.48	0.01054
108	sp|P40939|ECHA_HUMAN	Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2	0.42	0.01054
109	sp|P61247|RS3A_HUMAN	40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2	0.41	0.01054
110	sp|Q13617|CUL2_HUMAN	Cullin-2 OS=Homo sapiens GN=CUL2 PE=1 SV=2	0.52	0.01054
111	sp|Q9UGI8|TES_HUMAN	Testin OS=Homo sapiens GN=TES PE=1 SV=1	0.45	0.01060
112	sp|Q4LDE5|SVEP1_HUMAN	Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 OS=Homo sapiens GN=SVEP1 PE=1 SV=3	1.14	0.01065
113	sp|Q9Y5Y2|NUBP2_HUMAN	Cytosolic Fe-S cluster assembly factor NUBP2 OS=Homo sapiens GN=NUBP2 PE=1 SV=1	0.48	0.01071
114	sp|P01034|CYTC_HUMAN	Cystatin-C OS=Homo sapiens GN=CST3 PE=1 SV=1	2.40	0.01110
115	sp|Q96GD0|PLPP_HUMAN	Pyridoxal phosphate phosphatase OS=Homo sapiens GN=PDXP PE=1 SV=2	6.97	0.01167
116	sp|O60437|PEPL_HUMAN	Periplakin OS=Homo sapiens GN=PPL PE=1 SV=4	0.39	0.01172
117	sp|Q6ZMN7|PZRN4_HUMAN	PDZ domain-containing RING finger protein 4 OS=Homo sapiens GN=PDZRN4 PE=1 SV=3	7.62	0.01180
118	sp|Q6P4A8|PLBL1_HUMAN	Phospholipase B-like 1 OS=Homo sapiens GN=PLBD1 PE=1 SV=2	1.59	0.01180
119	sp|P09651|ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=5	0.37	0.01180
120	sp|O00151|PDLI1_HUMAN	PDZ and LIM domain protein 1 OS=Homo sapiens GN=PDLIM1 PE=1 SV=4	0.36	0.01180
121	sp|P20160|CAP7_HUMAN	Azurocidin OS=Homo sapiens GN=AZU1 PE=1 SV=3	2.67	0.01219
122	sp|Q9H7P6|F125B_HUMAN	Multivesicular body subunit 12B OS=Homo sapiens GN=FAM125B PE=1 SV=2	2.23	0.01243
123	sp|P52790|HXK3_HUMAN	Hexokinase-3 OS=Homo sapiens GN=HK3 PE=1 SV=2	0.26	0.01243
124	sp|Q15904|VAS1_HUMAN	V-type proton ATPase subunit S1 OS=Homo sapiens GN=ATP6AP1 PE=1 SV=2	1.94	0.01305
125	sp|P10619|PPGB_HUMAN	Lysosomal protective protein OS=Homo sapiens GN=CTSA PE=1 SV=2	2.82	0.01331
126	sp|P04264|K2C1_HUMAN	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	0.56	0.01331
127	sp|Q9ULV0|MYO5B_HUMAN	Unconventional myosin-Vb OS=Homo sapiens GN=MYO5B PE=1 SV=3	0.48	0.01331
128	sp|P57088|TMM33_HUMAN	Transmembrane protein 33 OS=Homo sapiens GN=TMEM33 PE=1 SV=2	0.48	0.01331
129	sp|Q96S59|RANB9_HUMAN	Ran-binding protein 9 OS=Homo sapiens GN=RANBP9 PE=1 SV=1	0.55	0.01331
130	sp|Q5K651|SAMD9_HUMAN	Sterile alpha motif domain-containing protein 9 OS=Homo sapiens GN=SAMD9 PE=1 SV=1	0.38	0.01331
131	sp|Q9ULV4|COR1C_HUMAN	Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1	0.44	0.01331
132	sp|O95394|AGM1_HUMAN	Phosphoacetylglucosamine mutase OS=Homo sapiens GN=PGM3 PE=1 SV=1	0.40	0.01331
133	sp|Q8WVN6|SCTM1_HUMAN	Secreted and transmembrane protein 1 OS=Homo sapiens GN=SECTM1 PE=1 SV=2	3.36	0.01338
134	sp|P04196|HRG_HUMAN	Histidine-rich glycoprotein OS=Homo sapiens GN=HRG PE=1 SV=1	2.10	0.01338
135	sp|P31947|1433S_HUMAN	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1	0.44	0.01338
136	sp|Q96SA4|SERC2_HUMAN	Serine incorporator 2 OS=Homo sapiens GN=SERINC2 PE=2 SV=3	4.55	0.01343
137	sp|P00736|C1R_HUMAN	Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2	2.20	0.01379
138	sp|O95967|FBLN4_HUMAN	EGF-containing fibulin-like extracellular matrix protein 2 OS=Homo sapiens GN=EFEMP2 PE=1 SV=3	1.80	0.01379
139	sp|Q15084|PDIA6_HUMAN	Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1	0.36	0.01452
140	sp|Q16270|IBP7_HUMAN	Insulin-like growth factor-binding protein 7 OS=Homo sapiens GN=IGFBP7 PE=1 SV=1	1.92	0.01458
141	sp|P63151|2ABA_HUMAN	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Homo sapiens GN=PPP2R2A PE=1 SV=1	0.47	0.01458
142	sp|O75390|CISY_HUMAN	Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2	0.35	0.01458
143	sp|Q8NCL4|GALT6_HUMAN	Polypeptide N-acetylgalactosaminyltransferase 6 OS=Homo sapiens GN=GALNT6 PE=2 SV=2	1.35	0.01487
144	sp|P30085|KCY_HUMAN	UMP-CMP kinase OS=Homo sapiens GN=CMPK1 PE=1 SV=3	0.52	0.01487
145	sp|P27824|CALX_HUMAN	Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2	0.45	0.01499
146	sp|P62826|RAN_HUMAN	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3	0.40	0.01499
147	sp|Q15149|PLEC_HUMAN	Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3	0.42	0.01548
148	sp|O14773|TPP1_HUMAN	Tripeptidyl-peptidase 1 OS=Homo sapiens GN=TPP1 PE=1 SV=2	2.00	0.01584
149	sp|P78527|PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3	0.42	0.01690
150	sp|Q92608|DOCK2_HUMAN	Dedicator of cytokinesis protein 2 OS=Homo sapiens GN=DOCK2 PE=1 SV=2	0.51	0.01690
151	sp|P35052|GPC1_HUMAN	Glypican-1 OS=Homo sapiens GN=GPC1 PE=1 SV=2	2.28	0.01707
152	sp|K2C1_HUMAN|	sp|K2C1_HUMAN|	0.57	0.01758
153	sp|Q07020|RL18_HUMAN	60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2	0.44	0.01791
154	sp|O14786|NRP1_HUMAN	Neuropilin-1 OS=Homo sapiens GN=NRP1 PE=1 SV=3	1.17	0.01833
155	sp|Q7Z5L0|VMO1_HUMAN	Vitelline membrane outer layer protein 1 homolog OS=Homo sapiens GN=VMO1 PE=1 SV=1	2.30	0.01833
156	sp|Q9BS26|ERP44_HUMAN	Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1	0.50	0.01833
157	sp|P00403|COX2_HUMAN	Cytochrome c oxidase subunit 2 OS=Homo sapiens GN=MT-CO2 PE=1 SV=1	0.52	0.01833
158	sp|Q00796|DHSO_HUMAN	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4	2.07	0.01970
159	sp|P13646|K1C13_HUMAN	Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 SV=4	0.48	0.01994
160	sp|HBA_HUMAN|	sp|HBA_HUMAN|	2.55	0.01995
161	sp|P53992|SC24C_HUMAN	Protein transport protein Sec24C OS=Homo sapiens GN=SEC24C PE=1 SV=3	0.50	0.02014

	Protein Annotation	Protein Name/Description	Ratio LS/HS	Adjusted *p* -value
162	sp|P26599|PTBP1_HUMAN	Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1	0.41	0.02199
163	sp|P16435|NCPR_HUMAN	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2	0.48	0.02217
164	sp|P41252|SYIC_HUMAN	Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2	0.44	0.02217
165	sp|Q9BUF5|TBB6_HUMAN	Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1	0.56	0.02221
166	sp|P13807|GYS1_HUMAN	Glycogen [starch] synthase, muscle OS=Homo sapiens GN=GYS1 PE=1 SV=2	0.41	0.02221
167	sp|Q86UX7|URP2_HUMAN	Fermitin family homolog 3 OS=Homo sapiens GN=FERMT3 PE=1 SV=1	0.47	0.02232
168	sp|P50914|RL14_HUMAN	60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4	0.35	0.02255
169	sp|Q93100|KPBB_HUMAN	Phosphorylase b kinase regulatory subunit beta OS=Homo sapiens GN=PHKB PE=1 SV=3	1.29	0.02273
170	sp|P13727|PRG2_HUMAN	Bone marrow proteoglycan OS=Homo sapiens GN=PRG2 PE=1 SV=2	1.49	0.02303
171	sp|P17900|SAP3_HUMAN	Ganglioside GM2 activator OS=Homo sapiens GN=GM2A PE=1 SV=4	2.89	0.02358
172	sp|Q9Y5P6|GMPPB_HUMAN	Mannose-1-phosphate guanyltransferase beta OS=Homo sapiens GN=GMPPB PE=1 SV=2	0.59	0.02368
173	sp|Q8WWI1|LMO7_HUMAN	LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=3	0.44	0.02397
174	sp|Q8WUH2|TGFA1_HUMAN	Transforming growth factor-beta receptor-associated protein 1 OS=Homo sapiens GN=TGFBRAP1 PE=1 SV=1	2.14	0.02404
175	sp|Q6UX73|CP089_HUMAN	UPF0764 protein C16orf89 OS=Homo sapiens GN=C16orf89 PE=2 SV=2	2.00	0.02404
176	sp|P09958|FURIN_HUMAN	Furin OS=Homo sapiens GN=FURIN PE=1 SV=2	1.45	0.02410
177	sp|Q8WZ75|ROBO4_HUMAN	Roundabout homolog 4 OS=Homo sapiens GN=ROBO4 PE=1 SV=1	2.09	0.02410
178	sp|Q96TA1|NIBL1_HUMAN	Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3	0.67	0.02410
179	sp|Q7Z589|EMSY_HUMAN	Protein EMSY OS=Homo sapiens GN=EMSY PE=1 SV=2	1.79	0.02447
180	sp|P11940|PABP1_HUMAN	Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2	0.50	0.02486
181	sp|Q15369|ELOC_HUMAN	Transcription elongation factor B polypeptide 1 OS=Homo sapiens GN=TCEB1 PE=1 SV=1	0.46	0.02486
182	sp|P23142|FBLN1_HUMAN	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4	2.24	0.02520
183	sp|P62753|RS6_HUMAN	40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	0.42	0.02520
184	sp|O14817|TSN4_HUMAN	Tetraspanin-4 OS=Homo sapiens GN=TSPAN4 PE=1 SV=1	3.32	0.02532
185	sp|Q15223|PVRL1_HUMAN	Poliovirus receptor-related protein 1 OS=Homo sapiens GN=PVRL1 PE=1 SV=3	1.53	0.02544
186	sp|P55084|ECHB_HUMAN	Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3	0.33	0.02544
187	sp|Q24JP5|T132A_HUMAN	Transmembrane protein 132A OS=Homo sapiens GN=TMEM132A PE=2 SV=1	0.34	0.02544
188	sp|Q9UFH2|DYH17_HUMAN	Dynein heavy chain 17, axonemal OS=Homo sapiens GN=DNAH17 PE=2 SV=2	0.53	0.02560
189	sp|Q9UBR1|BUP1_HUMAN	Beta-ureidopropionase OS=Homo sapiens GN=UPB1 PE=1 SV=1	1.13	0.02569
190	sp|Q9Y6R7|FCGBP_HUMAN	IgGFc-binding protein OS=Homo sapiens GN=FCGBP PE=1 SV=3	2.16	0.02569
191	sp|P05155|IC1_HUMAN	Plasma protease C1 inhibitor OS=Homo sapiens GN=SERPING1 PE=1 SV=2	1.95	0.02569
192	sp|Q13509|TBB3_HUMAN	Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2	0.65	0.02569
193	sp|P55786|PSA_HUMAN	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2	0.51	0.02569
194	sp|Q6Q0C0|TRAF7_HUMAN	E3 ubiquitin-protein ligase TRAF7 OS=Homo sapiens GN=TRAF7 PE=1 SV=1	0.49	0.02569
195	sp|Q13616|CUL1_HUMAN	Cullin-1 OS=Homo sapiens GN=CUL1 PE=1 SV=2	0.47	0.02569
196	sp|O95758|PTBP3_HUMAN	Polypyrimidine tract-binding protein 3 OS=Homo sapiens GN=PTBP3 PE=1 SV=2	0.53	0.02585
197	sp|P07437|TBB5_HUMAN	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	0.72	0.02592
198	sp|P09601|HMOX1_HUMAN	Heme oxygenase 1 OS=Homo sapiens GN=HMOX1 PE=1 SV=1	0.50	0.02670
199	sp|O60716|CTND1_HUMAN	Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1	0.46	0.02677
200	sp|O15231|ZN185_HUMAN	Zinc finger protein 185 OS=Homo sapiens GN=ZNF185 PE=1 SV=3	0.46	0.02687
201	sp|Q02809|PLOD1_HUMAN	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens GN=PLOD1 PE=1 SV=2	2.05	0.02718
202	sp|B2MG_HUMAN|	sp|B2MG_HUMAN|	2.23	0.02718
203	sp|Q7L2H7|EIF3M_HUMAN	Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1	0.58	0.02718
204	sp|Q7Z5L7|PODN_HUMAN	Podocan OS=Homo sapiens GN=PODN PE=1 SV=2	0.49	0.02726
205	sp|Q13867|BLMH_HUMAN	Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1	1.54	0.02756
206	sp|P16401|H15_HUMAN	Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3	0.40	0.02846
207	sp|Q9BRK5|CAB45_HUMAN	45 kDa calcium-binding protein OS=Homo sapiens GN=SDF4 PE=1 SV=1	1.64	0.02904
208	sp|P20742|PZP_HUMAN	Pregnancy zone protein OS=Homo sapiens GN=PZP PE=1 SV=4	2.90	0.02911
209	sp|Q53GQ0|DHB12_HUMAN	Estradiol 17-beta-dehydrogenase 12 OS=Homo sapiens GN=HSD17B12 PE=1 SV=2	0.48	0.02911
210	sp|Q9Y6N5|SQRD_HUMAN	Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1	0.41	0.03002
211	sp|P28331|NDUS1_HUMAN	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Homo sapiens GN=NDUFS1 PE=1 SV=3	0.46	0.03002
212	sp|P14550|AK1A1_HUMAN	Alcohol dehydrogenase [NADP(+)] OS=Homo sapiens GN=AKR1A1 PE=1 SV=3	1.75	0.03075
213	sp|O43240|KLK10_HUMAN	Kallikrein-10 OS=Homo sapiens GN=KLK10 PE=1 SV=3	1.70	0.03125
214	sp|P48047|ATPO_HUMAN	ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1	0.43	0.03125
215	sp|P39023|RL3_HUMAN	60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2	0.51	0.03125
216	sp|P83436|COG7_HUMAN	Conserved oligomeric Golgi complex subunit 7 OS=Homo sapiens GN=COG7 PE=1 SV=1	0.38	0.03125
217	sp|P16403|H12_HUMAN	Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2	0.44	0.03200
218	sp|O00571|DDX3X_HUMAN	ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3	0.55	0.03231
219	sp|Q8N0X7|SPG20_HUMAN	Spartin OS=Homo sapiens GN=SPG20 PE=1 SV=1	1.04	0.03266
220	sp|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	2.10	0.03266
221	sp|P68371|TBB4B_HUMAN	Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	0.70	0.03266
222	sp|P24752|THIL_HUMAN	Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1	0.33	0.03275
223	sp|Q71U36|TBA1A_HUMAN	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1	0.73	0.03276
224	sp|Q9UPT5|EXOC7_HUMAN	Exocyst complex component 7 OS=Homo sapiens GN=EXOC7 PE=1 SV=3	0.48	0.03276
225	sp|O95831|AIFM1_HUMAN	Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1	0.40	0.03280
226	sp|ANXA5_HUMAN|	sp|ANXA5_HUMAN|	1.53	0.03288
227	sp|P22735|TGM1_HUMAN	Protein-glutamine gamma-glutamyltransferase K OS=Homo sapiens GN=TGM1 PE=1 SV=4	0.50	0.03288
228	sp|P06748|NPM_HUMAN	Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	0.43	0.03288
229	sp|P37088|SCNNA_HUMAN	Amiloride-sensitive sodium channel subunit alpha OS=Homo sapiens GN=SCNN1A PE=1 SV=1	1.18	0.03297
230	sp|Q00325|MPCP_HUMAN	Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2	0.43	0.03308
231	sp|P01613|KV121_HUMAN	Ig kappa chain V-I region Ni OS=Homo sapiens PE=1 SV=1	1.32	0.03342
232	sp|O75116|ROCK2_HUMAN	Rho-associated protein kinase 2 OS=Homo sapiens GN=ROCK2 PE=1 SV=4	1.14	0.03342
233	sp|P08246|ELNE_HUMAN	Neutrophil elastase OS=Homo sapiens GN=ELANE PE=1 SV=1	1.88	0.03342
234	sp|P53396|ACLY_HUMAN	ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3	0.55	0.03342
235	sp|P19012|K1C15_HUMAN	Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3	0.49	0.03342
236	sp|P05091|ALDH2_HUMAN	Aldehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH2 PE=1 SV=2	0.56	0.03342
237	sp|P52597|HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3	0.61	0.03342
238	sp|P02533|K1C14_HUMAN	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	0.46	0.03342
239	sp|Q15080|NCF4_HUMAN	Neutrophil cytosol factor 4 OS=Homo sapiens GN=NCF4 PE=1 SV=2	0.46	0.03342
240	sp|Q8NBQ5|DHB11_HUMAN	Estradiol 17-beta-dehydrogenase 11 OS=Homo sapiens GN=HSD17B11 PE=1 SV=3	0.43	0.03342
241	sp|P02649|APOE_HUMAN	Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1	1.88	0.03372
242	sp|CAH2_HUMAN|	sp|CAH2_HUMAN|	2.03	0.03372

	Protein Annotation	Protein Name/Description	Ratio LS/HS	Adjusted *p* -value
243	sp|P13647|K2C5_HUMAN	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	0.47	0.03372
244	sp|P10412|H14_HUMAN	Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	0.45	0.03372
245	sp|P48444|COPD_HUMAN	Coatomer subunit delta OS=Homo sapiens GN=ARCN1 PE=1 SV=1	0.49	0.03372
246	sp|P53618|COPB_HUMAN	Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3	0.43	0.03372
247	sp|Q99798|ACON_HUMAN	Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2	0.35	0.03372
248	sp|P84243|H33_HUMAN	Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2	0.33	0.03372
249	sp|P08294|SODE_HUMAN	Extracellular superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD3 PE=1 SV=2	2.11	0.03433
250	sp|Q03252|LMNB2_HUMAN	Lamin-B2 OS=Homo sapiens GN=LMNB2 PE=1 SV=3	0.60	0.03433
251	sp|Q16836|HCDH_HUMAN	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3	0.41	0.03433
252	sp|Q9BZ11|ADA33_HUMAN	Disintegrin and metalloproteinase domain-containing protein 33 OS=Homo sapiens GN=ADAM33 PE=1 SV=2	0.43	0.03433
253	sp|P50552|VASP_HUMAN	Vasodilator-stimulated phosphoprotein OS=Homo sapiens GN=VASP PE=1 SV=3	0.44	0.03448
254	sp|Q7Z2K6|ERMP1_HUMAN	Endoplasmic reticulum metallopeptidase 1 OS=Homo sapiens GN=ERMP1 PE=1 SV=2	0.48	0.03448
255	sp|Q9Y5E6|PCDB3_HUMAN	Protocadherin beta-3 OS=Homo sapiens GN=PCDHB3 PE=2 SV=1	1.73	0.03484
256	sp|A1KZ92|PXDNL_HUMAN	Peroxidasin-like protein OS=Homo sapiens GN=PXDNL PE=2 SV=3	0.54	0.03544
257	sp|Q00610|CLH1_HUMAN	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	0.66	0.03625
258	sp|P98095|FBLN2_HUMAN	Fibulin-2 OS=Homo sapiens GN=FBLN2 PE=1 SV=2	1.37	0.03711
259	sp|P49447|CY561_HUMAN	Cytochrome b561 OS=Homo sapiens GN=CYB561 PE=2 SV=2	1.01	0.03711
260	sp|P05787|K2C8_HUMAN	Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7	0.56	0.03711
261	sp|CASK_BOVIN|	sp|CASK_BOVIN|	0.21	0.03711
262	sp|Q8WWA0|ITLN1_HUMAN	Intelectin-1 OS=Homo sapiens GN=ITLN1 PE=1 SV=1	1.40	0.03721
263	sp|P02751|FINC_HUMAN	Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	1.74	0.03721
264	sp|P05107|ITB2_HUMAN	Integrin beta-2 OS=Homo sapiens GN=ITGB2 PE=1 SV=2	0.46	0.03774
265	sp|Q5TCZ1|SPD2A_HUMAN	SH3 and PX domain-containing protein 2A OS=Homo sapiens GN=SH3PXD2A PE=1 SV=1	1.89	0.03799
266	sp|Q9ULT8|HECD1_HUMAN	E3 ubiquitin-protein ligase HECTD1 OS=Homo sapiens GN=HECTD1 PE=1 SV=3	0.47	0.03799
267	sp|P68036|UB2L3_HUMAN	Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1	2.01	0.03814
268	sp|Q58FF8|H90B2_HUMAN	Putative heat shock protein HSP 90-beta 2 OS=Homo sapiens GN=HSP90AB2P PE=1 SV=2	0.53	0.03814
269	sp|P08779|K1C16_HUMAN	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	0.46	0.03814
270	sp|Q6ZRV2|FA83H_HUMAN	Protein FAM83H OS=Homo sapiens GN=FAM83H PE=1 SV=3	0.45	0.03814
271	sp|P07814|SYEP_HUMAN	Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	0.41	0.03814
272	sp|Q7Z5N4|SDK1_HUMAN	Protein sidekick-1 OS=Homo sapiens GN=SDK1 PE=1 SV=3	1.58	0.03820
273	sp|O43511|S26A4_HUMAN	Pendrin OS=Homo sapiens GN=SLC26A4 PE=1 SV=1	2.86	0.03866
274	sp|Q14166|TTL12_HUMAN	Tubulin--tyrosine ligase-like protein 12 OS=Homo sapiens GN=TTLL12 PE=1 SV=2	0.52	0.03873
275	sp|P02765|FETUA_HUMAN	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	2.63	0.04040
276	sp|P16278|BGAL_HUMAN	Beta-galactosidase OS=Homo sapiens GN=GLB1 PE=1 SV=2	2.03	0.04040
277	sp|Q03013|GSTM4_HUMAN	Glutathione S-transferase Mu 4 OS=Homo sapiens GN=GSTM4 PE=1 SV=3	1.68	0.04040
278	sp|Q13885|TBB2A_HUMAN	Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1	0.70	0.04040
279	sp|P19013|K2C4_HUMAN	Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV=4	0.62	0.04040
280	sp|Q96LJ7|DHRS1_HUMAN	Dehydrogenase/reductase SDR family member 1 OS=Homo sapiens GN=DHRS1 PE=1 SV=1	0.57	0.04040
281	sp|P31153|METK2_HUMAN	S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1	0.50	0.04040
282	sp|P51659|DHB4_HUMAN	Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3	0.43	0.04040
283	sp|P05388|RLA0_HUMAN	60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	0.62	0.04051
284	sp|P48668|K2C6C_HUMAN	Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3	0.48	0.04084
285	sp|O75367|H2AY_HUMAN	Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4	0.44	0.04108
286	sp|P49368|TCPG_HUMAN	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4	0.63	0.04134
287	sp|Q08211|DHX9_HUMAN	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	0.46	0.04159
288	sp|P53621|COPA_HUMAN	Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2	0.50	0.04169
289	sp|Q15485|FCN2_HUMAN	Ficolin-2 OS=Homo sapiens GN=FCN2 PE=1 SV=2	1.89	0.04216
290	sp|P02538|K2C6A_HUMAN	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	0.50	0.04216
291	sp|P50897|PPT1_HUMAN	Palmitoyl-protein thioesterase 1 OS=Homo sapiens GN=PPT1 PE=1 SV=1	1.41	0.04244
292	sp|Q14134|TRI29_HUMAN	Tripartite motif-containing protein 29 OS=Homo sapiens GN=TRIM29 PE=1 SV=2	0.44	0.04244
293	sp|Q02388|CO7A1_HUMAN	Collagen alpha-1(VII) chain OS=Homo sapiens GN=COL7A1 PE=1 SV=2	1.16	0.04384
294	sp|P84095|RHOG_HUMAN	Rho-related GTP-binding protein RhoG OS=Homo sapiens GN=RHOG PE=1 SV=1	1.89	0.04430
295	sp|O43390|HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1	0.57	0.04432
296	sp|Q02413|DSG1_HUMAN	Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	0.47	0.04463
297	sp|Q8IWE2|NXP20_HUMAN	Protein NOXP20 OS=Homo sapiens GN=FAM114A1 PE=1 SV=2	0.56	0.04463
298	sp|Q8N0V5|GNT2A_HUMAN	N-acetyllactosaminide beta-1,6-N-acetylglucosaminyl-transferase, isoform A OS=Homo sapiens GN=GCNT2 PE=2 SV=1	1.50	0.04505
299	sp|Q02383|SEMG2_HUMAN	Semenogelin-2 OS=Homo sapiens GN=SEMG2 PE=1 SV=1	43.54	0.04546
300	sp|P04350|TBB4A_HUMAN	Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2	0.71	0.04546
301	sp|Q9H8L6|MMRN2_HUMAN	Multimerin-2 OS=Homo sapiens GN=MMRN2 PE=1 SV=2	2.28	0.04588
302	sp|O00560|SDCB1_HUMAN	Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1	2.11	0.04607
303	sp|Q09666|AHNK_HUMAN	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	0.50	0.04607
304	sp|Q13423|NNTM_HUMAN	NAD(P) transhydrogenase, mitochondrial OS=Homo sapiens GN=NNT PE=1 SV=3	0.40	0.04607
305	sp|Q14566|MCM6_HUMAN	DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1	2.60	0.04627
306	sp|P08865|RSSA_HUMAN	40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4	0.60	0.04627
307	sp|Q14203|DCTN1_HUMAN	Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 PE=1 SV=3	0.51	0.04627
308	sp|P50453|SPB9_HUMAN	Serpin B9 OS=Homo sapiens GN=SERPINB9 PE=1 SV=1	0.30	0.04651
309	sp|Q14CN4|K2C72_HUMAN	Keratin, type II cytoskeletal 72 OS=Homo sapiens GN=KRT72 PE=1 SV=2	0.42	0.04767
310	sp|Q99988|GDF15_HUMAN	Growth/differentiation factor 15 OS=Homo sapiens GN=GDF15 PE=1 SV=3	1.20	0.04791
311	sp|O95573|ACSL3_HUMAN	Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3	0.53	0.04791
312	sp|P62820|RAB1A_HUMAN	Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3	0.70	0.04821
313	sp|A8MVU1|NCF1C_HUMAN	Putative neutrophil cytosol factor 1C OS=Homo sapiens GN=NCF1C PE=5 SV=1	0.48	0.04821
314	sp|Q9P2K2|TXD16_HUMAN	Thioredoxin domain-containing protein 16 OS=Homo sapiens GN=TXNDC16 PE=2 SV=4	1.64	0.04871
315	sp|Q96G03|PGM2_HUMAN	Phosphoglucomutase-2 OS=Homo sapiens GN=PGM2 PE=1 SV=4	0.46	0.04967
316	sp|P35268|RL22_HUMAN	60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2	0.44	0.04996


Color Key
and Histogram
Count
2500
2000
1500
1000
500
0
−2
−1
0
1
2
Relative expression
(mean subtracted)
Subject 1
Subject 2
Subject 3
Subject 4
Subject 5
Subject 6
Subject 7
Subject 8
Subject 9
Subject 10
Subject 11
Subject 12
Subject 13
Subject 14