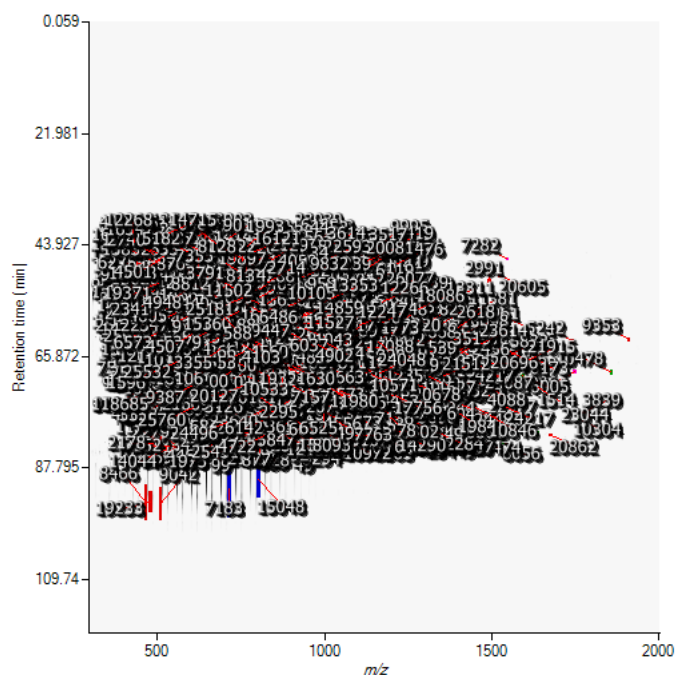


hjl

Report created: 10/3/2018 9:42:54 AM

Overview image



Data Processing Methods

Peak processing method	Profile data
Peptide ion detection method	High resolution











Experiment Design

Condition	0hr	1hr	2hr
Replicates	1	1	1

Proteins

Protein building options

Protein grouping	Group similar proteins
Protein quantitation	Relative Quantitation using Hi-3

Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances		
							0hr	1hr	2hr
Q5T200	56 (35)	286.55	---	1.05		Zinc finger CCCH domain-containing protein 13 OS=Homo sapiens GN=ZC3H13 PE=1 SV=1	1.14e+005	1.19e+005	1.13e+005
Q92817	25 (15)	119.14	---	1.66		Envoplakin OS=Homo sapiens GN=EVPL PE=1 SV=3	1.83e+005	1.63e+005	2.71e+005
A0A024R5M9	21 (16)	98.44	---	1.09		Nuclear mitotic apparatus protein 1_ isoform CRA_a OS=Homo sapiens GN=NUMA1 PE=4 SV=1	1.19e+005	1.14e+005	1.24e+005
Q9P2D3	23 (18)	94.69	---	1.19		HEAT repeat-containing protein 5B OS=Homo sapiens GN=HEATR5B PE=1 SV=2	7.64e+004	7.55e+004	8.97e+004
Q14966	19 (15)	89.20	---	1.16		Zinc finger protein 638 OS=Homo sapiens GN=ZNF638 PE=1 SV=2	7.71e+004	8.92e+004	8.03e+004
Q8N201	21 (15)	81.23	---	1.67		Integrator complex subunit 1 OS=Homo sapiens GN=INTS1 PE=1 SV=2	5.85e+004	4.60e+004	7.67e+004
Q9NV11	16 (11)	78.94	---	1.09		Fanconi anemia group I protein OS=Homo sapiens GN=FANCI PE=1 SV=4	1.24e+005	1.16e+005	1.26e+005
Q96N67	18 (13)	77.59	---	1.29		Dedicator of cytokinesis protein 7 OS=Homo sapiens GN=DOCK7 PE=1 SV=4	1.04e+005	8.96e+004	1.16e+005
P53675	18 (13)	74.57	---	1.08		Clathrin heavy chain 2 OS=Homo sapiens GN=CLTCL1 PE=1 SV=2	4.42e+004	4.09e+004	4.27e+004
Q92824	15 (12)	73.65	---	1.18		Proteinase convertase subtilisin/kexin type 5 OS=Homo sapiens GN=PCSK5 PE=1 SV=4	8.46e+004	7.20e+004	7.48e+004

Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances		
							0hr	1hr	2hr
B4DYG5	14 (9)	70.74	---	1.04		cDNA FLJ60960_ highly similar to Phosphatidylinositol 4-kinase alpha (EC 2.7.1.67) OS=Homo sapiens PE=2 SV=1	2.11e+004	2.04e+004	2.03e+004
Q8TDY2	17 (10)	69.81	---	1.07		RB1-inducible coiled-coil protein 1 OS=Homo sapiens GN=RB1CC1 PE=1 SV=3	9.44e+004	9.55e+004	8.94e+004
Q95996	17 (13)	69.75	---	1.14		Adenomatous polyposis coli protein 2 OS=Homo sapiens GN=APC2 PE=1 SV=1	1.14e+005	1.11e+005	1.26e+005
A0A0A0MTS5	15 (10)	69.18	---	1.14		HCG1811249_ isoform CRA_f OS=Homo sapiens GN=LAMA3 PE=1 SV=1	6.85e+004	7.32e+004	7.79e+004
Q95425	15 (9)	67.78	---	1.24		Supervillin OS=Homo sapiens GN=SVIL PE=1 SV=2	7.46e+004	8.12e+004	6.56e+004
Q9H583	15 (12)	65.88	---	1.04		HEAT repeat-containing protein 1 OS=Homo sapiens GN=HEATR1 PE=1 SV=3	1.01e+005	9.87e+004	1.03e+005
Q86X10	13 (12)	65.19	---	1.12		Ral GTPase-activating protein subunit beta OS=Homo sapiens GN=RALGAPB PE=1 SV=1	5.05e+004	5.12e+004	5.63e+004
A0A024RBR1	14 (8)	65.11	---	1.19		Restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)_ isoform CRA_b OS=Homo sapiens GN=RSN PE=4 SV=1	1.70e+005	1.50e+005	1.79e+005
Q9H650	15 (9)	65.09	---	1.12		Probable ATP-dependent RNA helicase YTHDC2 OS=Homo sapiens GN=YTHDC2 PE=1 SV=2	7.93e+004	8.23e+004	8.87e+004
E9PHY8	15 (14)	64.46	---	1.24		Maestro heat-like repeat-containing protein family member 1 OS=Homo sapiens GN=MROH1 PE=1 SV=1	1.14e+005	9.99e+004	1.24e+005
A0A0A0MQX1	14 (8)	62.92	---	1.09		Unconventional myosin-X OS=Homo sapiens GN=MYO10 PE=1 SV=1	9.12e+004	9.42e+004	9.94e+004
A2A3F7	13 (10)	61.39	---	1.13		Transient receptor potential cation channel subfamily M member 3 OS=Homo sapiens GN=TRPM3 PE=1 SV=1	8.91e+004	8.57e+004	9.67e+004
A0A140VJY5	12 (8)	60.72	---	1.15		Testicular tissue protein Li 212 OS=Homo sapiens PE=2 SV=1	7.59e+004	7.82e+004	8.70e+004
Q13796	16 (11)	60.63	---	1.06		Protein Shroom2 OS=Homo sapiens GN=SHROOM2 PE=1 SV=1	7.23e+004	7.46e+004	7.65e+004
L7RRS0	13 (11)	60.02	---	1.58		Phosphatidylinositol-4-phosphate 3-kinase_ catalytic subunit type 2 alpha OS=Homo sapiens GN=PIK3C2A PE=3 SV=1	1.04e+005	1.04e+005	1.64e+005
Q15440	14 (9)	59.80	---	1.06		Multidrug resistance-associated protein 5 OS=Homo sapiens GN=ABCC5 PE=1 SV=2	1.02e+005	9.68e+004	1.02e+005
Q14607	13 (12)	59.36	---	1.03		Histone demethylase UTY OS=Homo sapiens GN=UTY PE=1 SV=2	1.18e+005	1.14e+005	1.14e+005
Q7Z6E9	13 (12)	58.94	---	1.11		E3 ubiquitin-protein ligase RBBP6 OS=Homo sapiens GN=RBBP6 PE=1 SV=1	7.94e+004	7.91e+004	8.76e+004
F5H1U9	11 (6)	57.65	---	1.14		Multiple PDZ domain protein OS=Homo sapiens GN=MPDZ PE=1 SV=1	5.92e+004	5.54e+004	6.31e+004
Q8IZY2	13 (9)	57.61	---	1.03		ATP-binding cassette sub-family A member 7 OS=Homo sapiens GN=ABCA7 PE=1 SV=3	8.55e+004	8.52e+004	8.28e+004
E7EVA0	11 (8)	56.75	---	1.11		Microtubule-associated protein OS=Homo sapiens GN=MAP4 PE=1 SV=1	1.40e+004	1.47e+004	1.33e+004
A0A024R40Z	11 (8)	56.72	---	1.10		Microtubule-associated protein OS=Homo sapiens GN=MAP2 PE=4 SV=1	6.36e+004	5.78e+004	6.35e+004
Q60303	13 (11)	56.55	---	1.42		Protein KIAA0556 OS=Homo sapiens GN=KIAA0556 PE=1 SV=4	1.01e+005	9.23e+004	1.31e+005
Q14687	12 (11)	56.20	---	2.01		Genetic suppressor element 1 OS=Homo sapiens GN=GSE1 PE=1 SV=3	2.37e+005	3.35e+005	4.75e+005
Q9BX26	14 (9)	56.02	---	1.22		Synaptonemal complex protein 2 OS=Homo sapiens GN=SYCP2 PE=2 SV=2	5.51e+004	5.54e+004	6.70e+004
B5MCJ9	12 (11)	54.42	---	1.10		Tripartite motif-containing protein 66 OS=Homo sapiens GN=TRIM66 PE=4 SV=1	4.79e+004	5.04e+004	4.59e+004
Q2KHR3	12 (9)	53.76	---	1.26		Glutamine and serine-rich protein 1 OS=Homo sapiens GN=QSER1 PE=1 SV=3	6.02e+004	6.72e+004	5.34e+004
B1APH0	11 (6)	52.27	---	1.08		Zinc finger protein basonuclin-2 OS=Homo sapiens GN=BNC2 PE=1 SV=1	7.71e+004	7.31e+004	7.88e+004
Q15047	11 (8)	52.06	---	1.04		Histone-lysine N-methyltransferase SETDB1 OS=Homo sapiens GN=SETDB1 PE=1 SV=1	7.96e+004	7.65e+004	7.74e+004
H7BYL6	12 (9)	51.73	---	1.13		A-kinase anchor protein 9 (Fragment) OS=Homo sapiens GN=AKAP9 PE=1 SV=1	1.41e+005	1.25e+005	1.41e+005
Q15027	11 (7)	50.58	---	1.07		Protein transport protein Sec16A OS=Homo sapiens GN=SEC16A PE=1 SV=3	3.56e+004	3.79e+004	3.68e+004
A0A024QZ72	12 (8)	50.18	---	1.06		PR domain containing 2_ with ZNF domain_ isoform CRA_b OS=Homo sapiens GN=PRDM2 PE=4 SV=1	3.83e+004	4.00e+004	4.07e+004
Q5THK1	11 (8)	49.98	---	1.07		Protein PRR14L OS=Homo sapiens GN=PRR14L PE=1 SV=1	2.41e+004	2.24e+004	2.38e+004
Q38SD2	10 (9)	49.30	---	1.13		Leucine-rich repeat serine/threonine-protein kinase 1 OS=Homo sapiens GN=LRRK1 PE=1 SV=3	1.07e+005	9.68e+004	1.10e+005
D3DSQ0	11 (9)	49.13	---	1.04		Pericentriolar material 1_ isoform CRA_a OS=Homo sapiens GN=PCM1 PE=4 SV=1	2.96e+004	2.90e+004	2.84e+004
A0A0A0MQS9	10 (8)	48.25	---	1.57		Laminin subunit alpha-4 OS=Homo sapiens GN=LAMA4 PE=1 SV=1	2.41e+005	2.59e+005	3.77e+005
A8K8T9	11 (9)	47.69	---	1.27		cDNA FLJ71787_ highly similar to Homo sapiens cyclin B3 (CCNB3)_ transcript variant 3_ mRNA OS=Homo sapiens PE=2 SV=1	3.61e+005	4.02e+005	4.59e+005
M0QZQ3	12 (7)	47.69	---	1.19		Spectrin beta chain OS=Homo sapiens GN=SPTBN4 PE=1 SV=1	1.02e+005	8.61e+004	8.65e+004
Q6ZU65	10 (7)	47.23	---	2.01		Ubinuclein-2 OS=Homo sapiens GN=UBN2 PE=1 SV=2	5.69e+004	4.98e+004	1.00e+005
Q5T5P2	12 (8)	47.00	---	1.05		Sickle tail protein homolog OS=Homo sapiens GN=KIAA1217 PE=1 SV=2	5.44e+004	5.30e+004	5.58e+004
A0A024R854	11 (9)	46.88	---	1.48		Caspase recruitment domain family_ member 11_ isoform CRA_a OS=Homo sapiens GN=CARD11 PE=4 SV=1	1.01e+005	1.23e+005	1.49e+005
Q3T906	9 (7)	46.77	---	1.12		N-acetylglucosamine-1-phosphotransferase subunits alpha/beta OS=Homo sapiens GN=GNPTAB PE=1 SV=1	5.49e+004	5.23e+004	5.87e+004

Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances		
							0hr	1hr	2hr
A6QL64	11 (6)	46.76	---	1.07		Ankyrin repeat domain-containing protein 36A OS=Homo sapiens GN=ANKRD36 PE=2 SV=3	2.55e+004	2.72e+004	2.63e+004
P54132	12 (6)	46.53	---	1.30		Bloom syndrome protein OS=Homo sapiens GN=BLM PE=1 SV=1	2.71e+004	2.34e+004	3.04e+004
Q02952	10 (7)	46.44	---	1.19		A-kinase anchor protein 12 OS=Homo sapiens GN=AKAP12 PE=1 SV=4	8.09e+004	7.27e+004	8.63e+004
P06213	10 (7)	46.43	---	1.33		Insulin receptor OS=Homo sapiens GN=INSR PE=1 SV=4	4.48e+004	5.22e+004	3.94e+004
P13533	12 (9)	46.26	---	1.13		Myosin-6 OS=Homo sapiens GN=MYH6 PE=1 SV=5	8.54e+004	9.67e+004	8.68e+004
A0A024R250	9 (6)	46.25	---	1.08		Nucleolar protein 8_ isoform CRA_a OS=Homo sapiens GN=NOL8 PE=4 SV=1	2.81e+004	2.77e+004	2.60e+004
Q86V15	11 (8)	46.17	---	1.81		Zinc finger protein castor homolog 1 OS=Homo sapiens GN=CASZ1 PE=1 SV=4	1.88e+005	2.92e+005	3.41e+005
A0A0U1RR27	9 (6)	46.16	---	1.21		C-myc promoter-binding protein OS=Homo sapiens GN=DENND4A PE=1 SV=1	5.42e+004	4.47e+004	5.28e+004
P98155	10 (9)	45.59	---	2.47		Very low-density lipoprotein receptor OS=Homo sapiens GN=VLDLR PE=1 SV=1	4.47e+004	2.13e+004	1.81e+004
A0A0J9YW64	11 (6)	45.34	---	1.15		Dedicator of cytokinesis protein 11 (Fragment) OS=Homo sapiens GN=DOCK11 PE=1 SV=1	5.26e+004	6.07e+004	5.70e+004
Q86XA9	10 (6)	44.78	---	1.04		HEAT repeat-containing protein 5A OS=Homo sapiens GN=HEATR5A PE=1 SV=2	3.64e+005	3.80e+005	3.65e+005
B7Z7S9	10 (7)	44.48	---	1.09		cDNA FLJ61724_ highly similar to Shugoshin-like 2 OS=Homo sapiens PE=2 SV=1	2.78e+004	3.02e+004	2.89e+004
Q13459	11 (7)	43.92	---	1.15		Unconventional myosin-IXb OS=Homo sapiens GN=MYO9B PE=1 SV=3	4.59e+004	4.44e+004	5.11e+004
A0A1B0GTN0	10 (8)	43.79	---	1.15		Voltage-dependent L-type calcium channel subunit alpha OS=Homo sapiens GN=CACNA1D PE=3 SV=1	9.76e+004	1.10e+005	9.56e+004
A0A0S2Z5M1	10 (9)	43.66	---	1.10		SEC63-like (S. cerevisiae) (Fragment) OS=Homo sapiens GN=SEC63 PE=2 SV=1	6.58e+004	6.89e+004	7.23e+004
A0A140VJW1	10 (6)	43.16	---	1.06		Testicular tissue protein Li 188 OS=Homo sapiens PE=2 SV=1	1.03e+005	1.02e+005	1.09e+005
Q9BWH6	9 (6)	42.98	---	2.01		RNA polymerase II-associated protein 1 OS=Homo sapiens GN=RPAP1 PE=1 SV=3	6.80e+004	5.86e+004	1.17e+005
Q96NW7	10 (8)	42.80	---	1.19		Leucine-rich repeat-containing protein 7 OS=Homo sapiens GN=LRRC7 PE=1 SV=1	1.13e+005	1.03e+005	1.23e+005
B7ZM73	10 (7)	42.78	---	1.08		MON2 protein OS=Homo sapiens GN=MON2 PE=2 SV=1	1.01e+005	9.49e+004	1.03e+005
D3DYC4	9 (9)	42.76	---	1.17		Nestin_ isoform CRA_c OS=Homo sapiens GN=NES PE=3 SV=1	8.78e+004	7.53e+004	8.60e+004
Q6XZF7	10 (7)	42.17	---	1.08		Dynamin-binding protein OS=Homo sapiens GN=DNMBP PE=1 SV=1	3.77e+004	3.56e+004	3.48e+004
F8VPD4	9 (5)	42.17	---	1.06		CAD protein OS=Homo sapiens GN=CAD PE=1 SV=1	4.10e+004	3.85e+004	3.93e+004
A4DOS8	9 (6)	41.61	---	1.18		Dedicator of cytokinesis 4 OS=Homo sapiens GN=DOCK4 PE=3 SV=1	1.10e+005	9.86e+004	1.16e+005
Q9P227	8 (7)	41.49	---	1.08		Rho GTPase-activating protein 23 OS=Homo sapiens GN=ARHGAP23 PE=1 SV=2	1.47e+005	1.36e+005	1.47e+005
Q5VU65	10 (6)	41.37	---	1.05		Nuclear pore membrane glycoprotein 210-like OS=Homo sapiens GN=NUP210L PE=2 SV=1	1.89e+004	1.90e+004	1.98e+004
A0A1L1ZH79	7 (5)	41.04	---	1.15		NADH dehydrogenase subunit 5 OS=Homo sapiens GN=ND5 PE=4 SV=1	4.79e+004	5.53e+004	4.95e+004
E7EQN9	8 (7)	40.65	---	1.08		Type II inositol 3_4-bisphosphate 4-phosphatase OS=Homo sapiens GN=INPP4B PE=1 SV=1	6.54e+004	6.42e+004	6.06e+004
P49750	9 (5)	39.87	---	1.75		YLP motif-containing protein 1 OS=Homo sapiens GN=YLPM1 PE=1 SV=3	4.37e+004	4.12e+004	7.21e+004
Q8IVG5	9 (7)	39.76	---	1.15		Sterile alpha motif domain-containing protein 9-like OS=Homo sapiens GN=SAMD9L PE=1 SV=2	3.88e+004	3.62e+004	4.16e+004
C9J066	10 (8)	39.68	---	1.12		Ninein OS=Homo sapiens GN=NIN PE=1 SV=1	2.01e+005	1.92e+005	2.16e+005
B4DH14	9 (6)	39.64	---	1.02		cDNA FLJ60536_ highly similar to Death-associated protein kinase 1 (EC 2.7.11.1) OS=Homo sapiens PE=2 SV=1	3.11e+004	3.18e+004	3.13e+004
P56715	9 (5)	39.61	---	1.08		Oxygen-regulated protein 1 OS=Homo sapiens GN=RP1 PE=1 SV=1	7.67e+004	8.08e+004	8.31e+004
Q460N5	9 (6)	39.14	---	1.14		Poly [ADP-ribose] polymerase 14 OS=Homo sapiens GN=PARP14 PE=1 SV=3	8.93e+004	1.00e+005	1.02e+005
Q9C091	9 (6)	39.00	---	1.19		GREB1-like protein OS=Homo sapiens GN=GREB1L PE=2 SV=2	8.69e+004	9.94e+004	8.36e+004
A0A024R9B9	8 (7)	38.95	---	1.30		Matrilin 2_ isoform CRA_b OS=Homo sapiens GN=MATN2 PE=4 SV=1	7.53e+004	7.99e+004	9.83e+004
Q9Y6N6	9 (7)	38.88	---	1.22		Laminin subunit gamma-3 OS=Homo sapiens GN=LAMC3 PE=1 SV=3	4.47e+004	4.58e+004	3.76e+004
Q9BXL6	9 (8)	38.66	---	1.20		Caspase recruitment domain-containing protein 14 OS=Homo sapiens GN=CARD14 PE=1 SV=2	7.15e+004	7.70e+004	6.43e+004
Q60645	10 (8)	38.35	---	1.08		Exocyst complex component 3 OS=Homo sapiens GN=EXOC3 PE=1 SV=2	7.01e+004	6.48e+004	6.80e+004
A0A075B785	9 (5)	38.21	---	1.17		LisH domain and HEAT repeat-containing protein KIAA1468 OS=Homo sapiens GN=KIAA1468 PE=1 SV=7	4.72e+004	5.42e+004	5.54e+004
P10266	9 (2)	38.14	---	1.19		Endogenous retrovirus group K member 10 Pol protein OS=Homo sapiens GN=ERVK-10 PE=3 SV=2	2.69e+005	2.27e+005	2.45e+005
F2Z2S2	9 (7)	38.03	---	1.39		Protein furry homolog-like OS=Homo sapiens GN=FRYL PE=1 SV=1	1.22e+005	1.35e+005	1.69e+005
Q6ZV73	9 (8)	37.74	---	1.07		FYVE_ RhoGEF and PH domain-containing protein 6 OS=Homo sapiens GN=FGD6 PE=1 SV=2	5.35e+004	5.72e+004	5.45e+004
B3KWW9	8 (6)	37.66	---	1.72		cDNA FLJ44046 fis_ clone TEST14030505 OS=Homo sapiens PE=2 SV=1	4.56e+004	4.76e+004	7.82e+004
Q8N3P4	9 (5)	37.56	---	1.07		Vacuolar protein sorting-associated protein 8 homolog OS=Homo sapiens GN=VPS8 PE=1 SV=3	1.09e+005	1.04e+005	1.12e+005

Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances		
							0hr	1hr	2hr
Q9H2M9	8 (4)	37.49	---	1.18		Rab3 GTPase-activating protein non-catalytic subunit OS=Homo sapiens GN=RAB3GAP2 PE=1 SV=1	1.25e+004	1.06e+004	1.10e+004
Q9WJR5	9 (1)	37.47	---	1.21		Endogenous retrovirus group K member 19 Pol protein OS=Homo sapiens GN=ERVK-19 PE=2 SV=2	1.18e+004	9842.83	9752.40
Q86WG5	8 (7)	37.29	---	1.07		Myotubularin-related protein 13 OS=Homo sapiens GN=SBF2 PE=1 SV=1	3.13e+004	2.96e+004	3.16e+004
A0A087WT58	8 (7)	37.25	---	1.26		Maestro heat-like repeat-containing protein family member 2A OS=Homo sapiens GN=MROH2A PE=4 SV=1	2.31e+004	2.58e+004	2.91e+004
P18858	8 (6)	37.16	---	1.09		DNA ligase 1 OS=Homo sapiens GN=LIG1 PE=1 SV=1	5.55e+004	6.03e+004	5.89e+004
B1AJZ9	8 (7)	37.16	---	1.11		Forkhead-associated domain-containing protein 1 OS=Homo sapiens GN=FHAD1 PE=2 SV=2	1.47e+005	1.36e+005	1.51e+005
Q86US8	11 (8)	37.14	---	1.45		Telomerase-binding protein EST1A OS=Homo sapiens GN=SMG6 PE=1 SV=2	5.84e+004	5.53e+004	8.04e+004
A0A087WVQ6	7 (6)	36.97	---	1.06		Clathrin heavy chain OS=Homo sapiens GN=CLTC PE=1 SV=1	1.67e+005	1.61e+005	1.57e+005
Q13233	8 (7)	36.96	---	1.05		Mitogen-activated protein kinase kinase kinase 1 OS=Homo sapiens GN=MAP3K1 PE=1 SV=4	7.39e+004	7.25e+004	7.61e+004
Q14674	9 (7)	36.80	---	1.12		Separin OS=Homo sapiens GN=ESPL1 PE=1 SV=3	3.90e+004	4.09e+004	4.36e+004
P16157	8 (5)	36.64	---	1.20		Ankyrin-1 OS=Homo sapiens GN=ANK1 PE=1 SV=3	3.79e+004	4.53e+004	4.22e+004
Q15031	8 (6)	36.63	---	1.03		Plexin-B2 OS=Homo sapiens GN=PLXNB2 PE=1 SV=3	7.89e+004	7.75e+004	7.68e+004
P07814	7 (6)	36.23	---	1.04		Bifunctional glutamate/proline-tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	1.06e+005	1.03e+005	1.06e+005
A0A0A0MRJ3	8 (6)	36.18	---	1.12		Neuron navigator 1 OS=Homo sapiens GN=NAV1 PE=1 SV=1	9178.71	9438.69	8420.23
H0YA7Z	8 (5)	35.69	---	1.29		Protein JBT517 (Fragment) OS=Homo sapiens GN=C5orf42 PE=1 SV=1	5.93e+004	5.23e+004	6.73e+004
Q5T5U3	8 (5)	35.67	---	1.12		Rho GTPase-activating protein 21 OS=Homo sapiens GN=ARHGAP21 PE=1 SV=1	4.81e+004	4.31e+004	4.52e+004
B9EG73	9 (6)	35.66	---	1.14		DOCK9 protein OS=Homo sapiens GN=DOCK9 PE=2 SV=1	3.69e+004	3.75e+004	4.22e+004
Q75122	8 (6)	35.63	---	1.25		CLIP-associating protein 2 OS=Homo sapiens GN=CLASP2 PE=1 SV=2	6.49e+004	7.43e+004	8.08e+004
Q14BD4	7 (4)	35.62	---	1.46		ITSN1 protein OS=Homo sapiens GN=ITSN1 PE=2 SV=1	2.87e+005	3.50e+005	4.20e+005
Q60522	8 (5)	35.39	---	1.19		Tudor domain-containing protein 6 OS=Homo sapiens GN=TDRD6 PE=2 SV=2	1.84e+004	2.07e+004	1.74e+004
D3DSS6	8 (7)	35.22	---	1.10		Dedicator of cytokinesis 5_ isoform CRA_a OS=Homo sapiens GN=DOCK5 PE=3 SV=1	7.55e+004	6.97e+004	7.66e+004
Q86SQ0	8 (7)	35.22	---	1.15		Pleckstrin homology-like domain family B member 2 OS=Homo sapiens GN=PHLDB2 PE=1 SV=2	3.14e+004	2.72e+004	2.75e+004
B4DF80	8 (5)	35.22	---	1.09		cDNA FLJ58527_ highly similar to Nucleolar protein 6 OS=Homo sapiens PE=2 SV=1	5.17e+004	5.65e+004	5.24e+004
Q2M3CZ	8 (7)	34.91	---	2.32		A-kinase anchor protein SPHKAP OS=Homo sapiens GN=SPHKAP PE=1 SV=1	1.55e+005	1.71e+005	3.59e+005
B2RUT8	8 (4)	34.46	---	1.24		Benzodiazepine receptor (Peripheral) associated protein 1 OS=Homo sapiens GN=BZRAP1 PE=2 SV=1	8.21e+004	8.52e+004	1.02e+005
Q6GYQ0	7 (4)	34.31	---	1.10		Ral GTPase-activating protein subunit alpha-1 OS=Homo sapiens GN=RALGAP1 PE=1 SV=1	1.00e+004	1.03e+004	1.11e+004
Q94822	7 (5)	34.26	---	1.06		E3 ubiquitin-protein ligase listerin OS=Homo sapiens GN=LTN1 PE=1 SV=6	3.93e+004	3.72e+004	3.80e+004
Q92621	7 (6)	34.00	---	1.09		Nuclear pore complex protein Nup205 OS=Homo sapiens GN=NUP205 PE=1 SV=3	7.28e+004	7.34e+004	6.76e+004
A0A0B4J1W0	7 (6)	33.99	---	1.20		Mediator of RNA polymerase II transcription subunit 24 OS=Homo sapiens GN=MED24 PE=1 SV=1	3.54e+004	3.27e+004	3.91e+004
Q12879	8 (8)	33.99	---	1.51		Glutamate receptor ionotropic_NMDA 2A OS=Homo sapiens GN=GRIN2A PE=1 SV=1	4.70e+004	4.40e+004	6.67e+004
Q9HAR2	8 (3)	33.84	---	3.81		Adhesion G protein-coupled receptor L3 OS=Homo sapiens GN=ADGRL3 PE=1 SV=2	1.87e+004	1.97e+004	5155.61
A0A024QZ45	7 (6)	33.57	---	1.15		BRCA1 interacting protein C-terminal helicase 1_ isoform CRA_a OS=Homo sapiens GN=BRIP1 PE=4 SV=1	3.29e+004	3.12e+004	3.58e+004
A0A024R8L6	7 (5)	33.42	---	1.38		ATP-binding cassette_ sub-family A (ABC1)_ member 8_ isoform CRA_a OS=Homo sapiens GN=ABCA8 PE=4 SV=1	2.74e+005	2.35e+005	1.99e+005
A8K8P1	8 (6)	33.19	---	2.01		cDNA FLJ78752_ highly similar to Homo sapiens centromere protein J (CENPJ)_ mRNA OS=Homo sapiens PE=2 SV=1	3.47e+004	3.75e+004	6.97e+004
A0A1B0GVU7	7 (3)	33.17	---	1.06		Talin-2 OS=Homo sapiens GN=TLN2 PE=1 SV=1	3.62e+004	3.61e+004	3.43e+004
Q96BYZ	8 (6)	33.07	---	2.66		Autophagy-related protein 2 homolog B OS=Homo sapiens GN=ATG2B PE=1 SV=5	3.52e+004	3.24e+004	8.63e+004
A8K2VZ	7 (5)	33.05	---	2.36		cDNA FLJ76088_ highly similar to Homo sapiens dual oxidase 1 (DUOX1)_ transcript variant 1_ mRNA OS=Homo sapiens PE=2 SV=1	5.75e+004	5.12e+004	1.21e+005
D3U719	7 (5)	33.02	---	1.14		Conserved telomere capping protein 1 OS=Homo sapiens GN=CTC1 PE=2 SV=1	6.19e+004	5.44e+004	5.90e+004
Q70EL1	9 (7)	32.65	---	1.09		Inactive ubiquitin carboxyl-terminal hydrolase 54 OS=Homo sapiens GN=USP54 PE=1 SV=4	6.14e+004	6.36e+004	6.70e+004
Q5VW36	8 (6)	32.44	---	1.36		Focadhesin OS=Homo sapiens GN=FOCAD PE=1 SV=1	2.81e+004	2.58e+004	3.51e+004
P38935	7 (3)	32.19	---	1.19		DNA-binding protein SMUBP-2 OS=Homo sapiens GN=IGHMBP2 PE=1 SV=3	5.66e+004	6.52e+004	5.48e+004
A8K5J1	7 (6)	31.97	---	1.05		Uridine monophosphate synthetase (Orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)_ isoform CRA_b OS=Homo sapiens GN=UMPS PE=2 SV=1	1.06e+005	1.11e+005	1.11e+005
P13535	8 (5)	31.91	---	1.12		Myosin-8 OS=Homo sapiens GN=MYH8 PE=1 SV=3	4.61e+004	5.15e+004	4.64e+004

Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances		
							0hr	1hr	2hr
Q9UPU7	8 (6)	31.73	---	1.11		TBC1 domain family member 2B OS=Homo sapiens GN=TBC1D2B PE=1 SV=2	6.99e+004	6.57e+004	7.28e+004
A0JP08	7 (5)	31.58	---	1.12		Zinc finger E-box binding homeobox 2 OS=Homo sapiens GN=ZEB2 PE=1 SV=1	3.90e+004	3.76e+004	4.23e+004
Q9Y6J0	8 (8)	31.54	---	1.12		Calcineurin-binding protein cabin-1 OS=Homo sapiens GN=CABIN1 PE=1 SV=1	3.52e+004	3.49e+004	3.92e+004
Q63HK3	8 (6)	31.52	---	1.53		Zinc finger protein with KRAB and SCAN domains 2 OS=Homo sapiens GN=ZKSCAN2 PE=1 SV=2	6.27e+004	5.69e+004	8.67e+004
A0A0A0MR03	7 (5)	31.12	---	1.05		RNA polymerase II subunit A C-terminal domain phosphatase OS=Homo sapiens GN=CTDP1 PE=1 SV=1	5.80e+004	6.07e+004	5.98e+004
Q96K76	7 (5)	30.89	---	1.58		Ubiquitin carboxyl-terminal hydrolase 47 OS=Homo sapiens GN=USP47 PE=1 SV=3	5.39e+004	4.96e+004	7.81e+004
Q6ZMY3	7 (5)	30.62	---	1.03		SPOC domain-containing protein 1 OS=Homo sapiens GN=SPOCD1 PE=2 SV=1	1.57e+004	1.53e+004	1.56e+004
C1PHA2	7 (4)	30.62	---	1.02		Tyrosine-protein kinase receptor OS=Homo sapiens GN=KIF5B-ALK PE=2 SV=1	1.76e+004	1.78e+004	1.79e+004
J3KN16	7 (5)	30.58	---	1.14		KIAA0368 OS=Homo sapiens GN=KIAA0368 PE=1 SV=1	2.29e+004	2.05e+004	2.00e+004
A0AVI2	7 (5)	30.38	---	1.21		Fer-1-like protein 5 OS=Homo sapiens GN=FER1L5 PE=2 SV=2	5.71e+004	5.97e+004	6.92e+004
Q9NQW1	6 (3)	30.36	---	1.17		Protein transport protein Sec31B OS=Homo sapiens GN=SEC31B PE=1 SV=1	4.19e+004	3.97e+004	3.58e+004
P48357	7 (6)	30.35	---	1.20		Leptin receptor OS=Homo sapiens GN=LEPR PE=1 SV=2	1.46e+004	1.26e+004	1.51e+004
Q6ZU64	7 (6)	30.27	---	1.09		Cilia- and flagella-associated protein 65 OS=Homo sapiens GN=CFAP65 PE=1 SV=2	8.25e+004	7.63e+004	8.30e+004
A0A087WTD7	7 (5)	30.26	---	1.15		A-kinase anchor protein 13 OS=Homo sapiens GN=AKAP13 PE=1 SV=1	3.43e+004	3.11e+004	3.59e+004
P11277	8 (6)	30.21	---	1.12		Spectrin beta chain_ erythrocytic OS=Homo sapiens GN=SPTB PE=1 SV=5	6.27e+004	5.78e+004	6.45e+004
A0A024R104	7 (7)	30.12	---	1.09		Contactin 1_ isoform CRA_a OS=Homo sapiens GN=CNTN1 PE=4 SV=1	6.31e+004	6.79e+004	6.25e+004
Q60333	7 (5)	30.10	---	1.07		Kinesin-like protein KIF1B OS=Homo sapiens GN=KIF1B PE=1 SV=5	2.09e+004	1.95e+004	2.07e+004
A0A140VJN5	7 (5)	29.91	---	1.51		Testicular tissue protein Li 111 OS=Homo sapiens PE=2 SV=1	4.00e+004	3.51e+004	5.31e+004
Q5JU85	7 (5)	29.87	---	1.20		IQ motif and SEC7 domain-containing protein 2 OS=Homo sapiens GN=IQSEC2 PE=1 SV=1	1.66e+005	1.71e+005	1.99e+005
A0A024R6X4	6 (3)	29.80	---	1.10		Pleckstrin homology domain containing_ family G (With RhoGef domain) member 4_ isoform CRA_a OS=Homo sapiens GN=PLEKHG4 PE=4 SV=1	1.12e+004	1.22e+004	1.18e+004
Q2M3G0	6 (4)	29.80	---	1.11		ATP-binding cassette sub-family B member 5 OS=Homo sapiens GN=ABCB5 PE=1 SV=4	1.65e+004	1.84e+004	1.77e+004
A0A075B7B1	7 (5)	29.59	---	1.18		Desmuslin_ isoform CRA_a OS=Homo sapiens GN=SYNM PE=1 SV=1	1.83e+004	1.95e+004	2.15e+004
K7ER94	7 (5)	29.59	---	1.09		FH1/FH2 domain-containing protein 3 (Fragment) OS=Homo sapiens GN=FHOD3 PE=1 SV=1	2.15e+004	2.05e+004	2.23e+004
A8K0K2	7 (3)	29.58	---	1.20		cDNA FLJ75530_ highly similar to Human APC gene mRNA (Fragment) OS=Homo sapiens PE=2 SV=1	4.69e+004	3.90e+004	4.45e+004
Q15083	7 (5)	29.49	---	1.08		ERC protein 2 OS=Homo sapiens GN=ERC2 PE=1 SV=3	9.77e+004	9.45e+004	9.09e+004
E2RVJ0	6 (4)	29.18	---	1.25		Anion exchange protein OS=Homo sapiens GN=SLC4A1 PE=2 SV=1	2.14e+004	2.15e+004	2.67e+004
A0A0A0MT39	6 (5)	29.08	---	2.24		Sodium channel protein OS=Homo sapiens GN=SCN5A PE=3 SV=1	2.56e+004	2.58e+004	5.72e+004
Q9Y4K1	8 (3)	29.04	---	1.07		Absent in melanoma 1 protein OS=Homo sapiens GN=AIM1 PE=1 SV=3	6.00e+004	6.07e+004	6.43e+004
H0Y6I0	7 (5)	28.98	---	1.19		Golgin subfamily A member 4 (Fragment) OS=Homo sapiens GN=GOLGA4 PE=1 SV=1	7844.60	8385.96	7050.18
Q86WI3	7 (4)	28.97	---	1.13		Protein NLR5 OS=Homo sapiens GN=NLR5 PE=1 SV=3	9401.82	9454.37	8398.14
A0A087WYK2	7 (7)	28.95	---	2.32		Serine/threonine-protein kinase WNK3 OS=Homo sapiens GN=WNK3 PE=1 SV=1	7.66e+004	7.44e+004	1.73e+005
A5D6X1	6 (2)	28.94	---	1.13		MAP1B protein (Fragment) OS=Homo sapiens GN=MAP1B PE=2 SV=1	2.81e+004	2.67e+004	3.01e+004
Q96M83	7 (5)	28.90	---	2.57		Coiled-coil domain-containing protein 7 OS=Homo sapiens GN=CCDC7 PE=2 SV=3	5.71e+004	4.91e+004	1.26e+005
Q6ZMV9	8 (6)	28.81	---	2.21		Kinesin-like protein KIF6 OS=Homo sapiens GN=KIF6 PE=1 SV=3	4.34e+004	3.97e+004	8.80e+004
Q94988	7 (4)	28.41	---	1.21		Protein FAM13A OS=Homo sapiens GN=FAM13A PE=1 SV=2	2.30e+004	2.20e+004	2.67e+004
Q95373	6 (6)	28.41	---	1.05		Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1	7.45e+004	7.26e+004	7.65e+004
A0A024RDQ1	6 (6)	28.38	---	1.21		Furry homolog (Drosophila)_ isoform CRA_c OS=Homo sapiens GN=FRY PE=4 SV=1	4.22e+004	5.08e+004	4.39e+004
D3DS91	6 (3)	28.38	---	1.02		A kinase (PRKA) anchor protein 6_ isoform CRA_b OS=Homo sapiens GN=AKAP6 PE=4 SV=1	3.15e+004	3.09e+004	3.14e+004
A0A024R7N2	6 (6)	28.31	---	1.04		Cation-transporting ATPase OS=Homo sapiens GN=ATP13A1 PE=3 SV=1	4.96e+004	5.07e+004	5.17e+004
P12882	8 (2)	28.22	---	1.09		Myosin-1 OS=Homo sapiens GN=MYH1 PE=1 SV=3	2.05e+004	1.88e+004	2.00e+004
A0A087WWA5	7 (5)	28.03	---	1.21		Tenascin-X OS=Homo sapiens GN=TNXB PE=1 SV=1	1.07e+005	9.72e+004	1.17e+005
Q02779	7 (4)	28.01	---	1.13		Mitogen-activated protein kinase kinase kinase 10 OS=Homo sapiens GN=MAP3K10 PE=1 SV=3	1.48e+004	1.41e+004	1.32e+004
J3KQ21	6 (1)	27.85	---	1.40		Ankyrin repeat and MYND domain-containing protein 1 OS=Homo sapiens GN=ANKMY1 PE=4 SV=1	1.07e+004	1.33e+004	1.51e+004
Q92538	6 (3)	27.63	---	1.09		Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 OS=Homo sapiens GN=GBF1 PE=1 SV=2	8503.99	7786.77	8314.65

Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances		
							0hr	1hr	2hr
Q96T23	6 (1)	27.42	---	1.22		Remodeling and spacing factor 1 OS=Homo sapiens GN=RSF1 PE=1 SV=2	1.94e+004	1.59e+004	1.82e+004
Q86YA3	6 (4)	27.40	---	1.09		Protein ZGRF1 OS=Homo sapiens GN=ZGRF1 PE=1 SV=3	1.02e+005	9.31e+004	9.72e+004
Q9H2Y7	6 (4)	27.32	---	1.16		Zinc finger protein 106 OS=Homo sapiens GN=ZNF106 PE=1 SV=1	2.14e+004	2.13e+004	2.46e+004
Q13635	6 (5)	27.31	---	1.06		Protein patched homolog 1 OS=Homo sapiens GN=PTCH1 PE=1 SV=2	2.46e+004	2.32e+004	2.37e+004
B4DWC0	6 (3)	27.25	---	1.39		cDNA FLJ58290_ highly similar to Zinc finger MYM-type protein 6 (Fragment) OS=Homo sapiens PE=2 SV=1	5.06e+004	3.77e+004	5.25e+004
Q7RTU9	6 (2)	27.17	---	1.24		Stereocilin OS=Homo sapiens GN=STRC PE=2 SV=1	1.96e+004	1.76e+004	1.58e+004
Q71F56	6 (3)	27.14	---	1.24		Mediator of RNA polymerase II transcription subunit 13-like OS=Homo sapiens GN=MED13L PE=1 SV=1	3.27e+004	4.03e+004	4.05e+004
Q5JSZ5	6 (3)	27.06	---	1.14		Protein PRRC2B OS=Homo sapiens GN=PRRC2B PE=1 SV=2	1.70e+004	1.81e+004	1.60e+004
A0A024R209	6 (6)	26.82	---	1.05		Transient receptor potential cation channel_ subfamily M_ member 1_ isoform CRA_a OS=Homo sapiens GN=TRPM1 PE=4 SV=1	5.86e+004	5.92e+004	6.16e+004
Q01118	7 (7)	26.69	---	1.19		Sodium channel protein type 7 subunit alpha OS=Homo sapiens GN=SCN7A PE=1 SV=2	2.23e+004	2.08e+004	2.47e+004
Q14514	7 (6)	26.65	---	1.70		Brain-specific angiogenesis inhibitor 1 OS=Homo sapiens GN=BAI1 PE=1 SV=2	1.37e+004	1.42e+004	8380.32
A6NHR9	6 (4)	26.60	---	1.06		Structural maintenance of chromosomes flexible hinge domain-containing protein 1 OS=Homo sapiens GN=SMCHD1 PE=1 SV=2	1.08e+005	1.03e+005	1.09e+005
H0YJP0	6 (5)	26.57	---	1.17		E3 ubiquitin-protein ligase HECTD1 (Fragment) OS=Homo sapiens GN=HECTD1 PE=1 SV=2	2.36e+004	2.76e+004	2.75e+004
A0A024R1E6	5 (3)	26.49	---	1.29		Preferentially expressed antigen in melanoma_ isoform CRA_a OS=Homo sapiens GN=PRAME PE=4 SV=1	1.28e+004	1.31e+004	1.02e+004
A7E2A5	6 (3)	26.41	---	1.18		ARAP2 protein (Fragment) OS=Homo sapiens GN=ARAP2 PE=2 SV=1	8777.58	1.02e+004	1.04e+004
Q9Y6X0	6 (5)	26.37	---	1.15		SET-binding protein OS=Homo sapiens GN=SETBP1 PE=1 SV=3	2.30e+004	2.00e+004	2.26e+004
A6NEQ0	6 (4)	26.32	---	1.10		RNA-binding motif protein_ Y chromosome_ family 1 member E OS=Homo sapiens GN=RBM1Y1E PE=2 SV=1	4.65e+004	4.22e+004	4.44e+004
B7Z751	6 (4)	26.23	---	1.15		cDNA FLJ61721_ highly similar to Homo sapiens ring finger protein 17 (RNF17)_ mRNA OS=Homo sapiens PE=2 SV=1	3.82e+004	4.11e+004	3.57e+004
P01031	6 (4)	25.98	---	1.04		Complement C5 OS=Homo sapiens GN=C5 PE=1 SV=4	1.82e+004	1.80e+004	1.75e+004
G1UI29	6 (4)	25.90	---	1.28		Helicase SRCAP (Fragment) OS=Homo sapiens GN=SRCAP PE=2 SV=1	3.02e+004	2.93e+004	2.37e+004
B5TMG5	6 (6)	25.88	---	1.29		Histidine rich calcium binding protein OS=Homo sapiens GN=HRC PE=4 SV=1	4.88e+004	4.53e+004	3.79e+004
Q9HAU0	7 (4)	25.86	---	1.08		Pleckstrin homology domain-containing family A member 5 OS=Homo sapiens GN=PLEKHA5 PE=1 SV=1	3.32e+004	3.08e+004	3.24e+004
A0A158RFW1	5 (3)	25.79	---	1.07		Alpha 1 type XXI collagen OS=Homo sapiens GN=COL21A1 PE=4 SV=1	8.22e+004	8.06e+004	8.66e+004
B7ZKX1	6 (4)	25.74	---	1.29		RFX7 protein (Fragment) OS=Homo sapiens GN=RFX7 PE=2 SV=1	3.76e+004	4.84e+004	3.79e+004
B1AHL2	5 (3)	25.72	---	1.08		Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=1	3.73e+004	3.57e+004	3.45e+004
Q9P2R6	7 (5)	25.64	---	1.58		Arginine-glutamic acid dipeptide repeats protein OS=Homo sapiens GN=RERE PE=1 SV=2	3.81e+004	3.23e+004	5.10e+004
Q6ZUT9	7 (4)	25.64	---	1.16		DENN domain-containing protein 5B OS=Homo sapiens GN=DENND5B PE=1 SV=2	4.73e+004	4.24e+004	4.91e+004
Q13367	6 (6)	25.62	---	1.16		AP-3 complex subunit beta-2 OS=Homo sapiens GN=AP3B2 PE=1 SV=2	3.53e+004	3.04e+004	3.47e+004
B3KXB6	6 (6)	25.52	---	1.21		cDNA FLJ45101 fis_ clone BRAWH3032298_ highly similar to Tenascin-N OS=Homo sapiens PE=2 SV=1	3.26e+004	2.69e+004	2.97e+004
A5PKZ7	6 (4)	25.37	---	1.14		Phospholipase A2 OS=Homo sapiens GN=PLA2G4F PE=2 SV=1	1.50e+004	1.32e+004	1.46e+004
Q9UPR0	6 (4)	25.32	---	1.19		Inactive phospholipase C-like protein 2 OS=Homo sapiens GN=PLCL2 PE=1 SV=2	1.33e+004	1.45e+004	1.23e+004
A0A024R8E5	6 (4)	25.30	---	1.19		Collagen_ type V_ alpha 1_ isoform CRA_a OS=Homo sapiens GN=COL5A1 PE=4 SV=1	6277.40	5988.63	5254.09
A3KMH1	7 (5)	25.16	---	1.25		von Willebrand factor A domain-containing protein 8 OS=Homo sapiens GN=VWA8 PE=1 SV=2	2.23e+004	2.34e+004	2.77e+004
B4E2I4	5 (5)	25.13	---	1.09		cDNA FLJ58227_ highly similar to Glutamate--cysteine ligase catalytic subunit (EC 6.3.2.2) OS=Homo sapiens PE=2 SV=1	1.25e+004	1.18e+004	1.28e+004
J9R021	6 (4)	25.09	---	1.11		Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=eIF3a PE=2 SV=1	6.01e+004	6.12e+004	6.67e+004
A0AVK6	5 (5)	24.95	---	1.11		Transcription factor E2F8 OS=Homo sapiens GN=E2F8 PE=1 SV=1	8.96e+004	9.85e+004	8.83e+004
Q6ZUG5	5 (3)	24.79	---	1.13		Uncharacterized protein FLJ43738 OS=Homo sapiens PE=2 SV=1	1.31e+004	1.39e+004	1.23e+004
A0A087WTW5	6 (3)	24.76	---	1.25		CASP8-associated protein 2 OS=Homo sapiens GN=CASP8AP2 PE=1 SV=1	2.75e+004	2.28e+004	2.85e+004
Q6ZT12	6 (2)	24.71	---	1.07		E3 ubiquitin-protein ligase UBR3 OS=Homo sapiens GN=UBR3 PE=2 SV=2	3.05e+004	3.03e+004	3.24e+004
A8K182	5 (4)	24.70	---	1.47		Sortilin-related VPS10 domain containing receptor 1_ isoform CRA_d OS=Homo sapiens GN=SORCS1 PE=2 SV=1	3.39e+004	3.57e+004	4.97e+004
B1ALM3	6 (5)	24.68	---	1.92		Voltage-dependent L-type calcium channel subunit alpha OS=Homo sapiens GN=CACNA1S PE=1 SV=1	5.84e+004	5.00e+004	9.61e+004
Q96JE9	6 (4)	24.56	---	1.02		Microtubule-associated protein 6 OS=Homo sapiens GN=MAP6 PE=1 SV=2	8.97e+004	9.06e+004	8.84e+004
A0A0C4DG33	5 (4)	24.43	---	1.22		Peroxisome biogenesis factor 1 OS=Homo sapiens GN=PEX1 PE=1 SV=1	1.58e+004	1.93e+004	1.59e+004
B2RWP8	5 (2)	24.41	---	1.32		Phospholipase B1 OS=Homo sapiens GN=PLB1 PE=2 SV=1	2.30e+004	2.88e+004	2.17e+004

Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances		
							0hr	1hr	2hr
Q7Z3Z5	6 (5)	24.31	---	1.28		Mediator of RNA polymerase II transcription subunit 12 OS=Homo sapiens GN=TNRC11 PE=1 SV=1	2.99e+004	3.81e+004	3.56e+004
G3XAI2	6 (2)	24.17	---	1.08		Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=1 SV=1	1.17e+005	1.18e+005	1.26e+005
P19174	5 (5)	24.03	---	1.22		1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1 OS=Homo sapiens GN=PLCG1 PE=1 SV=1	3.67e+004	4.48e+004	4.15e+004
A0A024R3K9	5 (5)	23.98	---	1.29		Nuclear factor related to kappaB binding protein_ isoform CRA_c OS=Homo sapiens GN=NFRKB PE=4 SV=1	9.67e+004	9.35e+004	7.48e+004
A0A0J9YVZ6	6 (6)	23.95	---	1.11		Unconventional myosin-XVB OS=Homo sapiens GN=MYO15B PE=1 SV=1	9.11e+004	9.29e+004	8.38e+004
A8K1Y7	5 (4)	23.94	---	1.25		cDNA FLJ77273_ highly similar to Homo sapiens centaurin_ delta 3 (CENTD3)_ mRNA OS=Homo sapiens PE=2 SV=1	1.47e+004	1.67e+004	1.85e+004
A0A1B0GV47	5 (4)	23.92	---	1.06		Kinesin-like protein KIF21A (Fragment) OS=Homo sapiens GN=KIF21A PE=1 SV=1	4.69e+004	4.99e+004	4.69e+004
Q9UJF2	5 (3)	23.74	---	1.07		Ras GTPase-activating protein nGAP OS=Homo sapiens GN=RASAL2 PE=1 SV=2	1.92e+004	1.89e+004	1.80e+004
Q86TP1	5 (5)	23.73	---	1.42		Protein prune homolog OS=Homo sapiens GN=PRUNE PE=1 SV=2	1.60e+005	1.35e+005	1.12e+005
P35712	5 (4)	23.64	---	1.24		Transcription factor SOX-6 OS=Homo sapiens GN=SOX6 PE=1 SV=3	5.56e+004	4.47e+004	4.96e+004
B7ZLD0	5 (4)	23.47	---	1.09		LRP6 protein OS=Homo sapiens GN=LRP6 PE=2 SV=1	2.60e+004	2.58e+004	2.81e+004
Q76LX8	6 (4)	23.46	---	1.13		A disintegrin and metalloproteinase with thrombospondin motifs 13 OS=Homo sapiens GN=ADAMTS13 PE=1 SV=1	5.31e+004	4.71e+004	5.25e+004
Q5JYA6	5 (4)	23.44	---	1.20		Pleckstrin homology domain containing_ family G (With RhoGef domain) member 1 OS=Homo sapiens GN=PLEKHG1 PE=2 SV=1	2.11e+004	1.95e+004	2.35e+004
Q9Y2L6	5 (3)	23.29	---	3.57		FERM domain-containing protein 4B OS=Homo sapiens GN=FRMD4B PE=1 SV=4	2.61e+004	2.14e+004	7.64e+004
Q14008	6 (5)	23.20	---	1.07		Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5 PE=1 SV=3	6.20e+004	5.91e+004	5.80e+004
Q659C4	5 (2)	23.20	---	1.21		La-related protein 1B OS=Homo sapiens GN=LARP1B PE=1 SV=2	1.82e+004	1.63e+004	1.97e+004
B4DKD0	5 (4)	23.20	---	1.42		DNA topoisomerase 2 (Fragment) OS=Homo sapiens PE=2 SV=1	7.24e+004	7.08e+004	1.01e+005
Q5TYW1	5 (2)	23.16	---	1.41		Zinc finger protein 658 OS=Homo sapiens GN=ZNF658 PE=2 SV=2	1.78e+004	1.55e+004	1.26e+004
Q43424	6 (4)	23.15	---	1.18		Glutamate receptor ionotropic_ delta-2 OS=Homo sapiens GN=GRID2 PE=1 SV=2	1.28e+004	1.29e+004	1.51e+004
A8K5P7	5 (3)	23.06	---	1.99		cDNA FLJ75523_ highly similar to Homo sapiens glutamate receptor_ metabotropic 5 (GRM5)_ mRNA (Fragment) OS=Homo sapiens PE=2 SV=1	2.15e+004	1.66e+004	1.08e+004
A0A0A0MT08	5 (3)	23.03	---	1.29		MROH7-TTC4 readthrough (NMD candidate) OS=Homo sapiens GN=MROH7-TTC4 PE=4 SV=1	1.37e+005	1.77e+005	1.61e+005
Q13127	5 (3)	23.01	---	1.04		RE1-silencing transcription factor OS=Homo sapiens GN=REST PE=1 SV=3	5561.89	5419.48	5636.53
B7ZKS3	5 (4)	22.96	---	1.08		Ubiquitin specific peptidase 48 OS=Homo sapiens GN=USP48 PE=2 SV=1	5.37e+004	4.98e+004	5.38e+004
A0A024R9I5	5 (5)	22.88	---	1.71		Solute carrier family 12 (Potassium/chloride transporters)_ member 6_ isoform CRA_d OS=Homo sapiens GN=SLC12A6 PE=4 SV=1	2.32e+004	2.14e+004	3.66e+004
X5D9K3	5 (2)	22.73	---	1.08		Tuberous sclerosis 2 isoform E OS=Homo sapiens GN=TSC2 PE=2 SV=1	7.18e+004	7.74e+004	7.66e+004
Q5HYK7	6 (4)	22.73	---	1.14		SH3 domain-containing protein 19 OS=Homo sapiens GN=SH3D19 PE=1 SV=2	1.11e+004	1.09e+004	9736.90
Q6R327	5 (3)	22.72	---	1.06		Rapamycin-insensitive companion of mTOR OS=Homo sapiens GN=RICTOR PE=1 SV=1	4.26e+004	4.49e+004	4.23e+004
A0A024R9G7	5 (4)	22.60	---	1.10		ATPase family_ AAA domain containing 2_ isoform CRA_c OS=Homo sapiens GN=ATAD2 PE=4 SV=1	2.16e+004	2.32e+004	2.12e+004
D3DT71	5 (3)	22.56	---	1.48		Collagen_ type XI_ alpha 1_ isoform CRA_b OS=Homo sapiens GN=COL11A1 PE=4 SV=1	8421.82	8043.76	1.19e+004
Q8IWIY9	5 (5)	22.51	---	1.28		Codanin-1 OS=Homo sapiens GN=CDAN1 PE=1 SV=4	1.03e+004	1.25e+004	1.32e+004
Q15360	5 (2)	22.29	---	1.11		Fanconi anemia group A protein OS=Homo sapiens GN=FANCA PE=1 SV=2	6650.83	6913.95	6243.83
A0A024R8B6	5 (4)	22.25	---	1.10		Nucleoporin 214kDa_ isoform CRA_b OS=Homo sapiens GN=NUP214 PE=4 SV=1	2.20e+004	2.43e+004	2.40e+004
A8K4P8	5 (3)	22.18	---	1.26		cDNA FLJ75337 OS=Homo sapiens PE=2 SV=1	5.02e+004	5.28e+004	4.20e+004
A0A024RD55	5 (1)	22.11	---	1.39		EGF-like-domain_ multiple 9_ isoform CRA_a OS=Homo sapiens GN=EGFL9 PE=4 SV=1	4.22e+004	3.47e+004	3.03e+004
Q6PKG0	5 (4)	22.09	---	1.18		La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2	2.03e+004	1.90e+004	2.25e+004
Q658Y4	5 (5)	22.07	---	1.02		Protein FAM91A1 OS=Homo sapiens GN=FAM91A1 PE=1 SV=3	4.15e+004	4.20e+004	4.24e+004
Q9P2K1	5 (3)	22.00	---	1.01		Coiled-coil and C2 domain-containing protein 2A OS=Homo sapiens GN=CC2D2A PE=1 SV=3	1.93e+004	1.93e+004	1.95e+004
Q9UHF7	5 (3)	21.95	---	1.05		Zinc finger transcription factor Trps1 OS=Homo sapiens GN=TRPS1 PE=1 SV=2	1.50e+004	1.57e+004	1.57e+004
A0A0A0MRJ0	5 (4)	21.86	---	1.05		Serine/threonine-protein kinase MRCK alpha OS=Homo sapiens GN=CDC42BPA PE=1 SV=1	4.85e+004	5.02e+004	4.77e+004
Q8IZE3	5 (4)	21.85	---	1.28		Protein-associating with the carboxyl-terminal domain of ezrin OS=Homo sapiens GN=SCYL3 PE=1 SV=3	2.15e+005	2.14e+005	2.73e+005
A8K8V8	5 (4)	21.61	---	1.25		cDNA FLJ76444 OS=Homo sapiens PE=2 SV=1	2.44e+004	2.78e+004	2.22e+004
A0A024R7C7	4 (2)	21.59	---	1.09		Interleukin enhancer binding factor 3_ 90kDa_ isoform CRA_d OS=Homo sapiens GN=ILF3 PE=4 SV=1	6290.49	5942.94	5782.48
Q96QU1	6 (5)	21.51	---	1.09		Protocadherin-15 OS=Homo sapiens GN=PCDH15 PE=1 SV=2	9468.53	9104.14	9883.29

Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances		
							0hr	1hr	2hr
Q6FHF7	5 (3)	21.45	---	1.27		RABGGTA protein (Fragment) OS=Homo sapiens GN=RABGGTA PE=2 SV=1	8143.88	1.04e+004	8164.54
A0A0D9SFM0	5 (4)	21.43	---	1.12		E3 ubiquitin-protein ligase SHPRH OS=Homo sapiens GN=SHPRH PE=1 SV=1	2.04e+005	1.94e+005	2.16e+005
B4DM01	5 (3)	21.32	---	1.16		cDNA FLJ57529_ highly similar to Helicase SKI2W (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1	4.44e+004	3.82e+004	4.43e+004
Q9UBG0	5 (5)	21.25	---	1.38		C-type mannose receptor 2 OS=Homo sapiens GN=MRC2 PE=1 SV=2	4.66e+004	4.52e+004	6.24e+004
Q14676	5 (4)	21.22	---	1.20		Mediator of DNA damage checkpoint protein 1 OS=Homo sapiens GN=MDC1 PE=1 SV=3	5.02e+004	4.56e+004	5.47e+004
A8K6Q4	5 (4)	21.17	---	1.24		cDNA FLJ76888_ highly similar to Homo sapiens RNA binding motif protein 6 (RBM6)_ mRNA OS=Homo sapiens PE=2 SV=1	4.37e+004	3.52e+004	4.29e+004
A8MQ02	5 (4)	21.16	---	1.23		Afadin OS=Homo sapiens GN=AFDN PE=1 SV=2	2.30e+004	1.91e+004	2.36e+004
Q9BPX3	5 (3)	21.15	---	1.07		Condensin complex subunit 3 OS=Homo sapiens GN=NCAPG PE=1 SV=1	6.82e+004	6.36e+004	6.79e+004
B4DR53	5 (5)	21.11	---	1.24		Anion exchange protein OS=Homo sapiens PE=2 SV=1	4.71e+004	4.86e+004	5.84e+004
Q43719	5 (4)	21.06	---	2.12		HIV Tat-specific factor 1 OS=Homo sapiens GN=HTATSF1 PE=1 SV=1	2.22e+004	2.18e+004	4.63e+004
B2RNT9	5 (4)	20.99	---	1.23		UHRF1BP1 protein OS=Homo sapiens GN=UHRF1BP1 PE=2 SV=1	1.50e+004	1.75e+004	1.42e+004
Q13443	4 (2)	20.95	---	1.67		Disintegrin and metalloproteinase domain-containing protein 9 OS=Homo sapiens GN=ADAM9 PE=1 SV=1	1.85e+004	1.61e+004	2.68e+004
Q96BJ8	5 (4)	20.85	---	1.14		Engulfment and cell motility protein 3 OS=Homo sapiens GN=ELMO3 PE=1 SV=3	1.17e+005	1.33e+005	1.30e+005
G3V2A4	5 (4)	20.85	---	1.07		Telomerase protein component 1 OS=Homo sapiens GN=TEP1 PE=1 SV=1	3.77e+004	3.69e+004	3.51e+004
C9J5X1	5 (4)	20.81	---	1.23		Tyrosine-protein kinase receptor OS=Homo sapiens GN=IGF1R PE=1 SV=1	3.17e+004	3.06e+004	3.76e+004
B2R636	5 (4)	20.80	---	1.22		cDNA_FLJ92762_ highly similar to Homo sapiens ubiquitin specific protease 1 (USP1)_ mRNA OS=Homo sapiens PE=2 SV=1	2.29e+004	1.89e+004	2.31e+004
A6NKG5	5 (4)	20.79	---	1.08		Retrotransposon-like protein 1 OS=Homo sapiens GN=RTL1 PE=3 SV=3	1.41e+005	1.53e+005	1.52e+005
Q8IUD2	6 (3)	20.71	---	1.14		ELKS/Rab6-interacting/CAST family member 1 OS=Homo sapiens GN=ERC1 PE=1 SV=1	4.90e+004	5.37e+004	5.61e+004
A0A024R2H0	4 (2)	20.70	---	1.10		TBC1 domain family_ member 5_ isoform CRA_a OS=Homo sapiens GN=TBC1D5 PE=4 SV=1	8278.48	8878.42	8059.63
Q8NCN5	6 (4)	20.59	---	1.82		Pyruvate dehydrogenase phosphatase regulatory subunit_ mitochondrial OS=Homo sapiens GN=PDPR PE=1 SV=2	1.95e+004	3.54e+004	3.31e+004
P23229	5 (3)	20.58	---	1.09		Integrin alpha-6 OS=Homo sapiens GN=ITGA6 PE=1 SV=5	5.97e+004	6.51e+004	6.25e+004
P48634	6 (4)	20.54	---	1.26		Protein PRRC2A OS=Homo sapiens GN=PRRC2A PE=1 SV=3	6.72e+004	5.32e+004	5.88e+004
A0A024R1V5	5 (3)	20.54	---	1.16		Myeloid/lymphoid or mixed-lineage leukemia (Trithorax homolog_ Drosophila) translocated to_6_ isoform CRA_a OS=Homo sapiens GN=MLLT6 PE=4 SV=1	4.61e+004	4.44e+004	5.13e+004
Q9ULD2	5 (4)	20.35	---	1.10		Microtubule-associated tumor suppressor 1 OS=Homo sapiens GN=MTUS1 PE=1 SV=2	5.27e+004	5.81e+004	5.81e+004
Q6PIK7	5 (4)	20.33	---	1.86		Angiogenic factor with G patch and FHA domains 1 OS=Homo sapiens GN=AGGF1 PE=1 SV=1	2.59e+005	3.96e+005	4.82e+005
B4DNR7	4 (4)	20.19	---	1.19		cDNA FLJ51010_ highly similar to Latent-transforming growth factor beta-binding protein_ isoform 1S OS=Homo sapiens PE=2 SV=1	9.39e+004	9.96e+004	8.37e+004
A0A0A0MR60	4 (2)	20.18	---	1.25		Receptor-type tyrosine-protein phosphatase 5 OS=Homo sapiens GN=PTPRS PE=4 SV=1	5.07e+004	4.84e+004	6.07e+004
Q9NXD2	5 (2)	20.14	---	1.06		Myotubularin-related protein 10 OS=Homo sapiens GN=MTMR10 PE=1 SV=3	7029.13	6651.85	6683.75
Q13017	4 (3)	20.05	---	1.05		Rho GTPase-activating protein 5 OS=Homo sapiens GN=ARHGAP5 PE=1 SV=2	2.59e+004	2.46e+004	2.58e+004
A0A024RB84	4 (3)	20.00	---	1.17		V-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (Avian)_ isoform CRA_a OS=Homo sapiens GN=ERBB3 PE=4 SV=1	2.10e+004	2.06e+004	2.41e+004
A6H8W8	5 (3)	19.96	---	1.08		Intersectin 2 OS=Homo sapiens GN=ITSN2 PE=2 SV=1	6.04e+004	6.56e+004	6.40e+004
Q8N139	5 (4)	19.84	---	1.10		ATP-binding cassette sub-family A member 6 OS=Homo sapiens GN=ABCA6 PE=1 SV=2	3.91e+004	4.00e+004	4.29e+004
A0A0D9SGJ6	5 (2)	19.81	---	1.24		Synaptojanin-1 OS=Homo sapiens GN=SYNJ1 PE=1 SV=1	5768.49	6627.06	7180.97
A8K6J9	4 (3)	19.79	---	1.03		cDNA FLJ76879_ highly similar to Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 8 (DHX8)_ mRNA OS=Homo sapiens PE=2 SV=1	5.04e+004	5.06e+004	4.93e+004
B5MDV5	4 (4)	19.76	---	1.14		KIAA1244 OS=Homo sapiens GN=KIAA1244 PE=2 SV=1	1.95e+004	2.00e+004	2.22e+004
A8K7B7	4 (3)	19.70	---	1.14		Protein phosphatase 2 (Formerly 2A)_ regulatory subunit A (PR 65)_ alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=1	6.32e+004	6.31e+004	5.55e+004
Q43306	4 (4)	19.67	---	1.07		Adenylate cyclase type 6 OS=Homo sapiens GN=ADCY6 PE=1 SV=2	2.25e+004	2.28e+004	2.40e+004
Q9BY66	4 (3)	19.66	---	1.21		Lysine-specific demethylase 5D OS=Homo sapiens GN=KDM5D PE=1 SV=2	6909.05	8387.58	7286.44
Q5VVM6	4 (3)	19.64	---	1.19		Coiled-coil domain-containing protein 30 OS=Homo sapiens GN=CCDC30 PE=2 SV=1	2.25e+005	2.02e+005	2.40e+005
P37059	5 (4)	19.63	---	1.68		Estradiol 17-beta-dehydrogenase 2 OS=Homo sapiens GN=HSD17B2 PE=1 SV=1	2.29e+004	2.44e+004	1.45e+004
A4DOS4	6 (4)	19.62	---	1.18		Laminin subunit beta-4 OS=Homo sapiens GN=LAMB4 PE=2 SV=1	1.32e+004	1.12e+004	1.23e+004
Q9UPX0	4 (1)	19.62	---	1.12		Protein turtle homolog B OS=Homo sapiens GN=IGSF9B PE=2 SV=2	1.05e+005	1.00e+005	1.12e+005
Q12756	4 (4)	19.61	---	1.12		Kinesin-like protein KIF1A OS=Homo sapiens GN=KIF1A PE=1 SV=2	2.81e+004	2.51e+004	2.56e+004

Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances		
							0hr	1hr	2hr
A0A024R542	4 (4)	19.53	---	1.60		Tankyrase 1 binding protein 1_ 182kDa_ isoform CRA_a OS=Homo sapiens GN=TNKS1BP1 PE=2 SV=1	3.76e+004	2.36e+004	2.79e+004
Q7RTS5	4 (3)	19.35	---	1.21		Otopetrin-3 OS=Homo sapiens GN=OTOP3 PE=1 SV=1	1.65e+004	1.96e+004	1.62e+004
Q4L180	4 (3)	19.35	---	1.37		Filamin A-interacting protein 1-like OS=Homo sapiens GN=FILIP1L PE=1 SV=2	2.33e+004	2.32e+004	3.18e+004
A0A024RBR4	5 (2)	19.31	---	2.92		Huntingtin interacting protein 1 related_ isoform CRA_a OS=Homo sapiens GN=HIP1R PE=4 SV=1	3.33e+004	3.13e+004	9.14e+004
A0A024R9Q1	4 (3)	19.15	---	1.63		Thrombospondin 1_ isoform CRA_a OS=Homo sapiens GN=THBS1 PE=4 SV=1	1.68e+004	1.61e+004	2.63e+004
A8K322	5 (4)	19.14	---	1.16		cDNA FLJ76782_ highly similar to Homo sapiens RAD54 homolog B (S. cerevisiae) (RAD54B)_ transcript variant 1_ mRNA OS=Homo sapiens PE=2 SV=1	2.54e+004	2.38e+004	2.19e+004
Q14147	4 (3)	19.14	---	1.06		Probable ATP-dependent RNA helicase DHX34 OS=Homo sapiens GN=DHX34 PE=1 SV=2	5.59e+004	5.75e+004	5.91e+004
D3DN61	4 (4)	19.10	---	1.06		Zinc finger DAZ interacting protein 3_ isoform CRA_a OS=Homo sapiens GN=DZIP3 PE=4 SV=1	3.62e+004	3.74e+004	3.85e+004
Q9BXD5	4 (2)	19.09	---	1.06		N-acetylneuraminate lyase OS=Homo sapiens GN=NPL PE=1 SV=1	7924.63	8133.14	8415.69
B4DTX5	4 (4)	18.97	---	1.15		cDNA FLJ60072_ highly similar to Homo sapiens sorbin and SH3 domain containing 1 (SORBS1)_ transcript variant 6_ mRNA OS=Homo sapiens PE=2 SV=1	9.90e+004	9.43e+004	1.08e+005
D3DUC1	4 (3)	18.96	---	1.13		Zinc finger protein 263_ isoform CRA_a OS=Homo sapiens GN=ZNF263 PE=4 SV=1	1.84e+004	2.08e+004	2.01e+004
Q9P2Q2	4 (3)	18.94	---	1.23		FERM domain-containing protein 4A OS=Homo sapiens GN=FRMD4A PE=1 SV=3	3.33e+004	2.78e+004	3.42e+004
A4D0VZ	4 (2)	18.91	---	1.10		Cadherin-like and PC-esterase domain-containing protein 1 OS=Homo sapiens GN=CPED1 PE=2 SV=1	1.35e+004	1.48e+004	1.45e+004
H0Y7R9	4 (2)	18.90	---	1.07		Cadherin EGF LAG seven-pass G-type receptor 1 (Fragment) OS=Homo sapiens GN=CELSR1 PE=1 SV=1	6395.76	5952.82	6112.49
Q60568	4 (4)	18.82	---	1.01		Procollagen-lysine 2-oxoglutarate 5-dioxygenase 3 OS=Homo sapiens GN=PLOD3 PE=1 SV=1	2.61e+004	2.64e+004	2.62e+004
D9ZGF8	5 (4)	18.78	---	1.12		Rho-associated protein kinase OS=Homo sapiens GN=ROCK1 PE=3 SV=1	9.45e+004	8.74e+004	9.79e+004
A0A0G2JL54	4 (2)	18.76	---	1.29		Complement C4-B OS=Homo sapiens GN=C4B_2 PE=1 SV=1	5.72e+004	7.32e+004	5.69e+004
A0A024R9Q4	4 (4)	18.60	---	1.03		p21(CDKN1A)-activated kinase 6_ isoform CRA_a OS=Homo sapiens GN=PAK6 PE=4 SV=1	6.77e+004	6.91e+004	7.00e+004
P78314	4 (3)	18.56	---	1.15		SH3 domain-binding protein 2 OS=Homo sapiens GN=SH3BP2 PE=1 SV=2	1.19e+005	1.11e+005	1.03e+005
Q14432	4 (1)	18.53	---	3.83		cGMP-inhibited 3',5'-cyclic phosphodiesterase A OS=Homo sapiens GN=PDE3A PE=1 SV=3	3.07e+004	2.14e+004	8.21e+004
Q9UKX2	5 (0)	18.50	---	---		Myosin-2 OS=Homo sapiens GN=MYH2 PE=1 SV=1	---	---	---
A6NM62	4 (3)	18.46	---	1.66		Leucine-rich repeat-containing protein 53 OS=Homo sapiens GN=LRRC53 PE=4 SV=2	9.56e+004	1.39e+005	1.59e+005
P11055	5 (1)	18.45	---	1.12		Myosin-3 OS=Homo sapiens GN=MYH3 PE=1 SV=3	6301.65	7065.70	6647.00
B4DLD8	4 (2)	18.34	---	1.30		cDNA FLJ59295_ highly similar to Chromodomain-helicase-DNA-binding protein 6 (EC 3.6.1.-) (Fragment) OS=Homo sapiens PE=2 SV=1	6609.22	8148.14	6287.57
K7ER00	4 (4)	18.34	---	1.08		Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=1	4.27e+004	4.61e+004	4.63e+004
Q9H0E3	4 (3)	18.26	---	1.24		Histone deacetylase complex subunit SAP130 OS=Homo sapiens GN=SAP130 PE=1 SV=1	2.89e+004	2.66e+004	3.30e+004
H3BMQ0	4 (0)	18.23	---	---		Tuberin OS=Homo sapiens GN=TSC2 PE=1 SV=1	---	---	---
Q9Y5F8	4 (4)	17.98	---	1.05		Protocadherin gamma-B7 OS=Homo sapiens GN=PCDHGB7 PE=2 SV=1	2.45e+005	2.34e+005	2.38e+005
A0A024R6H5	4 (4)	17.95	---	1.13		MutL homolog 3 (E. coli)_ isoform CRA_b OS=Homo sapiens GN=MLH3 PE=4 SV=1	3.18e+004	3.28e+004	2.91e+004
Q96NW4	5 (5)	17.93	---	1.19		Ankyrin repeat domain-containing protein 27 OS=Homo sapiens GN=ANKRD27 PE=1 SV=2	2.54e+004	2.73e+004	2.29e+004
J3KNJ2	4 (3)	17.92	---	1.19		Eukaryotic translation initiation factor 3 subunit M (Fragment) OS=Homo sapiens GN=EIF3M PE=1 SV=1	1.08e+005	9.51e+004	1.13e+005
A0A024R8G5	4 (3)	17.92	---	1.38		Glutamate receptor_ ionotropic_ N-methyl D-aspartate 1_ isoform CRA_c OS=Homo sapiens GN=GRIN1 PE=3 SV=1	5.12e+004	5.51e+004	3.99e+004
A6NEM2	4 (2)	17.90	---	1.19		Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2	1.15e+005	1.37e+005	1.26e+005
P54762	4 (3)	17.88	---	1.17		Ephrin type-B receptor 1 OS=Homo sapiens GN=EPHB1 PE=1 SV=1	4.11e+004	4.18e+004	4.81e+004
B7WPN9	4 (3)	17.88	---	1.27		Cation-transporting ATPase OS=Homo sapiens GN=ATP13A4 PE=1 SV=1	1.61e+004	1.26e+004	1.48e+004
H0Y8C9	4 (4)	17.82	---	1.39		ATP-binding cassette sub-family A member 2 (Fragment) OS=Homo sapiens GN=ABCA2 PE=1 SV=1	4.34e+004	6.04e+004	4.37e+004
Q15399	4 (4)	17.80	---	1.20		Glutamate receptor ionotropic_ NMDA 2D OS=Homo sapiens GN=GRIN2D PE=1 SV=2	6.00e+004	6.11e+004	7.21e+004
Q60500	4 (4)	17.71	---	1.19		Nephrin OS=Homo sapiens GN=NPHS1 PE=1 SV=1	3.73e+004	4.45e+004	4.06e+004
D3DRH1	4 (3)	17.69	---	1.13		Dedicator of cytokinesis 8_ isoform CRA_a OS=Homo sapiens GN=DOCK8 PE=3 SV=1	3.82e+004	3.39e+004	3.62e+004
Q96AE7	4 (3)	17.64	---	1.21		Tetratricopeptide repeat protein 17 OS=Homo sapiens GN=TTC17 PE=1 SV=1	7.93e+005	9.26e+005	9.62e+005
Q9Y5F3	4 (4)	17.59	---	1.18		Protocadherin beta-1 OS=Homo sapiens GN=PCDHB1 PE=2 SV=2	2.58e+004	3.04e+004	2.57e+004
A0A087X208	4 (1)	17.58	---	1.17		Agrin OS=Homo sapiens GN=AGRN PE=1 SV=1	5.23e+004	4.48e+004	5.14e+004


Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances		
							0hr	1hr	2hr
Q9H7Z3	4 (3)	17.57	---	1.24		Protein NRDE2 homolog OS=Homo sapiens GN=NRDE2 PE=1 SV=3	9.08e+004	1.12e+005	9.77e+004
A0A024R229	4 (3)	17.56	---	1.28		Transmembrane protein 2_ isoform CRA_b OS=Homo sapiens GN=TMEM2 PE=4 SV=1	2.49e+004	2.39e+004	3.06e+004
A0A0A0MR42	4 (2)	17.55	---	1.29		Centrosomal protein of 192 kDa OS=Homo sapiens GN=CEP192 PE=1 SV=1	6824.80	8140.54	8824.05
Q75081	4 (3)	17.54	---	1.19		Protein CBFA2T3 OS=Homo sapiens GN=CBFA2T3 PE=1 SV=2	7638.00	8475.38	7112.17
D3DQT9	4 (4)	17.53	---	1.08		Dynein heavy chain domain 1_ isoform CRA_b OS=Homo sapiens GN=DNHD1 PE=4 SV=1	4.50e+004	4.21e+004	4.18e+004
P31327	5 (3)	17.49	---	1.28		Carbamoyl-phosphate synthase [ammonia]_ mitochondrial OS=Homo sapiens GN=CP51 PE=1 SV=2	6236.11	6493.25	5059.81
A0A140T9S5	4 (4)	17.49	---	1.11		von Willebrand factor A domain-containing protein 7 OS=Homo sapiens GN=VWA7 PE=1 SV=1	1.88e+004	1.80e+004	1.69e+004
P02452	4 (0)	17.40	---	---		Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=5	---	---	---
A0A087X1C5	4 (4)	17.40	---	1.45		Putative cytochrome P450 2D7 OS=Homo sapiens GN=CYP2D7 PE=5 SV=1	8417.77	8748.06	6024.18
P59045	4 (4)	17.25	---	1.12		NACHT_ LRR and PYD domains-containing protein 11 OS=Homo sapiens GN=NLRP11 PE=2 SV=2	7.68e+004	8.16e+004	7.26e+004
B9EH95	4 (3)	17.23	---	1.10		Armadillo repeat gene deletes in velocardiofacial syndrome OS=Homo sapiens GN=ARVCF PE=2 SV=1	2.85e+004	2.58e+004	2.75e+004
Q75QN2	4 (3)	17.20	---	1.04		Integrator complex subunit 8 OS=Homo sapiens GN=INTS8 PE=1 SV=1	3.53e+004	3.40e+004	3.48e+004
E7EMF1	4 (1)	17.19	---	2.82		Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	1.16e+004	9836.75	2.77e+004
Q75197	4 (3)	17.18	---	1.27		Low-density lipoprotein receptor-related protein 5 OS=Homo sapiens GN=LRP5 PE=1 SV=2	6946.98	7480.47	5903.67
Q17RH5	4 (3)	17.14	---	1.12		RAPGEF2 protein OS=Homo sapiens GN=RAPGEF2 PE=2 SV=1	1.46e+004	1.50e+004	1.64e+004
Q16720	4 (2)	17.14	---	1.03		Plasma membrane calcium-transporting ATPase 3 OS=Homo sapiens GN=ATP2B3 PE=1 SV=3	4309.88	4458.60	4376.35
A0A0J9YXNZ	4 (3)	17.13	---	1.08		Perilipin-4 OS=Homo sapiens GN=PLIN4 PE=1 SV=1	5.61e+004	6.08e+004	5.96e+004
Q6IMN6	4 (4)	17.12	---	1.06		Caprin-2 OS=Homo sapiens GN=CAPRIN2 PE=1 SV=1	4.64e+004	4.55e+004	4.37e+004
Q5SYE7	4 (3)	17.09	---	1.05		NHS-like protein 1 OS=Homo sapiens GN=NHSL1 PE=1 SV=2	5.73e+004	5.47e+004	5.69e+004
Q9Y5Z1	4 (1)	17.05	---	1.07		Nebulin (Fragment) OS=Homo sapiens GN=NEB PE=4 SV=1	6351.13	6255.36	6674.15
Q96RD9	5 (5)	17.02	---	1.04		Fc receptor-like protein 5 OS=Homo sapiens GN=FCRL5 PE=1 SV=3	3.31e+005	3.43e+005	3.32e+005
D3DVA5	4 (3)	16.85	---	1.10		Rho/rac guanine nucleotide exchange factor (GEF) 2_ isoform CRA_a OS=Homo sapiens GN=ARHGEF2 PE=4 SV=1	1.20e+004	1.23e+004	1.11e+004
Q86TC9	5 (3)	16.68	---	1.12		Myopalladin OS=Homo sapiens GN=MYPN PE=1 SV=2	5.06e+004	5.44e+004	4.85e+004
Q9H3N8	4 (3)	16.62	---	1.36		Histamine H4 receptor OS=Homo sapiens GN=HRH4 PE=1 SV=2	1.54e+004	1.42e+004	1.94e+004
Q6F5E8	4 (4)	16.56	---	1.11		Capping protein_ Arp2/3 and myosin-I linker protein 2 OS=Homo sapiens GN=CARMIL2 PE=1 SV=2	3.92e+004	3.74e+004	4.16e+004
B4DIT2	4 (4)	16.54	---	1.94		cDNA FLJ60067_ highly similar to Oligophrenin 1 OS=Homo sapiens PE=2 SV=1	2.99e+004	2.63e+004	5.09e+004
B4DH29	4 (2)	16.53	---	1.24		DNA-directed RNA polymerase subunit beta OS=Homo sapiens PE=2 SV=1	1.25e+004	1.43e+004	1.16e+004
Q2KJY2	6 (5)	16.41	---	1.18		Kinesin-like protein KIF26B OS=Homo sapiens GN=KIF26B PE=2 SV=1	3.39e+004	4.00e+004	3.58e+004
A0A0D9SF60	4 (2)	16.41	---	1.18		Plakophilin-4 OS=Homo sapiens GN=PKP4 PE=1 SV=1	3129.81	3341.83	2823.21
Q9HCD6	4 (2)	16.31	---	1.19		Protein TANC2 OS=Homo sapiens GN=TANC2 PE=1 SV=3	7.18e+004	6.03e+004	6.36e+004
A0A024R2N6	4 (3)	16.29	---	1.13		Natural killer-tumor recognition sequence_ isoform CRA_a OS=Homo sapiens GN=NKTR PE=4 SV=1	2.16e+004	2.43e+004	2.29e+004
Q9Y666	4 (4)	16.29	---	1.17		Solute carrier family 12 member 7 OS=Homo sapiens GN=SLC12A7 PE=1 SV=3	1.80e+004	1.71e+004	2.01e+004
A6BM72	4 (2)	16.22	---	1.11		Multiple epidermal growth factor-like domains protein 11 OS=Homo sapiens GN=MEGF11 PE=2 SV=3	8.52e+004	8.71e+004	7.82e+004
Q9H792	4 (4)	16.14	---	1.12		Pseudopodium-enriched atypical kinase 1 OS=Homo sapiens GN=PEAK1 PE=1 SV=4	3.15e+004	2.82e+004	3.15e+004
Q07617	4 (4)	16.10	---	1.10		Sperm-associated antigen 1 OS=Homo sapiens GN=SPAG1 PE=1 SV=3	5.04e+004	5.09e+004	5.54e+004
H0Y2S9	4 (1)	16.09	---	3.72		Myosin phosphatase Rho-interacting protein (Fragment) OS=Homo sapiens GN=MPRIIP PE=1 SV=3	7.39e+004	6.04e+004	2.25e+005
B4E2H5	4 (4)	16.03	---	1.17		cDNA FLJ58741_ highly similar to JmJc domain-containing histone demethylation protein 2A (EC 1.14.11.-) OS=Homo sapiens PE=2 SV=1	1.46e+004	1.68e+004	1.43e+004
A8KAB1	4 (2)	15.99	---	1.69		cDNA FLJ78685_ highly similar to Homo sapiens myosin binding protein C_ slow type (MYBPC1)_ transcript variant 2_ mRNA OS=Homo sapiens PE=2 SV=1	7445.55	5883.94	9921.90
Q7Z340	4 (4)	15.96	---	1.30		Zinc finger protein 551 OS=Homo sapiens GN=ZNF551 PE=1 SV=3	1.29e+004	1.68e+004	1.58e+004
P59510	4 (2)	15.64	---	1.25		A disintegrin and metalloproteinase with thrombospondin motifs 20 OS=Homo sapiens GN=ADAMTS20 PE=2 SV=2	3777.31	3691.30	4607.81
Q15015	4 (3)	15.58	---	1.15		Zinc finger protein 646 OS=Homo sapiens GN=ZNF646 PE=1 SV=1	1.80e+004	1.91e+004	2.06e+004
A0A024R2M8	4 (4)	15.54	---	1.16		Xeroderma pigmentosum_ complementation group C_ isoform CRA_a OS=Homo sapiens GN=XPC PE=4 SV=1	2.53e+004	2.29e+004	2.65e+004
A0A024RDV7	3 (2)	15.53	---	1.13		Importin subunit alpha OS=Homo sapiens GN=KPNA3 PE=3 SV=1	5.04e+004	5.67e+004	5.01e+004
P52179	3 (2)	15.45	---	1.54		Myomesin-1 OS=Homo sapiens GN=MYOM1 PE=1 SV=2	6823.44	6918.46	4504.07
Q5JW45	3 (2)	15.38	---	1.04		Myosin-7B (Fragment) OS=Homo sapiens GN=MYH7B PE=1 SV=1	2.30e+005	2.39e+005	2.30e+005

Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances		
							0hr	1hr	2hr
Q6ZSY0	3 (3)	15.30	---	2.07		cDNA FLJ45137 fis_ clone BRAWH3038827_ highly similar to Homo sapiens leucine-zipper-like transcriptional regulator_ 1 (LZTR1) OS=Homo sapiens PE=2 SV=1	9630.71	8780.57	1.82e+004
D3DUP2	4 (2)	15.28	---	1.11		WNK lysine deficient protein kinase 1_ isoform CRA_d OS=Homo sapiens GN=WNK1 PE=4 SV=1	3.05e+004	3.39e+004	3.05e+004
P14784	3 (1)	15.24	---	1.18		Interleukin-2 receptor subunit beta OS=Homo sapiens GN=IL2RB PE=1 SV=1	3.73e+004	4.42e+004	4.20e+004
B4DIF3	3 (2)	15.17	---	1.75		cDNA FLJ59282_ highly similar to Glutamate receptor-interacting protein 1 (Fragment) OS=Homo sapiens PE=2 SV=1	2.68e+004	4.29e+004	4.69e+004
Q6P2D8	3 (2)	15.13	---	1.04		X-ray radiation resistance-associated protein 1 OS=Homo sapiens GN=XRRA1 PE=2 SV=2	3.25e+004	3.14e+004	3.18e+004
A0A024R8J3	3 (1)	14.95	---	1.28		Solute carrier family 16 (Monocarboxylic acid transporters)_ member 6_ isoform CRA_a OS=Homo sapiens GN=SLC16A6 PE=4 SV=1	4.93e+004	5.20e+004	4.07e+004
B3KP18	3 (2)	14.90	---	1.19		cDNA FLJ30946 fis_ clone FEBRA2007622_ highly similar to RAD50-interacting protein 1 OS=Homo sapiens PE=2 SV=1	1.11e+004	1.32e+004	1.26e+004
Q14896	4 (2)	14.86	---	1.07		Myosin-binding protein C_ cardiac-type OS=Homo sapiens GN=MYBPC3 PE=1 SV=4	6.01e+004	6.40e+004	6.02e+004
Q8N6G6	5 (4)	14.84	---	1.13		ADAMTS-like protein 1 OS=Homo sapiens GN=ADAMTSL1 PE=1 SV=4	5335.35	4947.03	4738.88
B4E0G0	3 (2)	14.81	---	1.13		cDNA FLJ61513_ highly similar to DNA repair protein RAD51 homolog 3 OS=Homo sapiens PE=2 SV=1	1.19e+004	1.05e+004	1.05e+004
B9A018	3 (1)	14.79	---	1.11		U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens GN=USP39 PE=1 SV=1	6896.27	6412.13	6193.72
F5GXT3	3 (2)	14.74	---	2.43		Anoctamin OS=Homo sapiens GN=ANO2 PE=1 SV=2	1.62e+004	1.56e+004	3.79e+004
G3V258	3 (3)	14.66	---	1.13		Adenylate cyclase type 4 OS=Homo sapiens GN=ADCY4 PE=4 SV=1	7347.34	8043.12	7125.65
O00519	3 (2)	14.56	---	1.07		Fatty-acid amide hydrolase 1 OS=Homo sapiens GN=FAAH PE=1 SV=2	5.76e+004	5.53e+004	5.89e+004
B7ZLK1	3 (3)	14.53	---	1.63		KIAA0528 protein OS=Homo sapiens GN=KIAA0528 PE=2 SV=1	4.09e+004	4.01e+004	6.53e+004
P55287	3 (2)	14.42	---	1.21		Cadherin-11 OS=Homo sapiens GN=CDH11 PE=2 SV=2	3.44e+004	3.95e+004	4.16e+004
E5RFN6	3 (2)	14.39	---	1.26		ATP-binding cassette sub-family A member 10 OS=Homo sapiens GN=ABCA10 PE=1 SV=1	3.25e+004	3.12e+004	2.58e+004
A0A087WU80	3 (2)	14.38	---	1.11		Tumor necrosis factor alpha-induced protein 3 OS=Homo sapiens GN=TNFAIP3 PE=1 SV=1	6.92e+004	6.52e+004	7.21e+004
Q76MJ5	4 (2)	14.36	---	1.14		Serine/threonine-protein kinase/endoribonuclease IRE2 OS=Homo sapiens GN=ERN2 PE=1 SV=4	2.74e+004	3.13e+004	3.04e+004
A0A024R2K4	3 (3)	14.35	---	1.78		Leucine rich repeat (In FLII) interacting protein 2_ isoform CRA_b OS=Homo sapiens GN=LRRFIP2 PE=4 SV=1	2.33e+004	2.09e+004	3.73e+004
Q6ULP2	3 (3)	14.31	---	1.04		Aftiphilin OS=Homo sapiens GN=AFTPH PE=1 SV=2	9392.21	9809.33	9785.06
A0A024R2K6	3 (2)	14.31	---	1.21		Calcium-transporting ATPase OS=Homo sapiens GN=ATP2B2 PE=3 SV=1	1.79e+004	1.84e+004	2.16e+004
B7ZL06	3 (2)	14.31	---	1.09		SIGLEC10 protein OS=Homo sapiens GN=SIGLEC10 PE=2 SV=1	3.92e+004	4.10e+004	3.76e+004
Q15572	3 (1)	14.28	---	1.36		TATA box-binding protein-associated factor RNA polymerase I subunit C OS=Homo sapiens GN=TAF1C PE=1 SV=2	7751.22	5690.94	7489.78
Q8TD20	3 (2)	14.27	---	1.21		Solute carrier family 2_ facilitated glucose transporter member 12 OS=Homo sapiens GN=SLC2A12 PE=2 SV=1	2.49e+004	3.01e+004	2.59e+004
H0Y108	3 (3)	14.27	---	1.04		Protein MRV11 OS=Homo sapiens GN=MRV11 PE=1 SV=1	1.33e+004	1.32e+004	1.37e+004
Q00653	3 (2)	14.16	---	1.06		Nuclear factor NF-kappa-B p100 subunit OS=Homo sapiens GN=NFKB2 PE=1 SV=4	4.97e+004	5.03e+004	5.24e+004
B4DQY2	3 (1)	14.12	---	1.16		MICOS complex subunit MIC60 OS=Homo sapiens PE=2 SV=1	2.73e+004	2.64e+004	2.34e+004
B1ANR0	3 (3)	14.09	---	1.35		Polyadenylate-binding protein OS=Homo sapiens GN=PABPC4 PE=1 SV=1	1.49e+004	1.29e+004	1.74e+004
H0Y659	3 (1)	14.08	---	1.32		E3 ubiquitin-protein ligase HUWE1 (Fragment) OS=Homo sapiens GN=HUWE1 PE=1 SV=1	2407.69	1826.19	2220.78
Q5T6C5	3 (2)	14.07	---	1.33		Ataxin-7-like protein 2 OS=Homo sapiens GN=ATXN7L2 PE=1 SV=1	5.04e+004	5.37e+004	4.04e+004
Q43347	4 (4)	14.06	---	1.34		RNA-binding protein Musashi homolog 1 OS=Homo sapiens GN=MSI1 PE=1 SV=1	1.98e+004	2.65e+004	2.52e+004
Q86Y3Z	3 (3)	14.03	---	1.13		CDK2-associated and cullin domain-containing protein 1 OS=Homo sapiens GN=CACUL1 PE=1 SV=1	7.68e+004	7.43e+004	8.42e+004
Q9UPQ9	3 (2)	13.99	---	1.96		Trinucleotide repeat-containing gene 6B protein OS=Homo sapiens GN=TNRC6B PE=1 SV=4	3.83e+004	3.47e+004	1.96e+004
B2RDR6	3 (3)	13.98	---	1.13		Tyrosine-protein kinase OS=Homo sapiens PE=2 SV=1	4.31e+004	3.81e+004	4.07e+004
P17927	3 (0)	13.97	---	---		Complement receptor type 1 OS=Homo sapiens GN=CR1 PE=1 SV=3	---	---	---
B4DVM5	3 (2)	13.95	---	1.48		cDNA FLJ60907_ highly similar to WD repeat protein 24 OS=Homo sapiens PE=2 SV=1	5.07e+004	3.42e+004	4.18e+004
QZRTY7	3 (2)	13.95	---	1.12		Ovochymase-1 OS=Homo sapiens GN=OVCH1 PE=2 SV=2	2.51e+004	2.57e+004	2.81e+004
A0A024R1I2	3 (1)	13.92	---	1.62		Myotubularin related protein 3_ isoform CRA_d OS=Homo sapiens GN=MTMR3 PE=3 SV=1	827.51	854.81	527.63
B3KWQ9	3 (1)	13.91	---	2.00		cDNA FLJ43613 fis_ clone SPLEN2015679_ highly similar to TRAF3-interacting JNK-activating modulator (Fragment) OS=Homo sapiens PE=2 SV=1	7155.35	5306.18	3578.92
B2R8Z8	3 (3)	13.90	---	1.26		cDNA_FLJ94136_ highly similar to Homo sapiens synaptotagmin binding_ cytoplasmic RNA interacting protein (SYNCRIP)_ mRNA OS=Homo sapiens PE=2 SV=1	3.63e+005	4.40e+005	3.50e+005
A0A024R6W4	3 (3)	13.88	---	1.12		Lin-10 homolog (C. elegans)_ isoform CRA_b OS=Homo sapiens GN=LIN10 PE=4 SV=1	9525.35	9316.60	8515.47




Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances		
							0hr	1hr	2hr
A0A0D9SFB1	3 (2)	13.82	---	1.40		Dynamin-1 OS=Homo sapiens GN=DNM1 PE=1 SV=1	1.42e+004	1.72e+004	1.23e+004
Q13683	3 (2)	13.80	---	1.32		Integrin alpha-7 OS=Homo sapiens GN=ITGA7 PE=1 SV=3	1.10e+004	8325.03	8857.15
A8K1T7	3 (1)	13.73	---	1.07		cDNA FLJ75600_ highly similar to Homo sapiens cytochrome P450_ family 2_ subfamily U_ polypeptide 1(CYP2U1)_ mRNA OS=Homo sapiens PE=2 SV=1	1.77e+005	1.65e+005	1.67e+005
B2R825	3 (3)	13.69	---	1.33		Alpha-1,4 glucan phosphorylase OS=Homo sapiens PE=2 SV=1	3.56e+004	2.68e+004	3.21e+004
A0A024R0F1	3 (3)	13.63	---	1.22		Transcription termination factor_ RNA polymerase II_ isoform CRA_a OS=Homo sapiens GN=TTF2 PE=4 SV=1	2.80e+004	2.30e+004	2.61e+004
V9H1F4	3 (3)	13.63	---	1.30		Endogenous retrovirus ERV9 protein OS=Homo sapiens GN=endogenous retrovirus ERV9 PE=2 SV=1	1.40e+004	1.52e+004	1.82e+004
Q9Y2G1	3 (3)	13.58	---	1.63		Myelin regulatory factor OS=Homo sapiens GN=MYRF PE=1 SV=3	1.19e+004	1.42e+004	8732.00
Q58EX2	3 (1)	13.57	---	2.08		Protein sidekick-2 OS=Homo sapiens GN=SDK2 PE=1 SV=3	7435.09	3577.23	6095.17
A0A0C4DH07	3 (3)	13.52	---	1.12		Latent-transforming growth factor beta-binding protein 4 OS=Homo sapiens GN=LTBP4 PE=1 SV=1	1.24e+004	1.22e+004	1.36e+004
H7C269	3 (3)	13.52	---	1.17		Trinucleotide repeat-containing gene 6A protein (Fragment) OS=Homo sapiens GN=TNRC6A PE=1 SV=1	9525.22	1.11e+004	9784.03
A4QPE1	3 (3)	13.51	---	1.04		ENOX2 protein (Fragment) OS=Homo sapiens GN=ENOX2 PE=2 SV=1	6958.72	6700.54	6698.77
B4DY51	3 (3)	13.49	---	1.02		cDNA FLJ55546_ highly similar to Protein GPR89A OS=Homo sapiens PE=2 SV=1	2.39e+004	2.42e+004	2.38e+004
A7E228	3 (3)	13.46	---	1.09		ZNF536 protein OS=Homo sapiens GN=ZNF536 PE=2 SV=1	6.26e+004	6.52e+004	6.82e+004
P28223	3 (2)	13.46	---	1.04		5-hydroxytryptamine receptor 2A OS=Homo sapiens GN=HTR2A PE=1 SV=2	1.42e+005	1.42e+005	1.48e+005
Q9NR71	3 (3)	13.45	---	1.38		Neutral ceramidase OS=Homo sapiens GN=ASA2 PE=1 SV=2	8812.73	8226.29	6363.14
Q86T13	3 (2)	13.44	---	1.21		C-type lectin domain family 14 member A OS=Homo sapiens GN=CLEC14A PE=1 SV=1	2.67e+004	3.19e+004	3.23e+004
Q8N1W1	3 (3)	13.43	---	1.06		Rho guanine nucleotide exchange factor 28 OS=Homo sapiens GN=ARHGEF28 PE=1 SV=3	3.92e+004	4.18e+004	4.13e+004
Q5T2E6	3 (3)	13.43	---	1.05		UPF0668 protein C10orf76 OS=Homo sapiens GN=C10orf76 PE=1 SV=1	1.40e+005	1.46e+005	1.46e+005
Q14696	3 (2)	13.35	---	1.20		LDLR chaperone MESD OS=Homo sapiens GN=MESDC2 PE=1 SV=2	5.16e+004	4.32e+004	5.18e+004
A8K2F4	3 (3)	13.34	---	1.12		cDNA FLJ75620 OS=Homo sapiens PE=2 SV=1	1.25e+004	1.16e+004	1.30e+004
Q8TDC3	3 (2)	13.30	---	1.84		Serine/threonine-protein kinase BRSK1 OS=Homo sapiens GN=BRSK1 PE=1 SV=2	4.55e+004	4.59e+004	8.37e+004
Q5T0N1	3 (2)	13.23	---	1.11		Cilia- and flagella-associated protein 70 OS=Homo sapiens GN=CFAP70 PE=2 SV=3	3.86e+004	3.94e+004	4.27e+004
Q05BV3	3 (3)	13.22	---	1.08		Echinoderm microtubule-associated protein-like 5 OS=Homo sapiens GN=EML5 PE=2 SV=3	7761.60	7639.35	7171.67
Q15541	3 (2)	13.22	---	1.28		RING finger protein 113A OS=Homo sapiens GN=RNFI13A PE=1 SV=1	9558.19	8164.60	1.04e+004
Q9Y468	3 (3)	13.21	---	1.12		Lethal(3)malignant brain tumor-like protein 1 OS=Homo sapiens GN=L3MBTL1 PE=1 SV=3	2.96e+004	3.32e+004	3.25e+004
Q00629	3 (2)	13.20	---	1.06		Importin subunit alpha-3 OS=Homo sapiens GN=KPNA4 PE=1 SV=1	5.11e+004	5.41e+004	5.21e+004
Q1MSJ5	3 (2)	13.19	---	1.88		Centrosome and spindle pole-associated protein 1 OS=Homo sapiens GN=CSPP1 PE=1 SV=4	3.03e+004	2.53e+004	1.61e+004
A0A1B0GVL5	3 (1)	13.18	---	1.22		Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=1	9.05e+004	7.90e+004	9.63e+004
G3V256	3 (1)	13.08	---	1.36		Zinc finger CCCH domain-containing protein 14 OS=Homo sapiens GN=ZC3H14 PE=1 SV=1	9239.49	6959.96	9470.08
A0A087WXZ7	3 (3)	13.08	---	1.43		HEAT repeat-containing protein 6 OS=Homo sapiens GN=HEATR6 PE=1 SV=1	1.13e+004	1.17e+004	8223.67
F8WBX2	3 (1)	13.07	---	1.08		Transmembrane protease serine 12 OS=Homo sapiens GN=TMPRSS12 PE=1 SV=1	1.08e+004	1.07e+004	9945.02
A0A024RD21	3 (3)	13.04	---	1.25		ATP-binding cassette_ sub-family C (CFTR/MRP)_ member 10_ isoform CRA_b OS=Homo sapiens GN=ABCC10 PE=4 SV=1	7120.48	7418.11	5912.89
Q15746	3 (0)	13.00	---	---		Myosin light chain kinase_ smooth muscle OS=Homo sapiens GN=MYLK PE=1 SV=4	---	---	---
A0A0D9SF58	3 (1)	13.00	---	1.15		Chromosome transmission fidelity protein 18 homolog OS=Homo sapiens GN=CTTF18 PE=1 SV=1	4.51e+005	3.91e+005	4.18e+005
A0A024R125	3 (2)	13.00	---	1.15		Protein kinase_ AMP-activated_ gamma 1 non-catalytic subunit_ isoform CRA_a OS=Homo sapiens GN=PRKAG1 PE=4 SV=1	4.06e+004	3.65e+004	4.18e+004
Q96RT1	3 (3)	13.00	---	1.19		ErbB OS=Homo sapiens GN=ERBB PE=1 SV=2	7950.81	6666.81	7882.35
Q0D2K2	3 (3)	13.00	---	1.20		Kelch-like protein 30 OS=Homo sapiens GN=KLHL30 PE=2 SV=3	8179.81	8471.71	7043.59
E7EMB1	3 (3)	12.99	---	1.03		Switch-associated protein 70 OS=Homo sapiens GN=SWAP70 PE=1 SV=1	5.29e+005	5.42e+005	5.39e+005
Q8IVL6	3 (3)	12.98	---	1.20		Prolyl 3-hydroxylase 3 OS=Homo sapiens GN=P3H3 PE=1 SV=1	2.60e+004	3.13e+004	2.67e+004
Q60245	3 (1)	12.98	---	3.12		Protocadherin-7 OS=Homo sapiens GN=PCDH7 PE=1 SV=2	5.21e+004	6.48e+004	2.08e+004
B3KUQ8	3 (3)	12.86	---	1.15		Transmembrane channel-like protein OS=Homo sapiens PE=2 SV=1	1.43e+004	1.58e+004	1.36e+004
G5E9C8	3 (0)	12.85	---	---		Son of sevenless homolog 1 OS=Homo sapiens GN=SOS1 PE=1 SV=1	---	---	---
Q96EV2	3 (3)	12.80	---	1.12		RNA-binding protein 33 OS=Homo sapiens GN=RBM33 PE=1 SV=3	7.77e+004	7.06e+004	7.91e+004
Q6ZWH5	3 (3)	12.80	---	1.10		Serine/threonine-protein kinase Nek10 OS=Homo sapiens GN=NEK10 PE=2 SV=3	6.36e+004	6.98e+004	6.84e+004
F8WOU9	3 (1)	12.79	---	1.08		NACHT domain- and WD repeat-containing protein 1 OS=Homo sapiens GN=NWD1 PE=4 SV=1	2.49e+004	2.38e+004	2.58e+004

Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances		
							0hr	1hr	2hr
A0A024RBC7	3 (1)	12.78	---	1.13		Calcium-transporting ATPase OS=Homo sapiens GN=ATP2B1 PE=3 SV=1	1.55e+004	1.36e+004	1.50e+004
A3KMQ0	3 (3)	12.76	---	1.11		FYVE_ RhoGEF and PH domain containing 5 OS=Homo sapiens GN=FGD5 PE=2 SV=1	3.60e+004	3.71e+004	3.99e+004
A0A0G2JKR7	3 (2)	12.75	---	1.11		Retinoic acid receptor RXR-beta OS=Homo sapiens GN=RXRB PE=1 SV=1	4.66e+004	4.25e+004	4.71e+004
Q43167	3 (3)	12.74	---	1.55		Zinc finger and BTB domain-containing protein 24 OS=Homo sapiens GN=ZBTB24 PE=1 SV=2	1.84e+004	1.73e+004	2.68e+004
A0A0G2JP53	3 (2)	12.68	---	2.08		Thyroid peroxidase OS=Homo sapiens GN=TPO PE=1 SV=1	3419.83	3202.51	6673.58
Q05DH4	3 (2)	12.62	---	1.33		Protein FAM160A1 OS=Homo sapiens GN=FAM160A1 PE=2 SV=2	5.68e+004	6.07e+004	7.54e+004
Q5UXU0	3 (3)	12.57	---	1.09		F-box only protein 31 OS=Homo sapiens GN=FBXO31 PE=1 SV=2	7016.96	6478.22	6463.63
Q9NR16	3 (3)	12.54	---	1.04		Scavenger receptor cysteine-rich type 1 protein M160 OS=Homo sapiens GN=CD163L1 PE=1 SV=2	1.62e+004	1.68e+004	1.68e+004
Q8TED0	3 (3)	12.51	---	1.29		U3 small nucleolar RNA-associated protein 15 homolog OS=Homo sapiens GN=UTP15 PE=1 SV=3	9.22e+004	8.34e+004	1.07e+005
A0A0S2Z5J4	3 (3)	12.50	---	1.21		Adaptor-related protein complex 3 beta 1 subunit isoform 1 (Fragment) OS=Homo sapiens GN=AP3B1 PE=2 SV=1	7.90e+004	8.07e+004	6.64e+004
Q8IUV7	3 (3)	12.49	---	1.17		E3 ubiquitin-protein ligase UBR1 OS=Homo sapiens GN=UBR1 PE=1 SV=1	1.22e+004	1.05e+004	1.16e+004
A0A0A0MS01	3 (2)	12.32	---	1.35		T cell receptor gamma variable 10 (non-functional) (Fragment) OS=Homo sapiens GN=TRGV10 PE=4 SV=1	6521.41	4883.56	6577.55
Q6ZV29	3 (3)	12.31	---	1.07		Patatin-like phospholipase domain-containing protein 7 OS=Homo sapiens GN=PNPLA7 PE=1 SV=3	3.85e+004	3.77e+004	4.02e+004
Q08AF3	3 (2)	12.31	---	1.34		Schlafen family member 5 OS=Homo sapiens GN=SLFN5 PE=1 SV=1	1.08e+004	1.13e+004	8485.16
Q9NVH2	3 (3)	12.23	---	1.32		Integrator complex subunit 7 OS=Homo sapiens GN=INTS7 PE=1 SV=1	4.81e+004	4.58e+004	6.02e+004
B7Z855	3 (2)	12.11	---	1.20		cDNA FLJ50427_ highly similar to Ubiquitin carboxyl-terminal hydrolase 7 (EC3.1.2.15) OS=Homo sapiens PE=2 SV=1	1.73e+004	1.44e+004	1.63e+004
Q9UKP4	3 (2)	12.10	---	1.11		A disintegrin and metalloproteinase with thrombospondin motifs 7 OS=Homo sapiens GN=ADAMTS7 PE=1 SV=2	1.99e+004	1.80e+004	1.96e+004
Q8IZC6	3 (1)	12.07	---	1.16		Collagen alpha-1(XVII) chain OS=Homo sapiens GN=COL27A1 PE=1 SV=1	1.40e+004	1.27e+004	1.47e+004
P63128	3 (2)	12.06	---	1.12		Endogenous retrovirus group K member 9 Pol protein OS=Homo sapiens GN=ERVK-9 PE=3 SV=3	3436.47	3791.98	3862.90
P12110	3 (3)	12.01	---	1.11		Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2 PE=1 SV=4	3.21e+005	3.56e+005	3.43e+005
Q92834	3 (1)	11.96	---	1.28		X-linked retinitis pigmentosa GTPase regulator OS=Homo sapiens GN=RPGR PE=1 SV=2	5403.89	4838.90	6215.93
Q9Y2A7	3 (3)	11.91	---	1.09		Nck-associated protein 1 OS=Homo sapiens GN=NCKAP1 PE=1 SV=1	2.33e+004	2.39e+004	2.53e+004
C3VPR7	3 (1)	11.90	---	1.22		NLRC3 OS=Homo sapiens GN=NLRC3 PE=2 SV=1	3.11e+004	3.80e+004	3.49e+004
Q9UK80	3 (2)	11.80	---	1.22		Ubiquitin carboxyl-terminal hydrolase 21 OS=Homo sapiens GN=USP21 PE=1 SV=1	1.20e+004	1.08e+004	1.32e+004
Q9P241	3 (2)	11.43	---	1.33		Probable phospholipid-transporting ATPase VD OS=Homo sapiens GN=ATP10D PE=2 SV=3	8360.26	9712.68	1.11e+004
Q9H488	2 (2)	11.24	---	1.34		GDP-fucose protein O-fucosyltransferase 1 OS=Homo sapiens GN=POFUT1 PE=1 SV=1	7828.38	6810.76	5825.55
B4DRM3	3 (2)	10.74	---	1.05		cDNA FLJ54492_ highly similar to Eukaryotic translation initiation factor 4B OS=Homo sapiens PE=2 SV=1	3314.09	3476.75	3339.72
Q4VC12	2 (1)	10.55	---	1.16		Putative protein MSS51 homolog_ mitochondrial OS=Homo sapiens GN=MSS51 PE=1 SV=2	1.01e+005	1.17e+005	1.02e+005
Q9Y5Y0	2 (1)	10.42	---	1.47		Feline leukemia virus subgroup C receptor-related protein 1 OS=Homo sapiens GN=FLVCR1 PE=1 SV=1	4.88e+005	5.63e+005	7.19e+005
A0A0G2JLM7	2 (1)	10.40	---	1.24		Killer cell immunoglobulin-like receptor 3DL2 OS=Homo sapiens GN=KIR3DL2 PE=4 SV=1	6546.80	5280.03	5678.24
B3KWQ3	2 (2)	10.34	---	1.09		cDNA FLJ43573 fis_ clone RECTM2001691_ highly similar to Actin_ cytoplasmic 2 OS=Homo sapiens PE=2 SV=1	7.10e+005	7.18e+005	7.76e+005
A0A024RCC9	2 (1)	10.17	---	1.20		Nucleosome assembly protein 1-like 4_ isoform CRA_b OS=Homo sapiens GN=NAP1L4 PE=3 SV=1	2.97e+004	2.76e+004	3.32e+004
A0A024R5N1	2 (2)	10.14	---	1.23		Purinergic receptor P2Y_ G-protein coupled_ 2_ isoform CRA_a OS=Homo sapiens GN=P2RY2 PE=3 SV=1	7155.29	7837.01	6360.56
Q8TB52	2 (1)	10.09	---	1.11		F-box only protein 30 OS=Homo sapiens GN=FBXO30 PE=1 SV=3	1.46e+004	1.48e+004	1.33e+004
F8WCG9	2 (2)	10.08	---	1.09		Leucine-rich repeat-containing protein 75B OS=Homo sapiens GN=LRRC75B PE=4 SV=1	1.67e+004	1.60e+004	1.75e+004
A0A024R6N2	2 (2)	10.07	---	1.23		CDC42 binding protein kinase beta (DMPK-like)_ isoform CRA_a OS=Homo sapiens GN=CDC42BPB PE=3 SV=1	6966.02	8187.05	6631.81
Q92484	2 (0)	10.06	---	---		Acid sphingomyelinase-like phosphodiesterase 3a OS=Homo sapiens GN=SMPDL3A PE=1 SV=2	---	---	---
Q9C056	3 (3)	10.02	---	1.65		Homeobox protein Nkx-6.2 OS=Homo sapiens GN=NKX6-2 PE=2 SV=2	2.85e+004	3.27e+004	1.98e+004
B7Z5A2	2 (1)	10.01	---	1.44		cDNA FLJ57759_ moderately similar to Transgelin-2 OS=Homo sapiens PE=2 SV=1	3.43e+004	3.75e+004	2.60e+004
Q70J99	2 (1)	9.99	---	1.07		Protein unc-13 homolog D OS=Homo sapiens GN=UNC13D PE=1 SV=1	2.11e+005	1.97e+005	1.99e+005
Q16799	3 (3)	9.99	---	1.12		Reticulon-1 OS=Homo sapiens GN=RTN1 PE=1 SV=1	3.90e+004	3.47e+004	3.78e+004
A0A0D9SGI1	2 (2)	9.92	---	1.05		Membrane-associated guanylate kinase_ WW and PDZ domain-containing protein 2 OS=Homo sapiens GN=MAGI2 PE=1 SV=1	7.04e+004	6.74e+004	7.05e+004



Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances		
							0hr	1hr	2hr
Q9HAW8	3 (2)	9.82	---	1.37		UDP-glucuronosyltransferase 1-10 OS=Homo sapiens GN=UGT1A10 PE=1 SV=1	4418.81	5612.31	4104.60
B7Z1V0	2 (2)	9.76	---	1.16		cDNA FLJ59490_ highly similar to Beta-chimaerin OS=Homo sapiens PE=2 SV=1	7.47e+004	7.70e+004	8.67e+004
A0A0G2JLG2	2 (2)	9.73	---	1.19		IQ motif and SEC7 domain-containing protein 3 (Fragment) OS=Homo sapiens GN=IQSEC3 PE=1 SV=1	1.60e+004	1.90e+004	1.76e+004
Q9UHP6	2 (2)	9.72	---	1.04		Radial spoke head 14 homolog OS=Homo sapiens GN=RSPH14 PE=1 SV=1	1.23e+004	1.28e+004	1.26e+004
Q50KX5	2 (2)	9.68	---	1.09		Taste receptor type 2 (Fragment) OS=Homo sapiens GN=Hosa(Biaka)-T2R4 PE=3 SV=1	1.15e+005	1.25e+005	1.15e+005
Q9C029	2 (2)	9.67	---	1.13		Tripartite motif-containing protein 7 OS=Homo sapiens GN=TRIM7 PE=1 SV=2	2.09e+005	2.36e+005	2.30e+005
Q9BWP8	2 (2)	9.67	---	1.04		Collectin-11 OS=Homo sapiens GN=COLEC11 PE=1 SV=1	1.29e+004	1.24e+004	1.24e+004
Q14684	3 (2)	9.67	---	1.12		Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B PE=1 SV=3	1.43e+004	1.49e+004	1.59e+004
B4DXT6	2 (1)	9.67	---	1.37		cDNA FLJ55263 OS=Homo sapiens PE=2 SV=1	1233.52	1364.75	997.70
Q96P50	2 (1)	9.64	---	1.41		Arf-GAP with coiled-coil_ ANK repeat and PH domain-containing protein 3 OS=Homo sapiens GN=ACAP3 PE=1 SV=2	3676.86	2599.08	3460.13
A2RUL8	2 (2)	9.64	---	1.30		KCNS1 protein OS=Homo sapiens GN=KCNS1 PE=2 SV=1	1.52e+004	1.47e+004	1.90e+004
G3XAG5	2 (2)	9.61	---	1.08		Chloride channel protein OS=Homo sapiens GN=CLCN4 PE=1 SV=1	1.11e+004	1.13e+004	1.05e+004
A0A024R8M9	2 (2)	9.59	---	1.19		RecQ protein-like 5_ isoform CRA_a OS=Homo sapiens GN=RECQL5 PE=4 SV=1	5747.70	4876.74	5780.34
A0A0J9YVP0	2 (2)	9.56	---	1.11		E3 ubiquitin-protein ligase HERC2 (Fragment) OS=Homo sapiens GN=HERC2 PE=1 SV=1	1.01e+005	1.03e+005	9.29e+004
B3KU30	2 (0)	9.56	---	---		cDNA FLJ39125 fis_ clone NTONG2007034_ highly similar to Homo sapiens collagen_ type XXI_ alpha 1 (COL21A1)_ mRNA OS=Homo sapiens PE=2 SV=1	---	---	---
P08514	3 (3)	9.54	---	1.10		Integrin alpha-IIb OS=Homo sapiens GN=ITGA2B PE=1 SV=3	1.50e+004	1.56e+004	1.65e+004
A0A0A0MSG0	2 (1)	9.52	---	1.08		WAS/WASL-interacting protein family member 3 OS=Homo sapiens GN=WIPF3 PE=1 SV=1	1.73e+004	1.80e+004	1.87e+004
Q5TIA1	3 (2)	9.51	---	1.06		Meiosis inhibitor protein 1 OS=Homo sapiens GN=MEI1 PE=2 SV=2	5.98e+004	5.69e+004	6.01e+004
A0A024R9E9	2 (2)	9.50	---	1.22		Frizzled homolog 6 (Drosophila)_ isoform CRA_a OS=Homo sapiens GN=FZD6 PE=3 SV=1	1.89e+004	2.00e+004	1.63e+004
A6NKF1	2 (2)	9.50	---	1.12		SAC3 domain-containing protein 1 OS=Homo sapiens GN=SAC3D1 PE=1 SV=2	2.16e+004	1.93e+004	2.13e+004
B4DTK7	2 (1)	9.47	---	1.42		cDNA FLJ61387_ highly similar to Homo sapiens conserved nuclear protein NHN1 (NHN1)_ mRNA OS=Homo sapiens PE=2 SV=1	1.88e+004	1.75e+004	1.32e+004
A0A024R0L5	2 (2)	9.45	---	1.09		Glycogen synthase kinase 3 alpha_ isoform CRA_a OS=Homo sapiens GN=GSK3A PE=3 SV=1	9.39e+004	1.02e+005	9.80e+004
Q5VTJ3	2 (2)	9.44	---	1.04		Kelch domain-containing protein 7A OS=Homo sapiens GN=KLHDC7A PE=1 SV=5	3.67e+004	3.54e+004	3.62e+004
B3KS94	2 (1)	9.43	---	1.09		cDNA FLJ35791 fis_ clone TESTI2005743_ highly similar to ZINC FINGER PROTEIN 8 OS=Homo sapiens PE=2 SV=1	8458.65	8259.05	7743.35
B3KS74	2 (2)	9.41	---	1.12		cDNA FLJ35684 fis_ clone SPLEN2019169_ highly similar to DNA polymerase epsilon_ catalytic subunit A OS=Homo sapiens PE=2 SV=1	1.02e+004	9923.76	1.11e+004
D6RC52	2 (2)	9.40	---	1.11		H/ACA ribonucleoprotein complex subunit 2 (Fragment) OS=Homo sapiens GN=NHP2 PE=1 SV=1	9872.14	1.03e+004	1.10e+004
H0YFX2	2 (2)	9.40	---	1.30		DnaJ homolog subfamily B member 13 (Fragment) OS=Homo sapiens GN=DNAJB13 PE=1 SV=1	2.75e+004	2.78e+004	2.15e+004
B2R6N0	2 (2)	9.38	---	1.03		cDNA_FLJ93029_ highly similar to Homo sapiens COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis) (COPS2)_ mRNA OS=Homo sapiens PE=2 SV=1	7412.87	7662.59	7441.66
B4YCH1	2 (2)	9.36	---	1.24		ATP synthase protein 8 (Fragment) OS=Homo sapiens GN=ATP8 PE=3 SV=1	3158.54	3792.71	3916.26
P81408	2 (1)	9.35	---	1.25		Protein FAM189B OS=Homo sapiens GN=FAM189B PE=1 SV=2	2.62e+004	2.82e+004	3.29e+004
A0A024R65Z	2 (2)	9.33	---	1.08		AT rich interactive domain 4A (RBP1-like)_ isoform CRA_c OS=Homo sapiens GN=ARID4A PE=4 SV=1	2.29e+004	2.28e+004	2.46e+004
Q9BRP1	2 (2)	9.33	---	1.12		Programmed cell death protein 2-like OS=Homo sapiens GN=PPDC2L PE=1 SV=1	8.00e+004	8.21e+004	8.93e+004
Q8TE60	2 (2)	9.30	---	1.07		A disintegrin and metalloproteinase with thrombospondin motifs 18 OS=Homo sapiens GN=ADAMTS18 PE=1 SV=3	7.02e+004	6.91e+004	7.37e+004
Q53T07	2 (2)	9.25	---	1.09		Putative uncharacterized protein LOC91526 (Fragment) OS=Homo sapiens GN=LOC91526 PE=4 SV=1	2.27e+004	2.08e+004	2.12e+004
Q5JY77	2 (2)	9.25	---	1.04		G-protein coupled receptor-associated sorting protein 1 OS=Homo sapiens GN=GPRASP1 PE=1 SV=3	2.46e+004	2.56e+004	2.48e+004
G3XAK1	2 (1)	9.15	---	1.30		Hepatocyte growth factor-like protein OS=Homo sapiens GN=MST1 PE=1 SV=1	2.81e+004	3.12e+004	2.40e+004
B7Z5P7	2 (2)	9.12	---	1.23		Leupaxin OS=Homo sapiens GN=LPXN PE=1 SV=1	9678.87	1.12e+004	1.19e+004
P14616	2 (1)	9.11	---	1.08		Insulin receptor-related protein OS=Homo sapiens GN=INSRR PE=1 SV=2	1.07e+004	1.15e+004	1.07e+004
A0A024RAV2	2 (0)	9.10	---	---		RecQ protein-like (DNA helicase Q1-like)_ isoform CRA_a OS=Homo sapiens GN=RECQL PE=4 SV=1	---	---	---
A0A087WXZ6	2 (1)	9.06	---	1.08		High affinity immunoglobulin gamma Fc receptor 1B (Fragment) OS=Homo sapiens GN=FCGR1B PE=4 SV=6	6.77e+004	7.34e+004	6.88e+004
B4DZ87	2 (0)	9.03	---	---		cDNA FLJ57240_ highly similar to Mitochondrial proteins import receptor OS=Homo sapiens PE=2 SV=1	---	---	---

Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances		
							0hr	1hr	2hr
Q15482	2 (1)	9.03	---	2.97		Testis-specific protein TEX28 OS=Homo sapiens GN=TEX28 PE=2 SV=1	1.70e+005	1.40e+005	4.16e+005
A0A024R5U5	2 (1)	9.00	---	1.05		ADAM metalloproteinase domain 10_ isoform CRA_b OS=Homo sapiens GN=ADAM10 PE=4 SV=1	1.54e+004	1.58e+004	1.62e+004
Q8IX18	2 (1)	8.99	---	1.08		Probable ATP-dependent RNA helicase DHX40 OS=Homo sapiens GN=DHX40 PE=1 SV=2	2.01e+004	1.86e+004	1.89e+004
P08173	2 (1)	8.92	---	1.18		Muscarinic acetylcholine receptor M4 OS=Homo sapiens GN=CHRM4 PE=1 SV=2	1.41e+004	1.54e+004	1.31e+004
Q14568	2 (1)	8.91	---	1.37		Heat shock protein HSP 90-alpha A2 OS=Homo sapiens GN=HSP90AA2 PE=1 SV=2	1.55e+004	1.37e+004	1.88e+004
A0A140TA01	2 (1)	8.88	---	1.34		PHD finger protein 1 OS=Homo sapiens GN=PHF1 PE=1 SV=1	7024.83	5246.47	6444.29
D6RAS1	2 (2)	8.85	---	1.12		E3 SUMO-protein ligase ZNF451 (Fragment) OS=Homo sapiens GN=ZNF451 PE=1 SV=1	4.41e+004	3.96e+004	4.42e+004
Q9HBM0	2 (1)	8.82	---	1.38		Vezatin OS=Homo sapiens GN=VEZT PE=1 SV=3	1.91e+004	2.65e+004	2.36e+004
A0A024R6W0	2 (2)	8.75	---	1.76		Aspartate aminotransferase OS=Homo sapiens GN=GOT2 PE=4 SV=1	1.64e+004	1.64e+004	2.89e+004
A0A0A8K9B1	2 (2)	8.75	---	1.87		Up-regulated in lung cancer 6 OS=Homo sapiens GN=URLC6 PE=2 SV=1	1.56e+004	1.38e+004	2.58e+004
Q96MT7	2 (2)	8.74	---	1.12		Cilia- and flagella-associated protein 44 OS=Homo sapiens GN=CFAP44 PE=1 SV=1	9331.04	9059.73	1.01e+004
A0A024R1P7	2 (1)	8.74	---	3.65		Unc-84 homolog B (C. elegans)_ isoform CRA_b OS=Homo sapiens GN=UNC84B PE=4 SV=1	1947.72	2099.63	7105.02
A0A024R3X4	2 (1)	8.73	---	1.28		Heat shock 60kDa protein 1 (Chaperonin)_ isoform CRA_a OS=Homo sapiens GN=HSPD1 PE=2 SV=1	9427.11	1.21e+004	1.16e+004
B2R6L0	2 (0)	8.69	---	---		Tubulin beta chain OS=Homo sapiens PE=2 SV=1	---	---	---
B4DST2	2 (2)	8.66	---	1.17		cDNA FLJ54525_ highly similar to Intraflagellar transport 122 homolog OS=Homo sapiens PE=2 SV=1	1.54e+004	1.58e+004	1.80e+004
A0A0K0K1K3	2 (1)	8.62	---	1.25		Adenylate cyclase 8 (Brain) OS=Homo sapiens GN=HEL-S-172mP PE=2 SV=1	8.93e+004	7.62e+004	7.14e+004
Q9HCE9	2 (2)	8.61	---	1.10		Anoctamin-8 OS=Homo sapiens GN=ANO8 PE=1 SV=3	3.61e+004	3.28e+004	3.51e+004
A0A0A0MRE2	2 (2)	8.60	---	1.21		Double zinc ribbon and ankyrin repeat-containing protein 1 OS=Homo sapiens GN=DZANK1 PE=1 SV=1	3.48e+004	4.23e+004	4.12e+004
Q2Y0W8	2 (2)	8.59	---	1.45		Electroneutral sodium bicarbonate exchanger 1 OS=Homo sapiens GN=SLC4A8 PE=1 SV=1	4609.48	5653.78	3910.13
A0A0S2Z5Z8	2 (1)	8.58	---	1.24		1-aminocyclopropane-1-carboxylate synthase-like protein (Non-functional) isoform 2 OS=Homo sapiens GN=ACCS PE=2 SV=1	7412.24	5986.07	6643.29
A1L3A9	2 (2)	8.49	---	1.05		TBC1 domain family_ member 9B (With GRAM domain) OS=Homo sapiens GN=TBC1D9B PE=2 SV=1	5.10e+004	5.13e+004	4.87e+004
A0A0D9SEY3	2 (1)	8.47	---	1.13		Potassium channel subfamily T member 1 OS=Homo sapiens GN=KCNT1 PE=4 SV=1	5.23e+004	5.34e+004	4.73e+004
A0A0A0MSC1	2 (1)	8.43	---	1.96		Adenylate cyclase type 3 OS=Homo sapiens GN=ADCY3 PE=1 SV=1	1618.56	2742.59	1397.42
Q9P265	2 (0)	8.41	---	---		Disco-interacting protein 2 homolog B OS=Homo sapiens GN=DIP2B PE=1 SV=3	---	---	---
B9EGI2	2 (1)	8.39	---	1.17		Myosin phosphatase Rho interacting protein OS=Homo sapiens GN=MPRIIP PE=2 SV=1	8.22e+004	8.71e+004	7.45e+004
A0A024RDV9	2 (2)	8.38	---	1.21		Spastic paraplegia 20 isoform 1 OS=Homo sapiens GN=SPG20 PE=2 SV=1	6050.82	5650.26	4989.95
Q69YN4	3 (2)	8.35	---	1.27		Protein virilizer homolog OS=Homo sapiens GN=KIAA1429 PE=1 SV=2	1.14e+004	1.26e+004	9950.34
Q15884	2 (1)	8.34	---	1.31		Protein FAM189A2 OS=Homo sapiens GN=FAM189A2 PE=1 SV=3	7.58e+004	6.53e+004	8.56e+004
Q9NSJ8	2 (1)	8.31	---	1.35		SAM domain-containing protein SAMSN-1 OS=Homo sapiens GN=SAMSN1 PE=1 SV=1	1.99e+004	2.69e+004	2.15e+004
E7EQR6	2 (1)	8.31	---	1.14		T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1	1.25e+004	1.34e+004	1.17e+004
Q95219	2 (2)	8.30	---	1.13		Sorting nexin-4 OS=Homo sapiens GN=SNX4 PE=1 SV=1	3.09e+004	3.44e+004	3.05e+004
A8K3I0	2 (1)	8.30	---	1.03		cDNA FLJ78437_ highly similar to Homo sapiens cartilage oligomeric matrix protein (COMP)_ mRNA OS=Homo sapiens PE=2 SV=1	3935.65	3825.55	3861.17
Q60508	2 (2)	8.23	---	1.97		Pre-mRNA-processing factor 17 OS=Homo sapiens GN=CDC40 PE=1 SV=1	1.35e+004	1.54e+004	2.65e+004
Q8IVV2	2 (2)	8.21	---	1.46		Lipoxygenase homology domain-containing protein 1 OS=Homo sapiens GN=LOXHD1 PE=2 SV=3	2.59e+004	2.41e+004	1.77e+004
Q75911	2 (1)	8.18	---	1.13		Short-chain dehydrogenase/reductase 3 OS=Homo sapiens GN=DHRS3 PE=1 SV=2	5.45e+004	6.14e+004	5.71e+004
Q5JYT7	2 (1)	8.15	---	1.17		Uncharacterized protein KIAA1755 OS=Homo sapiens GN=KIAA1755 PE=2 SV=2	2.74e+004	2.45e+004	2.35e+004
Q06418	3 (1)	8.13	---	1.43		Tyrosine-protein kinase receptor TYRO3 OS=Homo sapiens GN=TYRO3 PE=1 SV=1	1.63e+004	1.84e+004	1.29e+004
A0A024R1Q0	2 (2)	8.08	---	1.48		Sterol regulatory element binding transcription factor 2_ isoform CRA_a OS=Homo sapiens GN=SREBF2 PE=4 SV=1	1.49e+005	1.41e+005	2.09e+005
H7C0U5	2 (2)	8.03	---	1.19		ATP-binding cassette sub-family A member 13 (Fragment) OS=Homo sapiens GN=ABCA13 PE=1 SV=2	4210.82	3770.88	3525.32
Q9C0J8	3 (1)	8.00	---	1.06		pre-mRNA 3' end processing protein WDR33 OS=Homo sapiens GN=WDR33 PE=1 SV=2	2574.91	2655.28	2740.25
A0A024R0Z3	2 (2)	7.98	---	1.35		DEAD (Asp-Glu-Ala-Asp) box polypeptide 23_ isoform CRA_b OS=Homo sapiens GN=DDX23 PE=4 SV=1	8047.00	8385.96	6189.10
A8KAH2	2 (2)	7.96	---	1.25		cDNA FLJ78748_ highly similar to Homo sapiens ADAMTS-like 4_ mRNA OS=Homo sapiens PE=2 SV=1	1.72e+004	1.76e+004	1.41e+004

Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances		
							0hr	1hr	2hr
Q09428	2 (2)	7.92	---	1.16		ATP-binding cassette sub-family C member 8 OS=Homo sapiens GN=ABCC8 PE=1 SV=6	1.32e+004	1.53e+004	1.35e+004
H3BN02	2 (1)	7.81	---	1.12		Integrin alpha-X OS=Homo sapiens GN=ITGAX PE=1 SV=1	1.84e+004	1.85e+004	1.66e+004
A0A087WU38	2 (1)	7.79	---	1.21		Glutamate receptor-interacting protein 2 OS=Homo sapiens GN=GRIP2 PE=1 SV=1	7018.61	7625.22	6310.14
Q9NQG7	2 (2)	7.72	---	1.11		Hermansky-Pudlak syndrome 4 protein OS=Homo sapiens GN=HPS4 PE=1 SV=2	8216.25	8204.13	9072.14
Q8TAQ5	2 (1)	7.65	---	1.06		Zinc finger protein 420 OS=Homo sapiens GN=ZNF420 PE=1 SV=1	2.37e+004	2.52e+004	2.50e+004
C9IZQ6	2 (1)	7.62	---	1.34		HCG2022551_ isoform CRA_j OS=Homo sapiens GN=KALRN PE=1 SV=1	5378.84	6861.63	5138.95
Q96JK2	2 (1)	7.60	---	1.20		DDB1- and CUL4-associated factor 5 OS=Homo sapiens GN=DCAF5 PE=1 SV=2	6453.64	6872.37	5710.11
Q86TB9	2 (2)	7.54	---	1.05		Protein PAT1 homolog 1 OS=Homo sapiens GN=PATL1 PE=1 SV=2	9.68e+004	1.02e+005	9.74e+004
B3KMK0	1 (1)	6.20	---	1.51		cDNA FLJ11217 fis_ clone PLACE1008044_ highly similar to NUCLEAR PORE COMPLEX PROTEIN NUP107 OS=Homo sapiens PE=2 SV=1	3.51e+004	4.32e+004	2.86e+004
A0A0G2JR68	1 (1)	5.49	---	1.06		MLX-interacting protein (Fragment) OS=Homo sapiens GN=MLXIP PE=1 SV=1	8.10e+004	7.94e+004	8.40e+004
Q9H0B6	1 (1)	5.47	---	5.53		Kinesin light chain 2 OS=Homo sapiens GN=KLC2 PE=1 SV=1	3.99e+004	3.19e+004	7222.57
H9ZYJ1	1 (1)	5.45	---	1.13		Negative elongation factor E OS=Homo sapiens GN=NELF-E PE=2 SV=1	7913.81	8377.67	8963.58
A0A0C4DFT5	1 (1)	5.33	---	1.21		Solute carrier family 26 member 6 OS=Homo sapiens GN=SLC26A6 PE=1 SV=1	1.31e+004	1.32e+004	1.58e+004
B4DF28	1 (1)	5.32	---	1.25		cDNA FLJ59014 OS=Homo sapiens PE=2 SV=1	7655.18	8946.20	7154.48
A0A024RCI0	1 (0)	5.29	---	---		Tetraspanin 6_ isoform CRA_a OS=Homo sapiens GN=TSPAN6 PE=3 SV=1	---	---	---
P05113	1 (1)	5.28	---	1.12		Interleukin-5 OS=Homo sapiens GN=IL5 PE=1 SV=1	1.09e+004	1.22e+004	1.13e+004
A0A0C4DH10	1 (1)	5.23	---	1.07		Adhesion G-protein-coupled receptor F1 OS=Homo sapiens GN=ADGRF1 PE=1 SV=1	8723.15	8139.23	8612.37
Q8IYS2	1 (1)	5.22	---	1.28		Uncharacterized protein KIAA2013 OS=Homo sapiens GN=KIAA2013 PE=1 SV=1	8.08e+004	1.03e+005	9.27e+004
P17039	1 (0)	5.17	---	---		Zinc finger protein 30 OS=Homo sapiens GN=ZNF30 PE=2 SV=5	---	---	---
L8EBA1	1 (1)	5.15	---	1.06		Alternative protein GPR98 OS=Homo sapiens GN=GPR98 PE=4 SV=1	3.25e+004	3.34e+004	3.44e+004
A0A024R305	1 (1)	5.13	---	1.53		Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=BAP1 PE=3 SV=1	8893.47	6962.30	5819.03
A0A024QZR6	1 (0)	5.04	---	---		Dual specificity phosphatase 13_ isoform CRA_a OS=Homo sapiens GN=DUSP13 PE=3 SV=1	---	---	---
C9J0I5	1 (1)	5.02	---	1.32		Solute carrier family 12 member 9 (Fragment) OS=Homo sapiens GN=SLC12A9 PE=1 SV=1	1.88e+005	1.42e+005	1.70e+005
A4D1L4	1 (0)	4.96	---	---		Nuclear interacting partner of anaplastic lymphoma kinase (ALK) OS=Homo sapiens GN=NIPA PE=4 SV=1	---	---	---
A0A024R230	1 (1)	4.92	---	1.59		Tyrosine-protein kinase receptor OS=Homo sapiens GN=NTRK2 PE=3 SV=1	1.80e+004	2.87e+004	2.57e+004
B4DEW2	1 (1)	4.92	---	1.05		Mitogen-activated protein kinase 4 OS=Homo sapiens GN=MAPK4 PE=1 SV=1	4.63e+004	4.71e+004	4.48e+004
M0QXX4	1 (1)	4.91	---	1.54		Kaptein (Fragment) OS=Homo sapiens GN=KPTN PE=1 SV=1	3789.72	4830.10	3134.76
A0A068BUX7	1 (0)	4.91	---	---		ATP synthase subunit a OS=Homo sapiens GN=ATP6 PE=4 SV=1	---	---	---
A0A087WU43	1 (1)	4.90	---	1.18		Cadherin-1 OS=Homo sapiens GN=CDH1 PE=1 SV=1	8355.22	7272.10	7085.93
C9J7T7	1 (0)	4.89	---	---		Nuclear receptor corepressor 2 OS=Homo sapiens GN=NCOR2 PE=1 SV=3	---	---	---
Q7L5L3	1 (1)	4.88	---	1.13		Glycerophosphodiester phosphodiesterase domain-containing protein 3 OS=Homo sapiens GN=GDPD3 PE=2 SV=3	2.39e+004	2.44e+004	2.69e+004
Q07001	1 (1)	4.88	---	1.41		Acetylcholine receptor subunit delta OS=Homo sapiens GN=CHRNA1 PE=1 SV=1	7690.05	5926.66	8363.60
A0A0S2Z4Z3	1 (1)	4.87	---	1.14		Fucose-1-phosphate guanylyltransferase isoform 3 (Fragment) OS=Homo sapiens GN=FPGT PE=2 SV=1	7628.49	6829.42	7775.72
H6WHI2	1 (1)	4.83	---	1.45		ATP synthase subunit a OS=Homo sapiens GN=ATP6 PE=4 SV=1	1.81e+004	1.76e+004	1.25e+004
A0A024R997	1 (1)	4.82	---	1.14		ELK4_ ETS-domain protein (SRF accessory protein 1)_ isoform CRA_a OS=Homo sapiens GN=ELK4 PE=3 SV=1	1551.96	1359.70	1448.59
A0A142I7X2	1 (0)	4.79	---	---		NUP98/PHF23 fusion 2 protein (Fragment) OS=Homo sapiens PE=2 SV=1	---	---	---
A0A024RDY4	1 (0)	4.78	---	---		Transcription factor Dp-1_ isoform CRA_a OS=Homo sapiens GN=TFDP1 PE=3 SV=1	---	---	---
Q17RM4	1 (0)	4.75	---	---		Coiled-coil domain-containing protein 142 OS=Homo sapiens GN=CCDC142 PE=2 SV=1	---	---	---
A5D8T4	1 (1)	4.73	---	1.38		TNFRSF8 protein (Fragment) OS=Homo sapiens GN=TNFRSF8 PE=2 SV=1	1.71e+004	2.05e+004	2.36e+004
P50443	1 (1)	4.67	---	1.13		Sulfate transporter OS=Homo sapiens GN=SLC26A2 PE=1 SV=2	2.97e+004	2.71e+004	3.06e+004
A8K0L9	1 (0)	4.67	---	---		cDNA FLJ76999_ highly similar to Homo sapiens cadherin-like 22 (CDH22)_ mRNA OS=Homo sapiens PE=2 SV=1	---	---	---
B3KSX4	1 (1)	4.66	---	1.20		cDNA FLJ37231 fis_ clone BRAMY2001068_ highly similar to Large neutral amino acids transporter small subunit 2 OS=Homo sapiens PE=2 SV=1	2.38e+004	1.99e+004	2.20e+004
K7EMK7	1 (1)	4.66	---	1.19		Transducin-like enhancer protein 2 OS=Homo sapiens GN=TLE2 PE=1 SV=1	1.03e+004	1.14e+004	9602.19

Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances		
							0hr	1hr	2hr
A0A024R0Q0	1 (1)	4.63	---	1.13		Uncharacterized protein OS=Homo sapiens GN=FLJ12886 PE=4 SV=1	7360.87	8155.91	8324.19
A8KAE4	1 (0)	4.62	---	---		cDNA FLJ75520 OS=Homo sapiens PE=2 SV=1	---	---	---
Q9UHB4	1 (1)	4.61	---	1.16		NADPH-dependent diflavin oxidoreductase 1 OS=Homo sapiens GN=NDOR1 PE=1 SV=1	8.40e+005	7.56e+005	7.23e+005
Q9Y2T7	1 (1)	4.60	---	1.49		Y-box-binding protein 2 OS=Homo sapiens GN=YBX2 PE=1 SV=2	4924.62	5875.90	3934.53
P11926	1 (1)	4.59	---	1.22		Ornithine decarboxylase OS=Homo sapiens GN=ODC1 PE=1 SV=2	4.50e+004	5.47e+004	4.60e+004
A0A0G2JIW1	1 (1)	4.57	---	1.10		Heat shock 70 kDa protein 1B OS=Homo sapiens GN=HSPA1B PE=1 SV=1	1.07e+004	1.16e+004	1.18e+004
A0A0S2Z4W1	1 (1)	4.55	---	1.66		Serine/arginine repetitive matrix 1 isoform 1 (Fragment) OS=Homo sapiens GN=SRRM1 PE=2 SV=1	1.39e+004	2.30e+004	1.96e+004
Q7L1V2	1 (1)	4.55	---	1.21		Vacuolar fusion protein MON1 homolog B OS=Homo sapiens GN=MON1B PE=1 SV=1	1.75e+005	2.03e+005	2.13e+005
C9JPG5	1 (1)	4.55	---	1.18		Semaphorin-3F OS=Homo sapiens GN=SEMA3F PE=1 SV=1	7.59e+004	6.43e+004	7.45e+004
Q9H7M6	1 (1)	4.53	---	1.45		Zinc finger SWIM domain-containing protein 4 OS=Homo sapiens GN=ZSWIM4 PE=2 SV=3	3.07e+004	3.68e+004	2.53e+004
Q8NH62	2 (2)	4.51	---	1.12		Olfactory receptor OS=Homo sapiens PE=3 SV=1	1.98e+004	1.94e+004	2.17e+004
A0A024RBK9	1 (1)	4.49	---	1.28		Thioredoxin reductase 1 OS=Homo sapiens GN=TXNRD1 PE=3 SV=1	7585.26	8019.68	6272.29
A0A024R244	1 (0)	4.47	---	---		Tyrosine-protein kinase OS=Homo sapiens GN=SYK PE=3 SV=1	---	---	---
A0A024RDN9	1 (1)	4.44	---	1.09		Uncharacterized protein OS=Homo sapiens GN=LOC283537 PE=4 SV=1	1.05e+004	1.06e+004	1.14e+004
A0A024R632	1 (1)	4.43	---	1.33		Kinesin-like protein OS=Homo sapiens GN=KIF22 PE=3 SV=1	4.02e+004	5.35e+004	5.14e+004
P04003	1 (0)	4.42	---	---		C4b-binding protein alpha chain OS=Homo sapiens GN=C4BPA PE=1 SV=2	---	---	---
Q14114	1 (0)	4.41	---	---		Low-density lipoprotein receptor-related protein 8 OS=Homo sapiens GN=LRP8 PE=1 SV=4	---	---	---
Q9NYZ4	2 (2)	4.40	---	1.10		Sialic acid-binding Ig-like lectin 8 OS=Homo sapiens GN=SIGLEC8 PE=1 SV=2	2.29e+005	2.09e+005	2.23e+005
D6W5Y8	1 (1)	4.39	---	1.30		Melanoma associated antigen (Mutated) 1_ isoform CRA_a OS=Homo sapiens GN=MUM1 PE=4 SV=1	6974.03	5786.30	5383.54
Q96RP8	1 (1)	4.37	---	1.04		Potassium voltage-gated channel subfamily A member 7 OS=Homo sapiens GN=KCNA7 PE=2 SV=1	1.07e+004	1.12e+004	1.12e+004
B4DL02	1 (1)	4.35	---	1.28		cDNA FLJ56101_ highly similar to SHC-transforming protein 1 OS=Homo sapiens PE=2 SV=1	6.46e+004	5.91e+004	7.54e+004
Q8N4B5	1 (1)	4.34	---	1.33		Proline-rich protein 18 OS=Homo sapiens GN=PRR18 PE=2 SV=2	2.83e+004	3.75e+004	3.04e+004
P34820	1 (0)	4.34	---	---		Bone morphogenetic protein 8B OS=Homo sapiens GN=BMP8B PE=2 SV=2	---	---	---
A7E240	1 (1)	4.34	---	1.15		SLC8A3 protein (Fragment) OS=Homo sapiens GN=SLC8A3 PE=2 SV=1	4.54e+004	3.95e+004	4.48e+004
H0YKG6	1 (0)	4.33	---	---		UPF0583 protein C15orf59 (Fragment) OS=Homo sapiens GN=C15orf59 PE=4 SV=1	---	---	---
A1A5CZ	1 (1)	4.32	---	1.64		Solute carrier family 22 member 23 OS=Homo sapiens GN=SLC22A23 PE=1 SV=2	5268.80	5346.01	3251.31
H3BNV0	1 (1)	4.32	---	1.13		Leucine-rich repeat-containing protein 36 OS=Homo sapiens GN=LRRC36 PE=4 SV=1	2.47e+004	2.80e+004	2.76e+004
A6NJB7	1 (1)	4.28	---	1.17		Proline-rich protein 19 OS=Homo sapiens GN=PRR19 PE=1 SV=1	5.22e+004	5.16e+004	6.03e+004
B3KRT0	1 (0)	4.28	---	---		cDNA FLJ34857 fis_ clone NT2NE2012533_ highly similar to Cadherin-12 OS=Homo sapiens PE=2 SV=1	---	---	---
Q02641	1 (1)	4.25	---	1.39		Voltage-dependent L-type calcium channel subunit beta-1 OS=Homo sapiens GN=CACNB1 PE=2 SV=3	1.14e+004	1.58e+004	1.54e+004
P19021	1 (1)	4.25	---	1.06		Peptidyl-glycine alpha-amidating monooxygenase OS=Homo sapiens GN=PAM PE=1 SV=2	1.17e+004	1.13e+004	1.11e+004
Q8TBM8	1 (1)	4.24	---	1.30		DnaJ homolog subfamily B member 14 OS=Homo sapiens GN=DNAJB14 PE=1 SV=1	6187.00	6406.20	4925.01
A8MWY0	1 (1)	4.24	---	1.08		UPF0577 protein KIAA1324-like OS=Homo sapiens GN=KIAA1324L PE=1 SV=2	3.25e+004	3.29e+004	3.05e+004
Q9Y2I6	1 (1)	4.21	---	2.58		Ninein-like protein OS=Homo sapiens GN=NINL PE=1 SV=2	3.69e+004	2.90e+004	7.47e+004
B2R7C2	1 (0)	4.20	---	---		cDNA_FLJ93375_ highly similar to Homo sapiens ZW10_ kinetochore associated_ homolog (Drosophila) (ZW10)_ mRNA OS=Homo sapiens PE=2 SV=1	---	---	---
A0A087WSW7	1 (1)	4.20	---	1.83		Helicase_ lymphoid-specific_ isoform CRA_d OS=Homo sapiens GN=HELLS PE=1 SV=1	1.19e+005	9.60e+004	6.49e+004
B3KQ68	1 (0)	4.20	---	---		cDNA FLJ32970 fis_ clone TESTI2008840_ highly similar to Protein transport protein Sec61 subunit alpha isoform 2 OS=Homo sapiens PE=2 SV=1	---	---	---
M0QXB4	1 (0)	4.17	---	---		Coatomer protein complex_ subunit epsilon_ isoform CRA_g OS=Homo sapiens GN=COPE PE=1 SV=1	---	---	---
A8MWA4	1 (1)	4.14	---	1.16		Putative zinc finger protein 705E OS=Homo sapiens GN=ZNF705E PE=3 SV=1	1.58e+004	1.39e+004	1.36e+004
Q8TAD4	1 (1)	4.13	---	1.35		Zinc transporter 5 OS=Homo sapiens GN=SLC30A5 PE=1 SV=1	4387.48	4361.05	5868.84
Q94885	1 (1)	4.12	---	1.15		SAM and SH3 domain-containing protein 1 OS=Homo sapiens GN=SASH1 PE=1 SV=3	2078.04	2350.27	2391.08
A4D0P7	1 (0)	4.04	---	---		Origin recognition complex_ subunit 5-like (Yeast) OS=Homo sapiens GN=ORC5L PE=1 SV=1	---	---	---
Q96EI5	1 (1)	4.04	---	1.15		Transcription elongation factor A protein-like 4 OS=Homo sapiens GN=TCEAL4 PE=1 SV=2	9.55e+004	1.03e+005	1.09e+005

Accession	Peptides	Score	Anova (p)*	Fold	Tags	Description	Average Normalised Abundances		
							0hr	1hr	2hr
Q13643	1 (0)	4.03	---	---		Four and a half LIM domains protein 3 OS=Homo sapiens GN=FHL3 PE=1 SV=4	---	---	---
B4E153	1 (1)	4.00	---	1.31		cDNA FLJ61525_ highly similar to Thyroglobulin OS=Homo sapiens PE=2 SV=1	3233.09	3898.22	2980.79
Q96BD5	1 (1)	3.99	---	1.23		PHD finger protein 21A OS=Homo sapiens GN=PHF21A PE=1 SV=1	9959.59	9093.99	8078.12
A0A0A0MRU5	1 (1)	3.99	---	1.33		Ceroid-lipofuscinosis neuronal protein 5 OS=Homo sapiens GN=CLN5 PE=1 SV=1	7582.69	5696.11	6549.27
D6RF86	1 (1)	3.98	---	1.19		Cadherin-6 OS=Homo sapiens GN=CDH6 PE=1 SV=1	1.14e+004	1.02e+004	1.21e+004
Q9Y2X7	2 (2)	3.97	---	1.45		ARF GTPase-activating protein GIT1 OS=Homo sapiens GN=GIT1 PE=1 SV=2	4030.24	3239.40	4709.07
Q5TCH6	1 (0)	3.96	---	---		Meiotic recombination protein SPO11 (Fragment) OS=Homo sapiens GN=SPO11 PE=4 SV=2	---	---	---
B2R708	1 (1)	3.95	---	1.14		cDNA_ FLJ93213_ highly similar to Homo sapiens protocadherin beta 15 (PCDHB15)_ mRNA OS=Homo sapiens PE=2 SV=1	2140.95	2012.31	1871.44
B2RDF2	1 (0)	3.95	---	---		Pescadillo homolog OS=Homo sapiens GN=PES1 PE=2 SV=1	---	---	---
B7Z3X3	1 (1)	3.86	---	1.14		cDNA FLJ56097_ highly similar to Homo sapiens dystrobrevin alpha (DTNA)_ transcript variant 2_ mRNA OS=Homo sapiens PE=2 SV=1	1.15e+004	1.01e+004	1.13e+004
A0A024R0X1	1 (1)	3.84	---	1.18		NEL-like 2 (Chicken)_ isoform CRA_b OS=Homo sapiens GN=NELL2 PE=4 SV=1	1.07e+004	9003.51	1.03e+004

Tags	
	Modification with Phosphoryl+STY
	Max fold change ≥ 1.2

Q5T200

Zinc finger CCCH domain-containing protein 13 OS=Homo sapiens GN=ZC3H13 PE=1 SV=1
56 peptides

Sequence	Peptide lon	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										0hr	1hr	2hr
AQDIIGHQSEDR	5720	4.56	1	1504.7127	2		0		no	1.61e+004	1.24e+004	3.21e+004
ARERDRERDRERERERERDREREKER	23793	5.06	1	4167.1040	4		0		no	1744.90	1583.21	952.98
AREREREREKERDRERDRDR	17276	4.65	1	2741.4063	3		0		no	2414.51	1682.18	1793.97
DADNLFELHFGALNMAALLR	1284	4.91	1	2212.0845	3		0		no	5.66e+004	6.07e+004	6.68e+004
DADNLFELHFGALNMAALLR	3895	---	---	2212.2568	2		0		no	2.62e+004	3.19e+004	3.05e+004
DAHVDYRDREGRDTHR	17686	5.12	1	1897.8799	3		0		no	5105.88	4567.75	4009.15
DGHDER	13002	4.97	1	727.2721	2		0		no	3827.66	2825.88	1655.25
DMRDSREMRDYSRDTK	14118	5.14	1	2059.9075	3		0		no	3532.49	2613.26	2591.76
DMRDSREMRDYSRDTKESR	2365	5.34	1	2432.0671	4		0		no	2.63e+004	1.93e+004	2.39e+004
DRDHREREREREREREKEREREREERERERER	17286	5.06	1	4891.3269	5		0		no	5458.47	7111.98	4516.35
DRDRDHRERERERER	2977	5.45	1	2224.0559	3		1		no	3.87e+004	3.46e+004	3.94e+004
DREKEREREERERER	588	5.40	1	2101.0659	3		0		yes	1.58e+005	1.54e+005	1.59e+005
DREKEREREERERERERER	18188	5.08	1	2671.2960	4		1		no	5066.21	4804.83	4122.34
DRERDRDRDHRERER	18781	4.62	1	2210.0611	3		0		no	3010.28	2109.72	2630.97
DRGRDFERQR	941	5.85	1	1333.6595	2		0		no	5.64e+004	8.24e+004	5.61e+004
DRYEHDR	15645	5.87	1	989.4221	2		0		no	2770.05	2610.18	2488.79
DYSRDTKESRDPDSR	11187	4.87	1	1981.9134	3		0		no	3.65e+004	3.41e+004	3.73e+004
DYSRDTKESRDPDSR	24321	5.05	1	1981.9375	3		0		no	1329.07	1394.07	1241.63
EDIKITKER	15710	4.98	1	1130.6148	2		2		no	5.83e+004	5.71e+004	8.32e+004
EKERDRERDRDRDHR	8451	4.74	1	2182.0336	3		0		no	2.92e+004	2.78e+004	3.09e+004
EKEREREEREERERER	12313	5.60	2	2115.0499	3		0		no	1.19e+004	1.29e+004	1.38e+004
EKEREREEREERERERERERERERERERERER	4023	---	---	4111.3043	3		1		no	5.19e+004	3.96e+004	5.16e+004
EKEREREEREERERERERERERERERERERER	6785	5.06	1	4111.0577	4		1		no	2.30e+004	1.76e+004	2.36e+004
ELRDSRDMRDSREMRDYSR	4873	5.00	1	2472.1579	3		1		no	5.03e+004	3.94e+004	4.72e+004
EMRDYSRDTK	1937	4.45	1	1299.6115	2		1		no	1.08e+005	8.63e+004	1.08e+005
EMRDYSRDTKESRDPDR	3830	4.74	1	2039.9610	3		2		no	6.36e+004	5.82e+004	6.85e+004
EPGAALLKFTPGAVMLR	1905	5.19	1	1785.9825	2		2	[15] Oxidation+M	no	6.60e+004	5.82e+004	6.66e+004
EPGAALLKFTPGAVMLR	399	---	---	1785.8069	3		2	[15] Oxidation+M	no	1.30e+005	1.24e+005	1.50e+005

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										0hr	1hr	2hr
ERDREKEREREREER	9845	5.30	1	2101.0462	3		2		no	3.18e+004	3.24e+004	2.93e+004
ERDRERERDRER	9577	5.17	1	1700.8494	2		1		no	2.45e+004	2.47e+004	2.33e+004
ERDRERERDRERERERERER	14532	5.15	1	2841.4100	3		0		no	6892.65	7488.38	5972.54
EREERERERERERERER	25840	5.07	1	2428.2051	3		0		no	2639.17	2762.63	1891.73
ERERDREKEREREREERERER	1049	5.90	1	2956.4580	4		1		no	7.34e+004	5.85e+004	7.50e+004
ERERDREKEREREREERERER	2160	---	---	2956.6529	3		1		no	6.89e+004	6.18e+004	7.11e+004
ERERDRERERERER	8222	4.91	1	1999.9638	3		0		no	6016.80	6108.65	5539.54
EREREKERDRERDRDRDHDR	7531	5.42	1	2752.3692	3		1		no	2.59e+004	2.10e+004	2.77e+004
ERERERDREKERER	16890	5.55	1	1971.9866	3		0		no	6506.96	7028.29	5784.24
ERERERDREREKERELER	5672	4.29	1	2499.2041	4		0		no	1.05e+004	1.01e+004	1.15e+004
ERERERDREREKERELER	6870	---	---	2499.3718	3		0		no	3.42e+004	3.10e+004	3.75e+004
EREREREERERERERER	20137	5.57	1	2428.1796	3		0		no	3514.70	3964.55	3674.14
ERERERERDREKEREREREERERERERERER	14286	---	---	4382.3999	4		0		no	9456.57	9242.60	6848.73
ERERERERDREKEREREREERERERERERER	15058	5.25	1	4382.2170	5		0		no	5961.71	5696.40	3872.14
ERERERERERDREREKERELERER	6727	5.41	1	3354.6839	4		0		no	1.72e+004	1.67e+004	1.58e+004
ESSRRYEEQELK	8408	5.31	1	1552.7484	2		0		no	4.45e+004	4.03e+004	4.28e+004
GNIETTSQVDFSPKK	1022	4.81	1	1835.9251	2		1		no	3.10e+005	2.59e+005	3.09e+005
HHSSSSQSGSSIQR	10516	4.38	1	1483.6637	3		0		no	2204.06	2557.04	2774.05
KEDTAFSDWSDVDVDR	17336	5.25	1	2010.9337	3		1		no	1.02e+004	9521.36	1.07e+004
KEDTYPEESR	4486	4.68	1	1252.5562	2		0		no	2.92e+004	2.63e+004	3.08e+004
LEGEHERDLESTSR	2714	4.71	1	1656.7996	2		0		yes	9.58e+004	8.66e+004	9.71e+004
LLEKPKDADNLFHELGALNMAALLR	12873	5.52	2	2920.5683	3		0		no	1.79e+004	2.00e+004	1.74e+004
LRERERERERDK	9179	5.00	1	1670.8735	2		1		no	5957.68	4396.23	1.99e+004
NTEESSPPV	5932	5.08	1	1104.4665	2		1		no	3.25e+004	2.69e+004	3.17e+004
QAYTSAPMVDNELLRLSLRFLK	2917	5.59	1	2580.3494	3		0	[8] Oxidation+M	no	2.74e+004	2.73e+004	3.12e+004
RDREKDSREEREYEQDQSSSRDHRDDR	21873	5.71	1	3478.5668	4		0		no	1839.51	1807.79	5950.81
REHSPDSDAYNSGDDK	7025	4.90	1	1791.7374	3		0		no	1.69e+004	1.51e+004	3.53e+004
RELRSRDMRDSREMRDYSRDTKESRDPR	5084	5.17	1	3712.7638	4		0		no	2.00e+004	1.51e+004	1.95e+004
RSS [~] LGNSRNSNR	670	5.17	1	1399.6307	3		1	[4] Phosphoryl+STY	no	7.00e+004	6.63e+004	5.20e+004
RSS [~] LGNSRNSNR	474	---	---	1399.7934	2		1	[4] Phosphoryl+STY	no	1.67e+005	1.69e+005	1.56e+005
STRDAHYDRDREGDRDTHR	19493	4.73	1	2242.0198	4		0		no	3815.48	4245.43	3100.10
STSPAGQHHSPISSR	443	4.64	1	1547.6313	3		1		no	9.47e+004	1.20e+005	1.09e+005
STSPAGQHHSPISSR	275	---	---	1547.7980	2		1		no	1.46e+005	1.76e+005	1.63e+005
SYGRNHLREESSR	4611	5.56	1	1750.6936	3		1		no	3.64e+004	3.13e+004	3.61e+004
TSAVSSPLLDQQRNSKTNQSKK	17756	---	---	2416.4693	2		0		yes	1.54e+004	2.00e+004	1.57e+004
TSAVSSPLLDQQRNSKTNQSKK	2295	4.94	1	2416.2507	3		0		yes	7.35e+004	9.52e+004	6.64e+004
VETPHVTIEDAQHR	22795	---	---	1630.9738	2		2		no	6089.75	7300.99	6154.79
VETPHVTIEDAQHR	4005	5.51	1	1630.8123	3		2		no	2.47e+004	2.53e+004	1.89e+004
YEEQELKEK	2667	5.01	1	1194.5615	2		1		no	2.43e+004	2.98e+004	2.81e+004

Tags

Modification with Phosphoryl+STY

Q92817

Envoplakin OS=Homo sapiens GN=EVPL PE=1 SV=3
25 peptides

Sequence	Peptide Ion	Score	Hits	Mass	Charge	Tags	Conflicts	Modifications	In quantitation	Average Normalised Abundances		
										0hr	1hr	2hr
AAEDAVYELQSK	16525	4.79	1	1322.6148	2		1		no	1.41e+004	1.29e+004	1.44e+004
APLSRPTPLEDLEGR	10970	4.39	1	1649.8522	2		0		no	3.64e+004	3.53e+004	3.79e+004
ASAVESLRPSQQAPSGSDLANPQAQK	23576	4.55	1	2636.2988	3		0		no	2105.69	3091.27	2453.29
DPLSGLLLLLPAALEGYR	13302	4.47	1	1796.9770	3		2		no	5921.24	7095.55	5725.76