Thongjuk Geetha et al., Supplemental Table 2. Unique peptides detected with a minimum of 95% confidence in at least 1 out of 10 samples

Gene Name	Protein Name	Protein IPI accession numbers	Protein molecular weight (Da)	Number of unique peptides	Number of total peptides	Number of unique sequence	Percentage sequence coverage	Peptide sequence	Previous scores	Best score	Mascot score	Mascot identity	Number of keypeptides	Variable modifications	Observed m/z	Actual peptide mass (MH+)	Calculated +1H Peptide Mass (MH+)	Actual minus calculated peptide mass	Peptide start	Peptide stop	Exclusion	Other Proteins
Gnb1	Guanine nucleotide-binding protein G(t) subunit alpha-1	IPI00308271;IPI00411511	40862	10	10	10	19.70%	AKDEGIVRTVR			551.1	28.3			551.7898	1,101.56	1,100.57	0.98	109	119	YES	
Pdzk1	Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit beta isoform	IPI00110896	123955	6	6	6	6.90%	AKVDGGMAEVDR			561.1	39.1			717.8347	1,433.67	1,432.68	0.98	315	326	YES	
Atf4	Activator 3 binary chain	IPI00369894	39913	14	14	14	47.60%	AKDMAAIAAIK			559.8	38.4		Mdh: Oxidation (+15.99); Mdh: Oxidation (+15.99);	558.7739	1,115.52	1,096.50	19.02	78	88	YES	
Cpa62	Carboxypeptidase A2 precursor	IPI00329958	102193	6	6	6	9.37%	AKVSLSDPTEYKNLPYGLK			551.6	39.7			1,103.61	2,860.65	2,845.65	0.03	786	802	YES	
Ca2	Carbonic anhydrase 2	IPI00279751	31138	6	6	6	22.60%	AKVLDDFIQTIKSPGEQHS			558.6	33.6			1,674.83	3,346.65	3,345.65	0.01	67	97	YES	
Cnr1	CB1CB2	IPI00421355	53659	10	10	10	27.60%	AKGDPRTSEMVGGSSSEAE			551.1	21		Mdh: Oxidation (+15.99)	1,102.97	2,203.91	2,182.93	0.98	120	137	YES	
Ccnb1	Cyclin B1	IPI00130080;IPI00420088	49196	6	6	6	14.50%	AKVQDEIDNVIQPKHVNTF			551.1	32.1			1,653.29	3,304.57	3,303.58	0.99	171	189

Sec61	Sec61 beta subunit	P60953/P61851/P60953/P61851	62/69	0/0	0/0	0/0	0/0	0.42%	DAEEQIFDEDGNTDKIK	K							883.95377	1,575.82	1,708.89	2	0.48	55	55	VALE					
Ran1	Ras-related nuclear protein	P62826/P62827	68/68	1/1	0/0	0/0	0/0	0.42%	GVDDVMFNV	K							972.7511	1,555.69	1,644.59	2	0.78	179	179	VALE					
Ssr1	Translocon associated protein alpha	P43308/Q91	60/60	1/1	0/0	0/0	0/0	0.42%	GVDEMMFTR	K							996.5879	1,574.92	1,672.59	2	0.80	230	230	VALE					
Hspa9	Stress-70 protein, mitochondrial	P38647/P63039	73/60	1/1	0/0	0/0	0/0	0.42%	DGGSSIIVLVKR	K							921.8669	1,551.67	1,592.68	2	0.12	597	597	VALE					
Tpd52	Tumor protein D54 protein	P55863/Q9	70/83	1/1	0/0	0/0	0/0	0.42%	DEETGAEIVQLK	K							1030.9511	1,546.87	1,599.68	2	0.29	172	172	VALE					
Hspa8	70 kDa glucose-regulated protein	P63017/P08109	72/65	1/1	0/0	0/0	0/0	0.42%	DAGTIQAEIKAAR	K							1027.5173	1,532.65	1,597.69	2	0.43	186	197	VALE					
Ssr2	Translocon associated protein beta (signal-binding protein 1 subunit 1)	P62866/P62868	67/67	1/1	0/0	0/0	0/0	0.42%	DAEEEVDTLVLK	K							1030.5511	1,530.87	1,597.69	2	0.29	172	172	VALE					
Ssr1	SSR alpha protein	P62866/P62868	67/67	1/1	0/0	0/0	0/0	0.42%	GVDEMMFTR	K							996.4879	1,571.62	1,672.59	2	0.80	230	230	VALE					
Ssr4	Translocon associated protein delta	P62866/P62868	67/67	1/1	0/0	0/0	0/0	0.42%	DAEEEVDTLVLK	K							1030.9511	1,529.87	1,597.69	2	0.29	172	172	VALE					
Ssr3	Translocon associated protein gamma	P62866/P62868	67/67	1/1	0/0	0/0	0/0	0.42%	DAEEEVDTLVLK	K							1030.9511	1,529.87	1,597.69	2	0.29	172	172	VALE					
Ssr2	Translocon associated protein beta	P62866/P62868	67/67	1/1	0/0	0/0	0/0	0.42%	DAEEEVDTLVLK	K							1030.9511	1,529.87	1,597.69	2	0.29	172	172	VALE					
Ssr1	SSR alpha protein	P62866/P62868	67/67	1/1	0/0	0/0	0/0	0.42%	GVDEMMFTR	K							996.4879	1,529.87

Rpl13	Ribosomal protein L13	P60866/6670	127848	15	5	15	5.00%	RGGRPKVAQLLR	S	P	90.7	18.4				834.1004	1,664.4	1,395.67	P	0.22	1330	1331	P0CG48/O15.1;P60866/2	
Ube2l6	Ubiquitin-conjugating enzyme E2 L6	P68036/9178	225825	14	4	14	4.00%	LIEEPNIQSELLR	S	P	93.1	20.1				1,302.6	1,302.6	1,301.66	P	0.02	1371	1371	P68036/2	VALID
Rpl23	Ribosome 0	P35265/6179	153862	10	10	10	10.10%	DIGFTMAMGR	S	P	94.8	19.5				993.1868	1,983.9	1,989.99	P	0.02	1771	1782	VALID
Rpl7a	Ribosomal protein L7a	P62424/6731	136418	10	10	10	10.10%	IRGVDSEEQLR	S	P	93.9	19.7				1,198.5985	2,394.9	2,380.07	P	0.03	1165	1176	VALID
Ezr;7	14057b	P15311/6269	136616	16	14	16	14.00%	VEGLKDERLNM	S	P	97.6	24				1,992.8302	1,987.68	1,988.67	P	0.12	1305	1305	VALID
Tpr	Tumor ex Filamentin binding protein 1	P12270/8875	143855	5	5	5	5.%	DIEAVAQQR	S	P	97.6	15.3				1,017.7987	1,113.98	1,116.95	P	0.21	1676	1681	VALID
Rpl32	60S ribo protein	P62910/6160	116855	15	14	15	14.00%	LEEVKEIK	S	P	99.8	17.8				1,872.2181	1,871.6821	1,871.6899	P	0.04	1210	1217	VALID
Rpl10a	60S ribo protein	P62908/6134	100846	14	14	14	14.00%	LIEEFNSAYR	S	P	99.8	17.8				1,198.6	1,197.6	1,197.6	P	0.04	1211	1220	VALID
Rpl4	Ribosome 0	P62888/6124	112030	22	22	22	22.00%	LEEIAKDIHPL	S	P	97.5	24.1				2,371.2666	2,369.5176	2,369.5128	P	0.03	1123	1132	VALID
Rpl9	Ribosome 0	P63150/6133	126826	12	12	12	12.00%	LEEFVKAIR	S	P	91.6	19.4				1,017.5321	1,072.61	1,073.62	P	0.09	1169	1179	VALID
Ezh2	Enhancer 2 of Zeste protein	P70349/9257	103983	5	5	5	5.%	LEEAVKSLR	S	P	99.8	19.7				1,001.6207	1,001.62	1,001.62	P	0.04	1816	1821	VALID
Tpp1	7-peptide protein 1 isolate alpha	P50100/9067	50593	5	5	5	5.78%	EGLAAKFQR	S	P	98.8	19.1				974.5131	1,166.61	1,167.61	P	0.19	1436	1441	VALID
Ezh2	Enhancer 0	P70349/9178	103983	15	15	15	15.00%	DEIAKLTR	S	P	97.6	19.6				1,673.8178	1,673.8	1,671.8271	P	0.05	1670	1677	VALID
Gnrs;12	Conopsin 0	P50237/8836	124010	15	15	15	15.00%	VEGLDVSQDVNETEL	S	P	91.1	15.4				1,854.0751	1,926.93	1,927.94	P	0.15	1549	1562	VALID
Ezh2	Enhancer 0	P70349/9178	103983	15	15	15	15.00%	DEIAKLTRGVNETEL	S	P	97.6	19.6				1,673.8178	1,673.8	1,671.8271	P	0.05	1670	1677	VALID
Rpl19	60S ribo protein	P62888/6117	108010	10	10	10	10.10%	LEEIAKDIHPL	S	P	97.5	24.1				1,371.2666	1,369.5176	1,369.5128	P	0.03	1123	1132	VALID
Rpl27	60S ribo protein	P61358/6155	15862	10	10	10	10.10%	LEEFVKAIRR	S	P	99.8	19.7				1,198.6	1,198.6	1,198.6	P	0.04	1211	1220	VALID
Rpl7	60S ribo protein	P62424/6131	136418	10	10	10	10.10%	IRGVDSEEQLR	S	P	93.9	19.7				1,198.5985	2,394.9	2,380.07	P	0.03	1165	1176	VALID
Rpl18	60S ribo protein	P62270/6125	117875	15	15	15	15.00%	LEGVDKTRAIVDEIR	S	P	99.8	19.7				1,598.8	1,598.8	1,598.8	P	0.04	1211	1220	VALID
Rpl29	60S ribo protein	P47963/6121	18275	10	10	10	10.10%	LEEIAKDIHPL	S	P	97.5	24.1				1,371.2666	1,369.5176	1,369.5128	P	0.03	1123	1132	VALID
Rpl15	60S ribo protein	P61313/6094	124010	15	15	15	15.00%	VEGLDVSQDVNETEL	S	P	91.1	15.4				1,854.0751	1,926.93	1,927.94	P	0.15	1549	1562	VALID
Ezh2	Enhancer 0	P70349/9257	103983	5	5	5	5.%	LEEAVKSLR	S	P	99.8	19.7				1,001.6207	1,001.62	1,001.62	P	0.04	1816	1821	VALID
Rpl32	60S ribo protein	P62910/6160	116855	15	14	15	14.00%	LEEVKEIK	S	P	99.8	17.8				1,872.2181	1,871.6821	1,871.6899	P	0.04	1210	1217	VALID
Rpl10a	60S ribo protein	P62908/6134	100846	14	14	14	14.00%	LIEEFNSAYR	S	P	99.8	17.8				1,198.6	1,197.6	1,197.6	P	0.04	1211	1220	VALID
Rpl4	Ribosome 0	P62888/6124	112030	22	22	22	22.00%	LEEIAKDIHPL	S	P	97.5	24.1				2,371.2666	2,369.5176	2,369.5128	P	0.03	1123	1132	VALID
Rpl9	Ribosome 0	P63150/6133	126826	12	12	12	12.00%	LEEFVKAIR	S	P	91.6	19.4				1,017.5321	1,072.61	1,073.62	P	0.09	1169	1179	VALID
Ezh2	Enhancer 0	P70349/9178	103983	15	15	15	15.00%	DEIAKLTRGVNETEL	S	P	97.6	19.6				1,673.8178	1,673.8	1,671.8271	P	0.05	1670	1677

Col1a1	Collagen, type I, alpha 1	P02454|B2RE48	137956	17	57	17	0.298%	GVVAGPVGP	K			16.7	17.2				1831.7619	1831.5301	1824.5161	7	0.17	1568	1601	TRUE					
Ptpn11	Protein-tyrosine phosphatase 1D, PTP-1D, PTP-2C, SH-PTP2, SH-PTP3, PTP2C, SHP-2, SHP2, SH-PTP2, PTEN2, PTP2D	P35235|Q62410|Q64510|Q9Z0H5|Q9Z0J0|Q9Z0J1|Q9Z0J2|Q9Z0J3	67284	12	6	11	0.146%	GVDPEGAAGGR	K			11.1	11.1				1183.6016	1183.5	1180.7	3	0.25	1446	1466	TRUE					
Nqo1	Quinone oxidoreductase	P05982|Q64519	17108	7	6	6	0.146%	GVDPEGAEGPGGR	K			7.5	7.5	28.8			1797.8850	1795.75	1804.75	2	0.15	528	541	TRUE					
Ccnb1	Cyclin B1	P24860|P97448|Q9Z0V8	91433	6	6	6	0.146%	GVFPPVAGR	K			6.4	6.4	27.8			1014.2197	1014.2	1009.5	2	0.19	230	238	TRUE					
Tnnipa	BTG3	P30533|Q61990|P80269|Q7	81751	5	5	5	0.146%	GVHVVEINV	K			5.1	5.1	18.2			1041.2992	1041.2	1041.2	2	0.19	230	239	TRUE					
Ttn	Titin	A2A3R0|Q8VZX6	2419.9897	5	5	5	0.146%	GVIAPPAGYGPVDPTA	K			5.1	5.1	17.7			1179.9	1177.95	1180.7	2	0.25	1420	1451	TRUE					
Acta	Actin, sarcoplasmic 1	P02566|P68135|P68033|P68032|P62736	41720	4	12	4.08	0.146%	GFVITTAER	K			41.8	27.3				1064.7978	1131.61	1132.13	2	0.13	1387	1396	TRUE					
Ccnd1	Cyclin D1 (PRAD1 oncogene)	P24385|Q9Z0V8	36245	4	4	4	0.146%	GFLLPPPPPGGGR	K			4.4	4.4	15.4			1284.6	1284.6	1284.6	2	0.15	275	287	TRUE					
Myh9	Myosin-9	P14105|Q8VDD5	226415	31	30	31	0.146%	GFLIQMTSER	K			30.1	19.4			MR: Oxidation (+16.00)	1731.8239	1731.67	1732.19	2	0.21	1911	1926	TRUE					
Myh7	Myosin-7	P02563|Q9JHI9	223842	29	29	29	0.146%	GFLIQMTSER	K			29	19.4				1662.8201	1679.66	1680.05	2	0.27	1907	1922	TRUE					
Myh10	Myosin-10	P13533|Q8VDD5	229819	28	28	28	0.146%	GFLIQMTSER	K			28	19.4				1716.8201	1688.98	1700.08	2	0.28	1712	1726	TRUE					
Myl6s1	ATP synthase subunit alpha, mitochondrial	P20788|P97450	59737	11	12	11	0.135%	GGLVFDSLM	K			11.4	9				1041.5532	1041.69	1041.79	2	0.15	306	316	TRUE					
Cfl1|2	Cofilin-1|2	P18760|P45591	18.5	3	3	3	0.135%	GGLTSLFGR	K			3.1	3.1	11.8			1139.6	1139.6	1139.6	2	0.19	1126	1135	TRUE					
Ldha	LDH-M chain	P06151|P52500	36669	10	10	10	0.135%	GGLVSDLVQSLQSER	K			10.1	10.1	28.4			1911.9772	1912.03	1911.98	2	0.16	1218	1231	TRUE					
Ldhb	LDH-B chain	P16125|P16125	36669	10	10	10	0.135%	GGLVSDLVQSLQSER	K			10.1	10.1	28.4			1911.9772	1912.03	1911.98	2	0.16	1218	1231	TRUE					
Ldhc	LDH-C chain	P16125|P16125	36669	10	10	10	0.135%	GGLVSDLVQSLQSER	K			10.1	10.1	28.4			1911.9772	1912.03	1911.98	2	0.16	1218	1231	TRUE					
Ptn	Pleiotrophin	P18772|P18772	13.4	3	3	3	0.135%	GGLVTGTAMNK	K			3.1	3.1	11.8		MR: Oxidation (+16.00)	1117.7	1117.6	1117.6	2	0.19	143	153	TRUE					
Ptn	Pleiotrophin	P18772|P18772	13.4	3	3	3	0.135%	GGLVTGTAMNK	K			3.1	3.1	11.8	

Rab9	Rab9a-B	P60228	Q9JI13	226262	138	222	2011	91.00%	QVDHEVDSLKSKMTEMAN	K	K	61.5	18.9			MS- Oxidation (+15.99)	1904.6873	1899.97	5, 100.07	F	0.08	11001	11017	TRUE		
Rab9	Rab9a-B	P60228	Q9JI13	226262	138	222	2011	91.00%	QVDHEVDSLKSKMTEMAN	K	K	61.5	18.9				1904.6873	1899.97	5, 100.07	F	0.08	11001	11017	TRUE		
Pdf	Polypeptide f and transcript release factor	P60202	Q3U0J2	51893	51	67	6	95.00%	GVFAMEAKLGR	K	K	26.1	25.9				1208.5886	1211.16	1, 614.79	F	0.77	1139	1149	TRUE		
Rab	Rabaptin-5	P62835	Q9D1K4	319716	151	167	6	95.00%	DLLDEIEAR	K	K	26.5	25.4				1021.5398	1024.56	1, 360.58	F	0.08	1502	1510	TRUE		
Rab8	Rabaptin-5	P59196	Q9D118	226326	150	166	666	95.00%	DLLDEIEAR	K	K	26.5	27.5			MS- Oxidation (+15.99)	1021.5398	1017.6768	1, 612.68	F	0.19	1503	1509	TRUE	P59196|Q9D118|P62835|Q9D1K4	
Cpm 1	Carboxypeptidase 1, alpha-isoform	P14092	56303	25	39	139	95.00%	DEVLDGLR	K	K	47.4	24.2				1017.9971	1015.78	1, 524.76	F	0.77	1138	1145	TRUE	P14092|P70001	
Cpm 1	Carboxypeptidase 1, alpha-isoform	P70001	Q9D0H5	52871	28	42	148	95.00%	DEVLDGLR	K	K	47.4	25.7				1002.0992	1, 766.96	1, 599.59	F	0.83	1148	1152	TRUE	P70001|P14092	
Ccp1	Cytosolic carboxypeptidase 1 beta isoform	P97436	Q9D0E1	66152	51	67	6	95.00%	DEVLDGLR	K	K	47.4	25.7				1002.0992	1, 766.96	1, 599.59	F	0.83	1148	1152	TRUE		
Rab7	Rabaptin-5	P59196	Q9D118	226326	150	166	666	95.00%	DLLDEIEAR	K	K	47.5	24.8				1026.5327	1, 026.67	1, 267.58	F	0.08	1502	1510	TRUE		
Rab7	Rabaptin-5	P62835	Q9D1K4	319716	151	167	6	95.00%	DLLDEIEAR	K	K	47.5	24.8				1026.5327	1, 026.67	1, 267.58	F	0.08	1503	1509	TRUE		
Rab9	Rabaptin-5	P59196	Q9D118	226326	150	166	666	95.00%	DLLDEIEARDSLKSKMTEMAN	K	K	47.5	19.5			MS- Oxidation (+15.99)	1709.8209	1, 112.65	1, 514.04	F	0.77	1503	1519	TRUE		
Rab9	Rabaptin-5	P62835	Q9D1K4	319716	151	167	6	95.00%	DLLDEIEARDSLKSKMTEMAN	K	K	47.5	19.5			MS- Oxidation (+15.99)	1, 109.65	1, 076.66	1, 377.31	F	0.25	1502	1519	TRUE		
Ccl16	Type I keratin 42.kb	P50162	Q7TS7	50760	1	10	11	95.00%	RNVIEIRNALIR	K	K	56.1	18.9			MS- Oxidation (+15.99)	1091.5565	1, 092.68	1, 395.64	F	0.61	1911	1921	TRUE		
Cpm 1	Carboxyl-terminal kinase	P28671	12878	25	39	139	95.00%	DEVLDGLR	K	K	47.4	25.7				1017.9971	1, 013.97	1, 179.86	F	0.77	1138	1145	TRUE		
		P60203|Q3U2K1,P|P60203|Q3U2K1																											
Tnnt3	Isoform 1 of Troponin T, fast skeletal muscle	P60206|Q9JJ|P|P60206|Q9JJ	83753	12	26	66	95.00%	RNAEHEAQIDELR	K	K	39	27				1516.7562	1, 802.95	1, 803.95	F	0.02	185	196	TRUE		
Fdxp2	Ferredoxin-like 4 dimerizer binding protein 2	P10109	Q8BTT9	110303	51	67	6	95.00%	DPFLSLIHPQLEVAVE	K	K	60.6	12.9				1797.9604	1, 569.91	1, 904.95	F	0.52	1103	1121	TRUE		
Cpm	Rabaptin-5	P62835	Q9D1K4	319716	151	166	666	95.00%	DLLDEIEAR	K	K	26.5	25.4				1005.5398	1, 014.65	1, 712.85	F	0.08	1502	1510	TRUE		
Rab10	Rab10a protein	P59196	Q9D118	226262	150	166	666	95.00%	DLLDEIEAR	K	K	26.4	28.3				1005.5398	1, 797.89	1, 798.90	F	0.66	1502	1510	TRUE		
Rab10	Rab10a protein	P62835	Q9D1K4	319716	151	167	6	95.00%	DLLDEIEARDSLKSKMTEMAN	K	K	26.4	19.5				1, 109.65	1, 076.66	1, 377.31	F	0.25	1502	1519	TRUE		
Rab13	Isoform 2 of Dedicator	P62227	Q3U0J0	229262	51	67	6	95.00%	DPFLSLIHPQLEVAVE	K	K	60.6	12.9				1797.9604	1, 569.91	1, 904.95	F	0.52	1103	1121	TRUE		
Rab13	Rab13a protein	P62227	Q3U0J0	229262	51	67	6	95.00%	DPFLSLIHPQLEVAVE	K	K	60.6	12.9				1797.9604	1, 569.91	1, 904.95	F	0.52	1103	1121	TRUE		
Rab13	Rab13a protein	P62227	Q3U0J0	229262	51	67	6	95.00%	DPFLSLIHPQLEVAVE	K	K	60.6	12.9				1797.9604	1, 569.91	1, 904.95	F	0.52	1103	1121	TRUE		
Rab8	Rabaptin-5	P59196	Q9D118	226326	150	166	666	95.00%	DLLDEIEARDSLKSKMTEMAN	K	K	26.5	19.5				1, 109.65	1, 076.66	1, 377.31	F	0.25	1503	1519	TRUE		
Rab8	Rabaptin-5	P62835	Q9D1K4	319716	151	167	6	95.00%	DLLDEIEARDSLKSKMTEMAN	K	K	26.5	19.5				1, 109.65	1, 076.66	1, 377.31	F	0.25	1502	1519	TRUE		
Rab7	Rabaptin-5	P59196	Q9D118	226326	150	166	666	95.00%	DLLDEIEARDSLKSKMTEMAN	K	K	47.5	19.5				1, 109.65	1, 076.66	1, 377.31	F	0.25	1502	1519	TRUE		
Rab7	Rabaptin-5	P62835	Q9D1K4	319716	151	167	6	95.00%	DLLDEIEARDSLKSKMTEMAN	K	K	47.5	19.5				1, 109.65	1, 076.66	1, 377.31	F	0.25	1502	1519	TRUE		
Rab9	Rab9a-B	P60228	Q9JI13	226262	138	222	2011	95.00%	QVDHEVDSLKSKMTEMAN	K	K	47.5	19.5				1, 109.65	1, 076.66	1, 377.31	F	0.25	11001	11019	TRUE		
Rab9	Rab9a-B	P60228	Q9JI13	226262	138	222	2011	95.00%	QVDHEVDSLKSKMTEMAN	K	K	47.5	19.5				1, 109.65	1, 076.66	1, 377.31	F	0.25	11001	11019	TRUE		
Rab13	Rab13a protein	P62227	Q3U0J0	229262	51	67	6	95.00%	DPFLSLIHPQLEVAVE	K	K	60.6	12.9				1797.9604	1, 569.91	1, 904.95	F	0.52	1103	1121

Rab30	RAS-like protein	P0DPH9|RAB	174643	16	32	100	100.00%	GIIIDGDVGVGKSAL	K	E	125	135.0				9571.9819	1183.97	1,384.08	F	0.85	1163	1359	TRUE						
Rab18	RAS-like protein	P0DPH9|RAB	171863	16	32	100	100.00%	GIIIDGDVGVGKSAL	K	E	125	135.0				9571.9819	1183.97	1,384.08	F	0.85	1163	1359	TRUE						
Rab8B	Myosin-9	P0DJI9|MYH9	156926	178	279	68%	100.00%	GVDEIQKLKEQIDNIQ	K	E	257	285.2				9976.5019	1368.84	1,369.09	F	0.99	1419	1423	TRUE						
Rab7A	RAS-like protein	P0DPH9|RAB	174643	16	32	100	100.00%	GIIIDGDVGVGKSAL	K	E	125	135.0				9571.9819	1183.97	1,384.08	F	0.85	1163	1359	TRUE						
Fibp2	Ankyrin-repeat domain-containing protein 1	P0DJI8|RFP2	118693	10	32	31	100.00%	GQEIWNLIR	K	E	95.1	106.8				550.8009	1,399.60	1,100.61	F	0.93	720	720	TRUE						
Cpn1a	Myosin-9	P0DJI9|MYH9	153813	16	32	50%	100.00%	GEEIDERLR	K	E	19.1	21.5				1074.0197	143.83	1,325.85	F	0.11	112	127	TRUE						
Myo1c	Myosin-9	P0DJI9|MYH9	114797	47	83	100	100.00%	GEQLFNKTDK	K	E	66.3	74.2				4074.0132	543.85	1,385.85	F	0.39	426	456	TRUE						
Rab1A	RAS-like protein	P0DPH9|RAB	174643	16	32	100	100.00%	GIIIDGDVGVGKSAL	K	E	125	135.0				9571.9819	1183.97	1,384.08	F	0.85	1163	1359	TRUE						
Rab8A	Myosin-9	P0DJI9|MYH9	156926	178	279	68%	100.00%	GVDEIQKLKEQIDNIQ	K	E	257	285.2			MR: Oxidation (+16.99)	9,243.16	1,367.37	1,384.08	F	0.98	1376	1381	TRUE						
Rab11	Ankyrin-repeat domain-containing protein 1	P0DJI8|RFP2	118693	10	32	31	100.00%	GQEIWNLIR	K	E	95.1	106.8			MT: Oxidation (+16.99)	572.4009	1,514.98	1,014.98	F	0.99	768	768	TRUE						
Rab5B	Myosin-9	P0DJI9|MYH9	156926	178	279	68%	100.00%	GVDEIQKLKEQIDNIQ	K	E	257	285.2				9976.5019	1368.84	1,369.09	F	0.99	1419	1423	TRUE						
Rab8B	Myosin-9	P0DJI9|MYH9	156926	178	279	68%	100.00%	GVDEIQKLKEQIDNIQ	K	E	257	285.2				9976.5019	1368.84	1,369.09	F	0.99	1419	1423	TRUE						
Rab12	Dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit 2	P0DJB8|RPN2	109860	6	7	14%	100.00%	GEVRSGNFQAGAVVR	K	E	84	93.5				9570.0078	1,758.69	1,759.01	F	0.91	290	296	TRUE						
Rab27A	Phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1, isoform CRA_a	P0DJH4|AIM1	41211	17	33	100	100.00%	GAEPPEEFTFLIR	K	E	40.6	47.6			MT: Oxidation (+15.99)	1,215.46	360.70	1,387.18	F	0.26	338	348	TRUE						
Rab3A	Isoform 2 of Dynein-2	P0DJD7|DYNC2H1	171969	6	7	14%	100.00%	GEEIFNTLFSTTLR	K	E	39.6	44.7				976.2957	244.89	1,309.88	F	0.19	220	225	TRUE						
Rab3	Ribosomal ostomator transport factor p115	P0DJD8|SEC18	107547	6	7	14%	100.00%	GIEEIGLIR	K	E	40.6	47.3				1043.8202	1,185.64	1,186.64	F	0.99	936	941	TRUE						
Rab7	Dynein-2	P0DJD7|DYNC2H1	156263	16	32	50%	100.00%	GEEIDERLR	K	E	19.1	21.5				1074.0197	143.83	1,325.85	F	0.11	112	127	TRUE						
Rab5C	Ankyrin-repeat domain-containing protein 1	P0DJI8|RFP2	118693	10	32	31	100.00%	GQEIWNLIR	K	E	95.1	106.8				1043.8202	1,386.81	1,386.81	F	0.99	1,000	1,000	TRUE						
Rab5A	Myosin-9	P0DJI9|MYH9	156926	178	279	68%	100.00%	GVDEIQKLKEQIDNIQ	K	E	257	285.2				9976.5019	1368.84	1,369.09	F	0.99	1419	1423	TRUE						
Rab5C	Dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit 2	P0DJB8|RPN2	109860	6	7	14%	100.00%	GEVRSGNFQAGAVVR	K	E	84	93.5				9570.0078	1,758.69	1,759.01	F	0.91	290	296	TRUE						
Rab5	Ribosomal ostomator transport factor p115	P0DJD8|SEC18	107547	6	7	14%	100.00%	GIEEIGLIR	K	E	40.6	47.3				1043.8202	1,185.64	1,186.64	F	0.99	936	941	TRUE						
Rab7	Myosin-9	P0DJI9|MYH9	156926	178	279	68%	100.00%	GVDEIQKLKEQIDNIQ	K	E	257	285.2				9976.5019	1368.84	1,369.09	F	0.99	1419	1423	TRUE						
Rab2	Ankyrin-repeat domain-containing protein 1	P0DJI8|RFP2	118693	10	32	31	100.00%	GQEIWNLIR	K	E	95.1	106.8				1043.8202	1,386.81	1,386.81	F	0.99	1,000	1,000	TRUE						
Rab1	Dynein-2	P0DJD7|DYNC2H1	156263	16	32	50%	100.00%	GEEIDERLR	K	E	19.1	21.5				1074.0197	143.83	1,325.85	F	0.11	112	127	TRUE						
Rab3	Ankyrin-repeat domain-containing protein 1	P0DJI8|RFP2	118693	10	32	31	100.00%	GQEIWNLIR	K	E	95.1	106.8			MT: Oxidation (+15.99)	1043.8202	1,386.81	1,386.81	F	0.99	1,000	1,000	TRUE						
Rab5	Myosin-9	P0DJI9|MYH9	156926	178	279	68%	100.00%	GVDEIQKLKEQIDNIQ	K	E	257	285.2				9976.5019	1368.84	1,369.09	F	0.99	1419	1423	TRUE						
Rab8	Myosin-9	P0DJI9|MYH9	156926	178	279	68%	100.00%	GVDEIQKLKEQIDNIQ	K	E	257	285.2				9976.5019	1368.84	1,369.09	F	0.99	1419	1423	TRUE						
Rab9	Ankyrin-repeat domain-containing protein 1	P0DJI8|RFP2	118693	10	32	31	100.00%	GQEIWNLIR	K	E	95.1	106.8				1043.8202	1,386.81	1,386.81	F	0.99	1,000	1,000	TRUE						
Rab11A	Dynein-2	P0DJD7|DYNC2H1	156263	16	32	50%	100.00%	GEEIDERLR	K	E	19.1	21.5				1074.0197	143.83	1,325.85	F	0.11	112	127	TRUE						
Rab11B	Ribosome-binding protein 1	P0DJD8|RRBP1	114693	10	32	31	100.00%	GQEIWNLIR	K	E	95.1	106.8				1043.8202	1,386.81	1,386.81	F	0.99	1,000	1,000	TRUE						
Rab11	Ribosome-binding protein 1	P0DJD8|RRBP1	114693	10	32	31	100.00%	GQEIWNLIR	K	E	95.1	106.8				1043.8202	1,386.81	1,386.81	F	0.99	1,000	1,000	TRUE						
Rab11B	Ankyrin-repeat domain-containing protein 1	P0DJI8|RFP2	118693	10	32	31	100.00%	GQEIWNLIR	K	E	95.1	106.8				1043.8202	1,386.81	1,386.81	F	0.99	1,000	1,000	TRUE						
Rab5	Myosin-9	P0DJI9|MYH9	156926	178	279	68%	100.00%	GVDEIQKLKEQIDNIQ	K	E	257	285.2				9976.5019	1368.84	1,369.09	F	0.99	1419	1423	TRUE						
Rab8	Myosin-9	P0DJI9|MYH9	156926	178	279	68%	100.00%	GVDEIQKLKEQIDNIQ	K	E	257	285.2				9976.5019	1368.84	1,369.09	F	0.99	1419	1423	TRUE						
Rab11	Ribosome-binding protein 1	P0DJD8|RRBP1	114693	10	32	31	100.00%	GQEIWNLIR	K	E	95.1	106.8				1043.8202	1,386.81	1,386.81	F	0.99	1,000	1,000	TRUE						
Rab11B	Ribosome-binding protein 1	P0DJD8	RRBP1	114

Ccl2	Chemokine (motif) ligand 2	P0C0W8	110340	15	51	84	0.000%	MKAGQIGAFVSFTPR	K		66.1	18.9			GGI-Phosphe (+79.97)	779.4009	1.00E-04	5.00E-05	F	0.00	1326	1326	VALID		
Ccl7	Chemokine (motif) ligand 7	P0C0W9	110341	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	18.9				779.4009	1.00E-04	5.00E-05	F	0.00	1377	1377	VALID		
Gapdh	Glyceraldehyde 3-phosphate dehydrogenase	P0C0W5	70005	15	51	84	0.000%	VDSVVDLTCRVDKVE	K		45.4	18.6				606.9157	1.27E-03	1.27E-03	F	0.00	1377	1378	VALID		
Ccl3a1	Scyllatoxin alpha-1(1)-chain	P0C0B9(1)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27				1004.5609	9.57E-05	9.57E-05	F	0.00	1391	1392	VALID		
Ccl3a2	Scyllatoxin alpha-2(1)-chain	P0C0B9(2)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27				1004.5609	9.57E-05	9.57E-05	F	0.00	1392	1393	VALID		
Ccl4	Chemokine (motif) ligand 4	P0C0W6	110342	15	51	84	0.000%	MKLGVALVVLVLIFR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1417	1418	VALID		
Gnb2	Guanine nucleotide-binding protein, beta-2	P0C0W4	110338	15	51	84	0.000%	MKEMEQLTQEAELAE	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1418	1419	VALID		
Ccl5	Chemokine (motif) ligand 5	P0C0W7	110343	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1420	1421	VALID		
Ccl3	Chemokine (motif) ligand 3	P0C0W3	110339	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1421	1422	VALID		
Ccl2	Chemokine (motif) ligand 2	P0C0W8	110340	15	51	84	0.000%	MKAGQIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1422	1423	VALID		
Ccl7	Chemokine (motif) ligand 7	P0C0W9	110341	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1423	1424	VALID		
Ccl4	Chemokine (motif) ligand 4	P0C0W6	110342	15	51	84	0.000%	MKLGVALVVLVLIFR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1424	1425	VALID		
Ccl5	Chemokine (motif) ligand 5	P0C0W7	110343	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1425	1426	VALID		
Ccl3	Chemokine (motif) ligand 3	P0C0W3	110339	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1426	1427	VALID		
Gnb2	Guanine nucleotide-binding protein, beta-2	P0C0W4	110338	15	51	84	0.000%	MKEMEQLTQEAELAE	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1427	1428	VALID		
Ccl3a1	Scyllatoxin alpha-1(1)-chain	P0C0B9(1)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1428	1429	VALID		
Ccl3a2	Scyllatoxin alpha-2(1)-chain	P0C0B9(2)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1429	1430	VALID		
Ccl4	Chemokine (motif) ligand 4	P0C0W6	110342	15	51	84	0.000%	MKLGVALVVLVLIFR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1430	1431	VALID		
Ccl5	Chemokine (motif) ligand 5	P0C0W7	110343	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1431	1432	VALID		
Ccl3	Chemokine (motif) ligand 3	P0C0W3	110339	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1432	1433	VALID		
Ccl2	Chemokine (motif) ligand 2	P0C0W8	110340	15	51	84	0.000%	MKAGQIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1433	1434	VALID		
Ccl7	Chemokine (motif) ligand 7	P0C0W9	110341	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1434	1435	VALID		
Ccl4	Chemokine (motif) ligand 4	P0C0W6	110342	15	51	84	0.000%	MKLGVALVVLVLIFR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1435	1436	VALID		
Ccl5	Chemokine (motif) ligand 5	P0C0W7	110343	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1436	1437	VALID		
Ccl3	Chemokine (motif) ligand 3	P0C0W3	110339	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1437	1438	VALID		
Gnb2	Guanine nucleotide-binding protein, beta-2	P0C0W4	110338	15	51	84	0.000%	MKEMEQLTQEAELAE	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1438	1439	VALID		
Ccl3a1	Scyllatoxin alpha-1(1)-chain	P0C0B9(1)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1439	1440	VALID		
Ccl3a2	Scyllatoxin alpha-2(1)-chain	P0C0B9(2)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1440	1441	VALID		
Ccl4	Chemokine (motif) ligand 4	P0C0W6	110342	15	51	84	0.000%	MKLGVALVVLVLIFR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1441	1442	VALID		
Ccl5	Chemokine (motif) ligand 5	P0C0W7	110343	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1442	1443	VALID		
Ccl3	Chemokine (motif) ligand 3	P0C0W3	110339	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1443	1444	VALID		
Ccl2	Chemokine (motif) ligand 2	P0C0W8	110340	15	51	84	0.000%	MKAGQIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1444	1445	VALID		
Ccl7	Chemokine (motif) ligand 7	P0C0W9	110341	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1445	1446	VALID		
Ccl4	Chemokine (motif) ligand 4	P0C0W6	110342	15	51	84	0.000%	MKLGVALVVLVLIFR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1446	1447	VALID		
Ccl5	Chemokine (motif) ligand 5	P0C0W7	110343	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1447	1448	VALID		
Ccl3	Chemokine (motif) ligand 3	P0C0W3	110339	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1448	1449	VALID		
Gnb2	Guanine nucleotide-binding protein, beta-2	P0C0W4	110338	15	51	84	0.000%	MKEMEQLTQEAELAE	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1449	1450	VALID		
Ccl3a1	Scyllatoxin alpha-1(1)-chain	P0C0B9(1)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1450	1451	VALID		
Ccl3a2	Scyllatoxin alpha-2(1)-chain	P0C0B9(2)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1451	1452	VALID		
Ccl4	Chemokine (motif) ligand 4	P0C0W6	110342	15	51	84	0.000%	MKLGVALVVLVLIFR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1452	1453	VALID		
Ccl5	Chemokine (motif) ligand 5	P0C0W7	110343	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1453	1454	VALID		
Ccl3	Chemokine (motif) ligand 3	P0C0W3	110339	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1454	1455	VALID		
Gnb2	Guanine nucleotide-binding protein, beta-2	P0C0W4	110338	15	51	84	0.000%	MKEMEQLTQEAELAE	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1455	1456	VALID		
Ccl3a1	Scyllatoxin alpha-1(1)-chain	P0C0B9(1)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1456	1457	VALID		
Ccl3a2	Scyllatoxin alpha-2(1)-chain	P0C0B9(2)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1457	1458	VALID		
Ccl4	Chemokine (motif) ligand 4	P0C0W6	110342	15	51	84	0.000%	MKLGVALVVLVLIFR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1458	1459	VALID		
Ccl5	Chemokine (motif) ligand 5	P0C0W7	110343	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1459	1460	VALID		
Ccl3	Chemokine (motif) ligand 3	P0C0W3	110339	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1460	1461	VALID		
Gnb2	Guanine nucleotide-binding protein, beta-2	P0C0W4	110338	15	51	84	0.000%	MKEMEQLTQEAELAE	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1461	1462	VALID		
Ccl3a1	Scyllatoxin alpha-1(1)-chain	P0C0B9(1)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1462	1463	VALID		
Ccl3a2	Scyllatoxin alpha-2(1)-chain	P0C0B9(2)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1463	1464	VALID		
Ccl4	Chemokine (motif) ligand 4	P0C0W6	110342	15	51	84	0.000%	MKLGVALVVLVLIFR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1464	1465	VALID		
Ccl5	Chemokine (motif) ligand 5	P0C0W7	110343	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1465	1466	VALID		
Ccl3	Chemokine (motif) ligand 3	P0C0W3	110339	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1466	1467	VALID		
Gnb2	Guanine nucleotide-binding protein, beta-2	P0C0W4	110338	15	51	84	0.000%	MKEMEQLTQEAELAE	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1467	1468	VALID		
Ccl3a1	Scyllatoxin alpha-1(1)-chain	P0C0B9(1)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1468	1469	VALID		
Ccl3a2	Scyllatoxin alpha-2(1)-chain	P0C0B9(2)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1469	1470	VALID		
Ccl4	Chemokine (motif) ligand 4	P0C0W6	110342	15	51	84	0.000%	MKLGVALVVLVLIFR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1470	1471	VALID		
Ccl5	Chemokine (motif) ligand 5	P0C0W7	110343	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1471	1472	VALID		
Ccl3	Chemokine (motif) ligand 3	P0C0W3	110339	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1472	1473	VALID		
Gnb2	Guanine nucleotide-binding protein, beta-2	P0C0W4	110338	15	51	84	0.000%	MKEMEQLTQEAELAE	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1473	1474	VALID		
Ccl3a1	Scyllatoxin alpha-1(1)-chain	P0C0B9(1)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1474	1475	VALID		
Ccl3a2	Scyllatoxin alpha-2(1)-chain	P0C0B9(2)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1475	1476	VALID		
Ccl4	Chemokine (motif) ligand 4	P0C0W6	110342	15	51	84	0.000%	MKLGVALVVLVLIFR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1476	1477	VALID		
Ccl5	Chemokine (motif) ligand 5	P0C0W7	110343	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1477	1478	VALID		
Ccl3	Chemokine (motif) ligand 3	P0C0W3	110339	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1478	1479	VALID		
Gnb2	Guanine nucleotide-binding protein, beta-2	P0C0W4	110338	15	51	84	0.000%	MKEMEQLTQEAELAE	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1479	1480	VALID		
Ccl3a1	Scyllatoxin alpha-1(1)-chain	P0C0B9(1)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1480	1481	VALID		
Ccl3a2	Scyllatoxin alpha-2(1)-chain	P0C0B9(2)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1481	1482	VALID		
Ccl4	Chemokine (motif) ligand 4	P0C0W6	110342	15	51	84	0.000%	MKLGVALVVLVLIFR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1482	1483	VALID		
Ccl5	Chemokine (motif) ligand 5	P0C0W7	110343	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1483	1484	VALID		
Ccl3	Chemokine (motif) ligand 3	P0C0W3	110339	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1484	1485	VALID		
Gnb2	Guanine nucleotide-binding protein, beta-2	P0C0W4	110338	15	51	84	0.000%	MKEMEQLTQEAELAE	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1485	1486	VALID		
Ccl3a1	Scyllatoxin alpha-1(1)-chain	P0C0B9(1)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1486	1487	VALID		
Ccl3a2	Scyllatoxin alpha-2(1)-chain	P0C0B9(2)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1487	1488	VALID		
Ccl4	Chemokine (motif) ligand 4	P0C0W6	110342	15	51	84	0.000%	MKLGVALVVLVLIFR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1488	1489	VALID		
Ccl5	Chemokine (motif) ligand 5	P0C0W7	110343	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1489	1490	VALID		
Ccl3	Chemokine (motif) ligand 3	P0C0W3	110339	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1490	1491	VALID		
Gnb2	Guanine nucleotide-binding protein, beta-2	P0C0W4	110338	15	51	84	0.000%	MKEMEQLTQEAELAE	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1491	1492	VALID		
Ccl3a1	Scyllatoxin alpha-1(1)-chain	P0C0B9(1)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1492	1493	VALID		
Ccl3a2	Scyllatoxin alpha-2(1)-chain	P0C0B9(2)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1493	1494	VALID		
Ccl4	Chemokine (motif) ligand 4	P0C0W6	110342	15	51	84	0.000%	MKLGVALVVLVLIFR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1494	1495	VALID		
Ccl5	Chemokine (motif) ligand 5	P0C0W7	110343	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1495	1496	VALID		
Ccl3	Chemokine (motif) ligand 3	P0C0W3	110339	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1496	1497	VALID		
Gnb2	Guanine nucleotide-binding protein, beta-2	P0C0W4	110338	15	51	84	0.000%	MKEMEQLTQEAELAE	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1497	1498	VALID		
Ccl3a1	Scyllatoxin alpha-1(1)-chain	P0C0B9(1)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1498	1499	VALID		
Ccl3a2	Scyllatoxin alpha-2(1)-chain	P0C0B9(2)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1499	1500	VALID		
Ccl4	Chemokine (motif) ligand 4	P0C0W6	110342	15	51	84	0.000%	MKLGVALVVLVLIFR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1500	1501	VALID		
Ccl5	Chemokine (motif) ligand 5	P0C0W7	110343	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1501	1502	VALID		
Ccl3	Chemokine (motif) ligand 3	P0C0W3	110339	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1502	1503	VALID		
Gnb2	Guanine nucleotide-binding protein, beta-2	P0C0W4	110338	15	51	84	0.000%	MKEMEQLTQEAELAE	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1503	1504	VALID		
Ccl3a1	Scyllatoxin alpha-1(1)-chain	P0C0B9(1)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1504	1505	VALID		
Ccl3a2	Scyllatoxin alpha-2(1)-chain	P0C0B9(2)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1505	1506	VALID		
Ccl4	Chemokine (motif) ligand 4	P0C0W6	110342	15	51	84	0.000%	MKLGVALVVLVLIFR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1506	1507	VALID		
Ccl5	Chemokine (motif) ligand 5	P0C0W7	110343	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1507	1508	VALID		
Ccl3	Chemokine (motif) ligand 3	P0C0W3	110339	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1508	1509	VALID		
Gnb2	Guanine nucleotide-binding protein, beta-2	P0C0W4	110338	15	51	84	0.000%	MKEMEQLTQEAELAE	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1509	1510	VALID		
Ccl3a1	Scyllatoxin alpha-1(1)-chain	P0C0B9(1)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1510	1511	VALID		
Ccl3a2	Scyllatoxin alpha-2(1)-chain	P0C0B9(2)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1511	1512	VALID		
Ccl4	Chemokine (motif) ligand 4	P0C0W6	110342	15	51	84	0.000%	MKLGVALVVLVLIFR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1512	1513	VALID		
Ccl5	Chemokine (motif) ligand 5	P0C0W7	110343	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1513	1514	VALID		
Ccl3	Chemokine (motif) ligand 3	P0C0W3	110339	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1514	1515	VALID		
Gnb2	Guanine nucleotide-binding protein, beta-2	P0C0W4	110338	15	51	84	0.000%	MKEMEQLTQEAELAE	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1515	1516	VALID		
Ccl3a1	Scyllatoxin alpha-1(1)-chain	P0C0B9(1)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1516	1517	VALID		
Ccl3a2	Scyllatoxin alpha-2(1)-chain	P0C0B9(2)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1517	1518	VALID		
Ccl4	Chemokine (motif) ligand 4	P0C0W6	110342	15	51	84	0.000%	MKLGVALVVLVLIFR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1518	1519	VALID		
Ccl5	Chemokine (motif) ligand 5	P0C0W7	110343	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1519	1520	VALID		
Ccl3	Chemokine (motif) ligand 3	P0C0W3	110339	15	51	84	0.000%	MKAGLIGAFVSFTPR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1520	1521	VALID		
Gnb2	Guanine nucleotide-binding protein, beta-2	P0C0W4	110338	15	51	84	0.000%	MKEMEQLTQEAELAE	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1521	1522	VALID		
Ccl3a1	Scyllatoxin alpha-1(1)-chain	P0C0B9(1)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1522	1523	VALID		
Ccl3a2	Scyllatoxin alpha-2(1)-chain	P0C0B9(2)	109147	15	51	84	0.000%	MKNIFVAFLR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1523	1524	VALID		
Ccl4	Chemokine (motif) ligand 4	P0C0W6	110342	15	51	84	0.000%	MKLGVALVVLVLIFR	K		66.1	27.7				1117.6509	1.00E-04	5.00E-05	F	0.00	1524	1525	VALID		
Ccl5	Chemokine (motif) ligand 5	P0C0W7	110343	15	51	84	0.

Ccs	Copaborn	P0DP0H0W0,P0DP0H1L0	80484	G	G	G	G	0.00%	RGGDGCVCGD	K			86.9	105.3				8307.0808	1103.96	1,104.07	F	0.00	1803	1805	VALUE						
Ppp1r7	Phosphatase binding protein 7	P0DJI8,P0DJI9	50463	G	G	G	G	0.00%	GGGGGGGGGGGR	K			49.2	52.4				8562.9666	1127.51	1,128.51	F	0.00	1804	1806	VALUE						
Gpr17	Isoform 2 of Transmembrane beta-sheet	P0DJB7,P11	12561	G	G	G	G	0.00%	GGGGRRVFFR	K			29.7	35.4				9278.8006	1303.65	1,304.69	F	0.00	1806	1808	VALUE						
Ccdc47	Coiled-coil domain-containing protein 47	P0DJB7,P11	63943	G	G	G	G	0.00%	GGGGGGGGGGGR	K			62.0	69.1				8.6E+05	1304.69	1,305.69	F	0.00	1808	1810	VALUE						
Spns1l	Sympin-1	P0DJY3,P0DJ	130164	G	G	G	G	0.00%	GGGGRRVFFVDVDDR	K			66.6	74.5				8771.3283	1310.99	1,311.00	F	0.00	1809	1811	VALUE						
Ccl5a1	Chaperonin, type 1, alpha 1	P0DJB4,P0	147799	G	G	G	G	0.00%	GGGGRRVFLR	K			66.1	75.5				7798.0127	1315.83	1,315.85	F	0.00	1809	1811	VALUE						
Ccnno2	RCNA1280, isoform CRA_a	P0DJD0,P0	77802	G	G	G	G	0.00%	GGGGGGRRGGGLLR	K			35.8	38.8				6691.0332	1362.86	1,363.98	F	0.07	1808	1815	VALUE						
Ccl5	Chaperonin, type 1, alpha 1	P0DJB4,P0	147799	G	G	G	G	0.00%	GGGGRRVFLR	K			66.1	75.5				7798.0127	1315.83	1,315.85	F	0.00	1809	1811	VALUE						
Ccl2	Kinesin-like protein subfamily 1	P0DJD3,P0	130432	G	G	G	G	0.00%	GGGGGGGGGGGR	K			60.0	65.1				9166.6609	1364.71	1,365.73	F	0.00	1809	1811	VALUE						
Ccl7	CBDTb	P0DJD4,P0	130432	G	G	G	G	0.00%	GGGGGGGGGGGR	K			60.0	65.1				9163.6775	1365.73	1,366.74	F	0.00	1810	1812	VALUE						
Ccl8	Kinesin 5	P0DJD5,P0	113868	G	G	G	G	0.00%	GGGGTTGR	K			59.6	67.9				8663.3775	1365.92	1,366.94	F	0.00	1810	1812	VALUE						
Ccl1a1	Collagen, type 1, alpha 1	P0DJD6,P0	117936	G	G	G	G	0.00%	GGGGGRR	K			63.6	69.3				5961.8202	1366.66	1,367.66	F	0.00	1326	1335	VALUE						
Ccl1a2	Kinesin 14	P0DJD7,P0	113870	G	G	G	G	0.00%	GGGGGRR	K			63.6	69.3				5911.7882	1371.66	1,372.65	F	0.00	1326	1335	VALUE						
Ccl3	Kinesin 2	P0DJD8,P0	113870	G	G	G	G	0.00%	GGGGGRR	K			63.6	69.3				5917.7882	1371.66	1,372.65	F	0.00	1327	1336	VALUE						
Ccl4	Kinesin-like protein KIF20A	P0DJD9,P0	113870	G	G	G	G	0.00%	GGGGGRR	K			63.6	69.3				5917.7882	1371.66	1,372.65	F	0.00	1327	1336	VALUE						
Ccl11	Kinesin 3 heavy chain	P0DJE0,P0	109111	G	G	G	G	0.00%	GGGGTGGRVGR	K			59.1	64.6				7741.6755	1401.75	1,402.76	F	0.00	1345	1356	VALUE						
Ccl2b1b1	Kinesin-like protein KIF3B isoa	P0DJE7,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				7914.6798	1526.74	1,527.75	F	0.00	1507	1518	VALUE						
Ccl2b2	Cytokine-like Nimnaline 5	P0DJE8,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8168.9196	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b3	cytokine-like Nimnaline 5	P0DJE9,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b4	cytokine-like Nimnaline 5	P0DJF0,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b5	cytokine-like Nimnaline 5	P0DJF1,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b6	cytokine-like Nimnaline 5	P0DJF2,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b7	cytokine-like Nimnaline 5	P0DJF3,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b8	cytokine-like Nimnaline 5	P0DJF4,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b9	cytokine-like Nimnaline 5	P0DJF5,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b10	cytokine-like Nimnaline 5	P0DJF6,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b11	cytokine-like Nimnaline 5	P0DJF7,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b12	cytokine-like Nimnaline 5	P0DJF8,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b13	cytokine-like Nimnaline 5	P0DJF9,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b14	cytokine-like Nimnaline 5	P0DJG0,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b15	cytokine-like Nimnaline 5	P0DJG1,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b16	cytokine-like Nimnaline 5	P0DJG2,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b17	cytokine-like Nimnaline 5	P0DJG3,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b18	cytokine-like Nimnaline 5	P0DJG4,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b19	cytokine-like Nimnaline 5	P0DJG5,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b20	cytokine-like Nimnaline 5	P0DJG6,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b21	cytokine-like Nimnaline 5	P0DJG7,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b22	cytokine-like Nimnaline 5	P0DJG8,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b23	cytokine-like Nimnaline 5	P0DJG9,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b24	cytokine-like Nimnaline 5	P0DJH0,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b25	cytokine-like Nimnaline 5	P0DJH1,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b26	cytokine-like Nimnaline 5	P0DJH2,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b27	cytokine-like Nimnaline 5	P0DJH3,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b28	cytokine-like Nimnaline 5	P0DJH4,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b29	cytokine-like Nimnaline 5	P0DJH5,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b30	cytokine-like Nimnaline 5	P0DJH6,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b31	cytokine-like Nimnaline 5	P0DJH7,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b32	cytokine-like Nimnaline 5	P0DJH8,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b33	cytokine-like Nimnaline 5	P0DJH9,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b34	cytokine-like Nimnaline 5	P0DJI0,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b35	cytokine-like Nimnaline 5	P0DJI1,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b36	cytokine-like Nimnaline 5	P0DJI2,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b37	cytokine-like Nimnaline 5	P0DJI3,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b38	cytokine-like Nimnaline 5	P0DJI4,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b39	cytokine-like Nimnaline 5	P0DJI5,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b40	cytokine-like Nimnaline 5	P0DJI6,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b41	cytokine-like Nimnaline 5	P0DJI7,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b42	cytokine-like Nimnaline 5	P0DJI8,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b43	cytokine-like Nimnaline 5	P0DJI9,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b44	cytokine-like Nimnaline 5	P0DJJ0,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b45	cytokine-like Nimnaline 5	P0DJJ1,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b46	cytokine-like Nimnaline 5	P0DJJ2,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b47	cytokine-like Nimnaline 5	P0DJJ3,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b48	cytokine-like Nimnaline 5	P0DJJ4,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b49	cytokine-like Nimnaline 5	P0DJJ5,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b50	cytokine-like Nimnaline 5	P0DJJ6,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b51	cytokine-like Nimnaline 5	P0DJJ7,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b52	cytokine-like Nimnaline 5	P0DJJ8,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b53	cytokine-like Nimnaline 5	P0DJJ9,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b54	cytokine-like Nimnaline 5	P0DJK0,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b55	cytokine-like Nimnaline 5	P0DJK1,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b56	cytokine-like Nimnaline 5	P0DJK2,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b57	cytokine-like Nimnaline 5	P0DJK3,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b58	cytokine-like Nimnaline 5	P0DJK4,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b59	cytokine-like Nimnaline 5	P0DJK5,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b60	cytokine-like Nimnaline 5	P0DJK6,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b61	cytokine-like Nimnaline 5	P0DJK7,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b62	cytokine-like Nimnaline 5	P0DJK8,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b63	cytokine-like Nimnaline 5	P0DJK9,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b64	cytokine-like Nimnaline 5	P0DJL0,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b65	cytokine-like Nimnaline 5	P0DJL1,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b66	cytokine-like Nimnaline 5	P0DJL2,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b67	cytokine-like Nimnaline 5	P0DJL3,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b68	cytokine-like Nimnaline 5	P0DJL4,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b69	cytokine-like Nimnaline 5	P0DJL5,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b70	cytokine-like Nimnaline 5	P0DJL6,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b71	cytokine-like Nimnaline 5	P0DJL7,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b72	cytokine-like Nimnaline 5	P0DJL8,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b73	cytokine-like Nimnaline 5	P0DJL9,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b74	cytokine-like Nimnaline 5	P0DJM0,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b75	cytokine-like Nimnaline 5	P0DJM1,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b76	cytokine-like Nimnaline 5	P0DJM2,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b77	cytokine-like Nimnaline 5	P0DJM3,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b78	cytokine-like Nimnaline 5	P0DJM4,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b79	cytokine-like Nimnaline 5	P0DJM5,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b80	cytokine-like Nimnaline 5	P0DJM6,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b81	cytokine-like Nimnaline 5	P0DJM7,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b82	cytokine-like Nimnaline 5	P0DJM8,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b83	cytokine-like Nimnaline 5	P0DJM9,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b84	cytokine-like Nimnaline 5	P0DJN0,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b85	cytokine-like Nimnaline 5	P0DJN1,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b86	cytokine-like Nimnaline 5	P0DJN2,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b87	cytokine-like Nimnaline 5	P0DJN3,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b88	cytokine-like Nimnaline 5	P0DJN4,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b89	cytokine-like Nimnaline 5	P0DJN5,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b90	cytokine-like Nimnaline 5	P0DJN6,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b91	cytokine-like Nimnaline 5	P0DJN7,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b92	cytokine-like Nimnaline 5	P0DJN8,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b93	cytokine-like Nimnaline 5	P0DJN9,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b94	cytokine-like Nimnaline 5	P0DJO0,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b95	cytokine-like Nimnaline 5	P0DJO1,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b96	cytokine-like Nimnaline 5	P0DJO2,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b97	cytokine-like Nimnaline 5	P0DJO3,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00	1507	1519	VALUE						
Ccl2b98	cytokine-like Nimnaline 5	P0DJO4,P0	93248	G	G	G	G	0.00%	GGTGGGGRGLGR	K			57.1	63				8.0E+05	1574.63	1,575.65	F	0.00

Sec61	Sec61 beta-fulfilled protein beta in complexes	P60470/P61	60774	5	5	0	0	100%	PIGUPSFQVK	K	K	16.7	18.4			9960.6813	1.13 E-5	1.12 E-05	0.23	686	675	FALSE		
Sec61A1	Sec61 alpha 1	P61619/Q9	61700	6	6	0	0	100%	TTGTLLLLLGLGLR	K	K	7.5	8.4		MS: Oxidation (+15.99)	1361.9966	1.34 E-5	1.34 E-05	0.27	1132	1121	FALSE		
Sec61A2	Sec61 alpha subunit isoform alpha-2	P55735/Q96	61369	6	6	0	0	100%	CYVVLLLR	K	K	16	17.8			1008.7329	1.71 E-5	1.71 E-05	0.28	1322	1315	FALSE		
Sec61B	Sec61b, type II protein beta 1	P60953/P62	12.3	3.6	3.6	0.6	0.6	100%	DYVNFIMEV	K	K	19.5	19.7		MS: Oxidation (+15.99)	1049.5195	1.29 E-5	1.28 E-05	0.21	1212	1211	FALSE		
Sec61G	Sec61g, type II protein beta 1	P60953/Q13	11.9	3.8	3.8	0.6	0.6	100%	TTVNFIMFVMVAV	K	K	19.6	19.6		MS: Oxidation (+15.99)	976.2674	1.25 E-5	1.24 E-05	0.07	260	271	FALSE		
Sec31a	Sec31a 1 of Protein transport protein Sec31A	P53378/O75	115.9	2	2	0	0	100%	TFEEILLLR	K	K	1.1	1.1			1061.7962	1.11 E-5	1.11 E-05	0.19	1130	1131	FALSE		
Sec62	Translocon nucleotide-binding protein 62G, alpha-2 subunit	P60033/O15	61601	6	6	0	0	100%	TTGAEIMTTFA	K	K	16.9	16.2			1003.9657	1.19 E-5	1.18 E-05	0.18	1182	1192	FALSE		
Sec63	Sec63 homolog (S. cerevisiae)	P61969/Q9	93.1	3	3	0	0	100%	TTLLLLLLLLLLLPGPVGFGLFVGLFVGLFVGLFNGAVR	K	K	1.1	1.1		MS: Oxidation (+15.99)	3.2 E+06	1.19 E-5	1.19 E-05	0.23	1177	1176	FALSE	P38067-2	
Sec8	Sec8a, isoform 1	P30926/P38	91.7	3	3	0	0	100%	LLNAEIQSSGCTVTVPTCEDAQTNAQLR	K	K	1.1	1.1		MS: Oxidation (+15.99)	3.1 E+06	1.19 E-5	1.19 E-05	0.23	1176	1177	FALSE		
Sdf2	Sdf2-like protein	P35251/Q9	15.8	2.9	2.9	0.5	0.5	100%	CYVPFQR	K	K	15.4	17.6			1017.7201	9.5 E-06	9.5 E-06	0.23	1109	1103	FALSE		
Sdf2l2	Sdf2-like protein	P35251/Q9	15.8	2.9	2.9	0.5	0.5	100%	TTLEEFLLRTTLLAEAF	K	K	19.1	19.1			1997.9895	1.79 E-5	1.79 E-05	0.23	1170	1163	FALSE		
Sdh	Phosphatidylinositol 3 kinase, regulatory subunit, alpha/beta/delta 1, isoform CRA_a	P42336/E9	61251	16	16	16	16	100%	TTLFSAVVK	K	K	35.9	35.2			1031.7386	9.6 E-06	9.6 E-06	0.11	108	175	FALSE		
Sdpr2	Serum 70 protein, mitochondrial	P53396/Q5	43.6	4	4	0	0	100%	TTFVAAATTFEGER	K	K	7.1	10.8			1734.8725	1.47 E-5	1.47 E-05	0.19	186	185	FALSE		
Sdr9c7	Short chain dehydrogenase 7 1 isoform 1	P49753/Q96	35.9	3	3	0	0	100%	TTLLTTLLTTLLT

Cacng8	Voltage-gated calcium channel gamma-8 subunit	P62955|P48617	111845	0	0	0	0.00%	KYTSLDPVSYSVQLRLR	K	K	42	45.7	0		1764.1714	1,381.92	1,391.20	0	0.28	1511	1510	TRUE	
Cacng4	Voltage-gated calcium channel gamma-4 subunit	P62955|P48651	111511	0	0	0	0.00%	KYTSLDPVSYSVQLRLR	K	K	42	45.7	0		1811.9344	1,381.92	1,392.58	0	0.28	1110	1109	TRUE	
Ptk7	Inactive tyrosine-protein kinase 7	P34925|P48962	131160	0	0	0	0.00%	GPGSTMGFSPVLTQEIEAVGAGEVLIAR	K	K	45.5	55.5	0	MT: Oxidation (+15.99); Phosphorylation (+79.97)	3,324.77	2,202.22	2,201.23	0	0.72	689	705	TRUE	
Ptk7	Inactive tyrosine-protein kinase 7	P34925|P48962	131160	10	10	100	90.90%	GPGSTMGFSPVLTQEIEAVGAGEVLIAR	K	K	45.5	55.5	0	MT: Oxidation (+15.99); MS: Phosphorylation (+79.97)	3,324.77	2,202.22	2,201.23	0	0.72	689	705	TRUE	
Ncs1	Neuronal calcium sensor 1	P62166|P62162	191560	10	10	100	90.90%	KPAGTMAGFSPAQTQEIKAGAGEVLDMR	K	K	73.6	71.7	0	Phosphorylation (+79.97)	3011.0707	2,700.20	2,701.19	0	0.19	189	215	TRUE	
Ccr1	C-C chemokine receptor type 1	P35454|P51679|P51677	67721	0	0	0	0.00%	KYTSSLLILQCTR	K	K	35.6	36.3	0		1710.8767	1,426.73	1,426.74	0	0.06	179	191	TRUE	
Ppp1r1a	DARPP-32 family of cAMP-dependent protein kinase inhibitors	P63329|P63330	117855	10	10	100	90.90%	KRQPTTGLGLK	K	K	61.1	56.8	0		1722.0919	1,462.77	1,469.77	0	0.48	1127	1138	TRUE	
Ptpn1	Tyrosine-protein phosphatase non-receptor type 1	P18031|P18032	19042	10	10	100	90.90%	KAPSGEAANYIRAGPKFKTER	K	K	45.5	45.5	0	MT: Oxidation (+15.99)	3,324.77	2,202.22	2,201.23	0	0.72	689	705	TRUE	
Ccdc124/Ccdc124	Coiled-coil domain-containing protein 124	P60169|P60170|Q5U117	80169	0	0	0	0.00%	CLGRPALCTSR	K	K	55.2	58	0		1042.5206	1,114.61	1,114.60	0	0.08	1331	1321	TRUE	
Myo1b	Isoform 2 of Myosin-Ib	P24331|Q61939|P70570|P70571|P70572|Q61938	110808	0	0	0	0.00%	CVGLLRNLR	K	K	47.2	55.5	0		1030.6211	1,075.62	1,074.61	0	0.10	1328	1316	TRUE	
Ugt1a	Bilirubin UDP-glucuronosyltransferase	P35504|Q64637	114707	10	10	100	90.90%	VLLLWRTGR	K	K	51.2	59.5	0	MT: Oxidation (+15.99)	1042.5909	1,114.57	1,114.58	0	0.16	1120	1111	TRUE	
Ttc3gc	Isoform 9 of Isoform 1 of Tetratricopeptide repeat protein 3	P59019|P59020|P59021|P59022|P59023	56850	0	0	0	0.00%	KQGEFVNNR	K	K	38.7	38.5	0		1039.5297	1,276.66	1,277.66	0	0.59	385	390	TRUE	
Cang2	Calmodulin, gamma 2	P62158|P62.1	56299	0	0	0	0.00%	EVEETVFGDFDFVQSQR	K	K	53	61.5	0		1914.0141	1,763.83	1,765.85	0	0.77	1127	1147	TRUE	
Cadb1a	Cadherin-beta 1A, short	P70587|Q62929	105897	0	0	0	0.00%	KTSGLGAFR	K	K	48.4	52	0		1127.5897	1,252.60	1,253.60	0	0.50	1142	1132	TRUE	
Cdh23	Cadherin-23 (Fragment) OS=Mus musculus GN=Cdh23	Q99PF4	114.1	0	0	0	0.00%	KTSGLGAFR	K	K	48.4	52	0		1127.5897	1,252.60	1,253.60	0	0.50	1142	1132	TRUE	
Cdh8	Cadherin, type 8	P55291|P55292	103915	0	0	0	0.00%	LTSSATVFR	K	K	42.1	54	0		1101.5551	1,268.60	1,269.60	0	0.25	1102	1118	TRUE	
Cdh4/Ncad	CDH2 (Rap-like-Rho-like-Ras-like polypeptide 1, X-linked	P15116|P18138	13130	11	11	100	90.90%	KVLDLDLNGR	K	M	47.1	57.9	0		1147.1853	1,266.54	1,265.55	0	0.21	1303	1311	TRUE	
Cpm5	Carboxypeptidase M	P16150|P15.1	115656	122	106	107	87.00%	LTVTVR	K	R	19.7	25.6	0		850.4537	704.5118	703.4705	0	0.28	71	57	TRUE	
Myo1d	Myosin-Id	P24330|P70469	110361	10	10	100	90.90%	RNDRRSFLK	K	K	28.1	27.9	0	MT: Oxidation (+15.99)	1034.7409	1,207.61	1,208.61	0	0.61	530	573	TRUE	
Myo1d	Myosin-Id	P24330|P70469	110361	10	10	100	90.90%	RNDRRSFLK	K	K	28.1	27.9	0	MT: Oxidation (+15.99)	1034.7409	1,207.61	1,208.61	0	0.61	530	573	TRUE	
Myo1c	Myosin-Ic	P23397|P70460	117757	10	10	100	90.90%	RNDRLQCDR	K	K	23.5	27.9	0	MT: Oxidation (+15.99)	1051.7487	1,207.57	1,208.56	0	0.60	530	573	TRUE	
Myo1c	Myosin-Ic	P23397|P70460	117757	10	10	100	90.90%	RNDRLQCDR	K	K	23.5	27.9	0	MT: Oxidation (+15.99)	1051.7487	1,207.57	1,208.56	0	0.60	530	573	TRUE	
Gnao12	G-protein O	P46087|P59073	110.1512	11	11	100	90.90%	VNDLLQQR	K	K	41.7	47.2	0	MT: Oxidation (+15.99)	1042.7282	1,014.6948	1,015.6921	0	0.39	489	496	TRUE	
Ptprd	Protein tyrosine phosphatase, receptor type, D	P26.0|P80.0	11.5.9	0	0	0	0.00%	VNFGSLVTR	K	K	51.4	55.7	0		1044.5116	1,197.62	1,197.62	0	0.07	1169	1176	TRUE	
Prmt8	Protein arginine methyltransferase 8	P70120|Q9ER.0	51.9.9	0	0	0	0.00%	VNFGSLVTR	K	K	51.4	55.7	0	MT: Oxidation (+15.99)	1044.5116	1,197.62	1,197.62	0	0.07	1169	1176	TRUE	
Prmt8	PRT-10	P70120|Q9ER.0|P60606|P63.7	51.7.5	0	0	0	0.00%	ENLLETNTRGR	K	M	38.1	18.9	0	MT: Oxidation (+15.99); MS: Phosphorylation (+79.97)	1249.6519	1,167.69	1,168.69	0	0.47	1309	1312	TRUE	
Myo1b	Isoform 2 of Myosin-Ib	P24331|Q61939|P70570|P70571|P70572|Q61938	110808	0	0	0	0.00%	VNTLLDSAA	K	K	45.9	55.5	0		1047.2761	1,173.57	1,172.58	0	0.07	1122	1121	TRUE	
Ppp2r5b	Serine/threonine-protein phosphatase PP2 beta catalytic subunit	P63.0|Q63.0	117.7.5	0	0	0	0.00%	VPGNIELLK	K	K	51.4	57	0		1009.6219	1,167.63	1,168.63	0	0.09	1115	1121	TRUE	
Kcnk9	Potassium channel subfamily K member 9	P56550|Q8BX.0	117.7.5	0	0	0	0.00%	SPGNIELLK	K	K	51.4	57	0		1009.6219	1,167.63	1,168.63	0	0.09	1115	1121	TRUE	
Kcnk9	Acidic, alpha-dentinal-matrix	P56550|Q8BX.0	111.9.0	0	0	0	0.00%	KYNLNGTRGNDMDR	K	K	27.4	33.1	0	MT: Oxidation (+15.99)	1666.7825	1,975.90	1,976.91	0	0.38	73	90	TRUE	P35234|Q8K7
Dmp1	Acidic, alpha-dentinal-matrix	P70349|Q8K1.0	11.9.9.4	0	0	0	0.00%	KYNLNGTRGNDMDR	K	K	27.4	33.1	0		1662.7827	1,969.91	1,969.91	0	0.00	71	88	TRUE	P35234|Q8K7
Ppp2r5	Isoform 2 of Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform	P30154|P63.0	11.9.9.9.3	0	0	0	0.00%	VGLLQEFDNR	K	K	42.7	49.5	0	MT: Oxidation (+15.99)	1242.6211	1,383.69	1,384.69	0	0.03	1171	1181	TRUE	
Pdzk1	Isoform pdz1-alpha of Phosphodiesterase 4 DHHC-type containing protein 3	P70157|Q7.0.0	119.1.0	13	13	13	1.17%	VGLDCVVVRSTRERVVSR	K	K	35.1	19.5	0		1914.999	1,961.97	1,962.98	0	0.96	431	477	TRUE	
Pdzk1	Phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha) OS=Mus musculus GN=p_d	P60.0|Q3.0.0.0	11.1.7.1	10	10	11	0.90%	VGDDCVVVRSTRERVAVGEA	K	F	35.8	28.6	0		1935.384	1,243.19	1,243.19	0	0.00	427	451	TRUE	
Cnnm3	Cyclin-M3 OS=Mus musculus GN=Cnnm3	P60.0|Q8.0.0.7.1|P60.0|Q8.0.0.8	11.9.0.0	0	0	0	0.00%	VRGVRDSLGALTRDGLR	K	F	35.5	50.2	0		1962.9766	2,278.11	2,279.12	0	0.14	18	35	TRUE	
Gpr1	Sequestosome-1, alpha-endocrine	P70.0|Q3.0.0.0	11.9.1	11	11	11	0.90%	VRVLAEEAQDR	K	F	37.5	28.8	0		1211.6272	1,260.63	1,261.63	0	0.28	50	70	TRUE	P35234|Q8K
Gpr1	Sequestosome-1, alpha-endocrine	P70.0|Q3.0.0.0	11.9.1	11	11	11	0.90%	VRVLAEEAQDRLAGR	K	K	37.5	27.7	0		1414.2379	1,564.82	1,565.82	0	0.38	53	71	TRUE	P35234|Q8K
Tpm2	Isoform 2 of Tropomyosin beta chain	P70.0|Q8.7.7.0	11.9.1.1	0	0	0	0.00%	VRVVAEQDR	K	K	44	19.6	0		1011.5151	1,262.60	1,261.61	0	0.11	60	79	TRUE	P35234|Q7.7
Tpm2	Isoform 2 of Tropomyosin beta chain	P70.0|Q8.7.7.0	11.9.1.1	0	0	0	0.00%	VRVVAEQDRLLDKV	K	K	44	19.5	0		1411.8161	1,563.87	1,561.87	0	0.26	61	81	TRUE	P35234|Q7.7
Gpr1	Sequestosome-1, alpha-endocrine	P70.0|Q3.0.0.0	11.9.1	11	11	11	0.90%	VRVLAEEAQDRLAGR	K	K	37.5	27.7	0		1414.2379	1,564.82	1,565.82	0	0.38	53	71	TRUE	P35234|Q8K
Gpr1	Sequestosome-1, alpha-endocrine	P70.0|Q3.0.0.0	11.9.1	11	11	11	0.90%	VRVLAEEAQDRLAGRE	K	K	37.5	27.7	0		1543.2379	1,692.83	1,693.83	0	0.38	53	71	TRUE	P35234|Q8K
Tpm2	Isoform 2 of Tropomyosin beta chain	P70.0|Q8.7.7.0	11.9.1.1	0	0	0	0.00%	VRVVAEQDRLLDKVK	K	K	44	19.6	0		1411.5151	1,262.60	1,261.61	0	0.11	60	79	TRUE	P35234|Q7.7
Tpm2	Isoform 2 of Tropomyosin beta chain	P70.0|Q8.7.7.0	11.9.1.1	0	0	0	0.00%	VRVVAEQDRLLDKVKE	K	K	44	19.5	0		1611.8161	1,563.87	1,561.87	0	0.26	61	81	TRUE	P35234|Q7.7
Gpr1	Sequestosome-1, alpha-endocrine	P70.0|Q3.0.0.0	11.9.1	11	11	11	0.90%	VRVLAEEAQDRLAGRE	K	K	37.5	27.7	0		1543.2379	1,692.83	1,693.83	0	0.38	53	71	TRUE	P35234|Q8K
Gpr1	Sequestosome-1, alpha-endocrine	P70.0|Q3.0.0.0	11.9.1	11	11	11	0.90%	VRVLAEEAQDRLAGREL	K	K	37.5	28.2	0		1656.4379	1,807.89	1,808.89	0	0.55	53	71	TRUE	P35234|Q8K
Tpm2	Isoform 2 of Tropomyosin beta chain	P70.0|Q8.7.7.0	11.9.1.1	0	0	0	0.00%	VRVVAEQDRLLDKVKE	K	K	44	19.5	0		1611.8161	1,563.87	1,561.87	0	0.26	61	81	TRUE	P35234|Q7.7
Clp2	CLP-1 like protein	P70.0|Q7.7.7.0	11.1.9.0.2	0	0	0	0.00%	VVGDTTGPLK	K	K	38.1	19.7	0		1171.1.9.0.2	1,118.68	1,119.69	0	0.12	1318	1332	TRUE	
Cnnm3b	Cyclin-M3 isoform, mitochondrial precursor, OS	P70.0|Q7.0.0.0	11.9.0.0	0	0	0	0.00%	VRGVRDSLGALTRDGLR	K	K	35.5	50.7	0	MT: Oxidation (+15.99)	1962.9766	2,247.11	2,248.12	0	0.28	1337	1353	TRUE	
Pacsin2	PACSIN2 SH3 isoform 1 OS=Mus musculus GN=Pacsin2	P70.0|Q8.0.0.0.0	11.7.8.0.1	0	0	0	0.00%	VPVFTDSLPVR	K	F	39.8	28.2	0		1647.9.1.8	1,292.61	1,293.62	0	0.58	1.7.6	1.9.5	TRUE	
Cadb1a	Cadherin-beta 1A, short	P70.0|Q8.9.2.9	11.1.9.0.4	0	0	0	0.00%	VRVTSGAFNR	K	K	41.9	48.7	0	MT: Oxidation (+15.99)	1.9.9.0.4	1,165.75	1,166.75	0	0.86	1.8.5	1.9.5	TRUE	
Cadb1a	Cadherin-beta 1A, short	P70.0|Q8.9.2.9	11.1.9.0.4	0	0	0	0.00%	VRVTSGAFNR	K	K	41.9	48	0		1.9.9.0.4	1,165.75	1,166.75	0	0.86	1.8.5	1.9.5	TRUE	
Cadb1a	Cadherin-beta 1A, short	P70.0|Q8.9.2.9	11.1.9.0.4	0	0	0	0.00%	VRVTSGAFNRE	K	K	41.9	48	0		1.9.9.0.4	1,165.75	1,166.75	0	0.86	1.8.5	1.9.5	TRUE	
Cadb1a	Cadherin-beta 1A, short	P70.0|Q8.9.2.9	11.1.9.0.4	0	0	0	0.00%	VRVTSGAFNREL	K	K	41.9	48	0		1.9.9.0.4	1,165.75	1,166.75	0	0.86	1.8.5	1.9.5	TRUE	
Cadb1a	Cadherin-beta 1A, short	P70.0|Q8.9.2.9	11.1.9.0.4	0	0	0	0.00%	VRVTSGAFNRELL	K	K	41.9	48	0		1.9.9.0.4	1,165.75	1,166.75	0	0.86	1.8.5	1.9.5	TRUE	
Cadb1a	Cadherin-beta 1A, short	P70.0|Q8.9.2.9	11.1.9.0.4	0	0	0	0.00%	VRVTSGAFNRELLK	K	K	41.9	48	0		1.9.9.0.4	1,165.75	1,166.75	0	0.86	1.8.5	1.9.5	TRUE	
Cadb1a	Cadherin-beta 1A, short	P70.0|Q8.9.2.9	11.1.9.0.4	0	0	0	0.00%	VRVTSGAFNRELLKE	K	K	41.9	48	0		1.9.9.0.4	1,165.75	1,166.75	0	0.86	1.8.5	1.9.5	TRUE	
Cadb1a	Cadherin-beta 1A, short	P70.0|Q8.9.2.9	11.1.9.0.4	0	0	0	0.00%	VRVTSGAFNRELLKEL	K	K	41.9	48	0		1.9.9.0.4	1,165.75	1,166.75	0	0.86	1.8.5	1.9.5	TRUE	
Cadb1a	Cadherin-beta 1A, short	P70.0|Q8.9.2.9	11.1.9.0.4	0	0	0	0.00%	VRVTSGAFNRELLKELL	K	K	41.9	48	0		1.9.9.0.4	1,165.75	1,166.75	0	0.86	1.8.5	1.9.5	TRUE	
Cadb1a	Cadherin-beta 1A, short	P70.0|Q8.9.2.9	11.1.9.0.4	0	0	0	0.00%	VRVTSGAFNRELLKELLE	K	K	41.9	48	0		1.9.9.0.4	1,165.75	1,166.75	0	0.86	1.8.5	1.9.5	TRUE	
Cadb1a	Cadherin-beta 1A, short	P70.0|Q8.9.2.9	11.1.9.0.4	0	0	0	0.00%	VRVTSGAFNRELLKELLEL	K	K	41.9	48	0		1.9.9.0.4	1,165.75	1,166.75	0	0.86	1.8.5	1.9.5	TRUE	
Cadb1a	Cadherin-beta 1A, short	P70.0|Q8.9.2.9	11.1.9.0.4	0	0	0	0.00%	VRVTSGAFNRELLKELLEL	K	K	41.9	48	0		1.9.9.0.4	1,165.75	1,166.75	0	0.86	1.8.5	1.9.5	TRUE	
Cacng8	Voltage-gated calcium channel gamma-8 subunit	P62955|P48617	111845	0	0	0	0.00%	KYTSLDPVSYSVQLRLR	K	K	42	45.7	0		1764.1714	1,381.92	1,391.20	0	0.28	1511	1510	TRUE	
Cacng4	Voltage-gated calcium channel gamma-4 subunit	P62955|P48651	111511	0	0	0	0.00%	KYTSLDPVSYSVQLRLR	K	K	42	45.7	0		1811.9344	1,381.92	1,392.58	0	0.28	1110	1109	TRUE	
Ptk7	Inactive tyrosine-protein kinase 7	P34925|P48962	131160	0	0	0	0.00%	GPGSTMGFSPVLTQEIEAVGAGEVLIAR	K	K	45.5	55.5	0	MT: Oxidation (+15.99); Phosphorylation (+79.97)	3,324.77	2,202.22	2,201.23	0	0.72	689	705	TRUE	
Ptk7	Inactive tyrosine-protein kinase 7	P34925|P48962	131160	10	10	100	90.90%	GPGSTMGFSPVLTQEIEAVGAGEVLIAR	K	K	45.5	55.5	0	MT: Oxidation (+15.99); MS: Phosphorylation (+79.97)	3,324.77	2,202.22	2,201.23	0	0.72	689	705	TRUE	
Ncs1	Neuronal calcium sensor 1	P62166|P62162	191560	10	10	100	90.90%	KPAGTMAGFSPAQTQEIKAGAGEVLDMR	K	K	73.6	71.7	0	Phosphorylation (+79.97)	3011.0707	2,700.20	2,701.19	0	0.19	189	215	TRUE	
Ccr1	C-C chemokine receptor type 1	P35454|P51679|P51677	67721	0	0	0	0.00%	KYTSSLLILQCTR	K	K	35.6	36.3	0		1710.8767	1,426.73	1,426.74	0	0.06	179	191	TRUE	
Ppp1r1a	DARPP-32 family of cAMP-dependent protein kinase inhibitors	P63329|P63330	117855	10	10	100	90.90%	KRQPTTGLGLK	K	K	61.1	56.8	0		1722.0919	1,462.77	1,469.77	0	0.48	1127	1138	TRUE	
Ptpn1	Tyrosine-protein phosphatase non-receptor type 1	P18031|P18032	19042	10	10	100	90.90%	KAPSGEAANYIRAGPKFKTER	K	K	45.5	45.5	0	MT: Oxidation (+15.99)	3,324.77	2,202.22	2,201.23	0	0.72	689	705	TRUE	
Ccdc124/Ccdc124	Coiled-coil domain-containing protein 124	P60169|P60170|Q5U117	80169	0	0	0	0.00%	CLGRPALCTSR	K	K	55.2	58	0		1042.5206	1,114.61	1,114.60	0	0.08	1331	1321	TRUE	
Myo1b	Isoform 2 of Myosin-Ib	P24331|Q61939|P70570|P70571|P70572|Q61938	110808	0	0	0	0.00%	CVGLLRNLR	K	K	47.2	55.5	0		1030.6211	1,075.62	1,074.61	0	0.10	1328	1316	TRUE	
Ugt1a	Bilirubin UDP-glucuronosyltransferase	P35504|Q64637	114707	10	10	100	90.90%	VLLLWRTGR	K	K	51.2	59.5	0	MT: Oxidation (+15.99)	1042.5909	1,114.57	1,114.58	0	0.16	1120	1111	TRUE	
Ttc3gc	Isoform 9 of Isoform 1 of Tetratricopeptide repeat protein 3	P59019|P59020|P59021|P59022|P59023	56850	0	0	0	0.00%	KQGEFVNNR	K	K	38.7	38.5	0		1039.5297	1,276.66	1,277.66	0	0.59	385	390	TRUE	
Cang2	Calmodulin, gamma 2	P62158|P62.1	56299	0	0	0	0.00%	EVEETVFGDFDFVQSQR	K	K	53	61.5	0		1914.0141	1,763.83	1,765.85	0	0.77	1127	1147	TRUE	
Cadb1a	Cadherin-beta 1A, short	P70587|Q62929	105897	0	0	0	0.00%	KTSGLGAFR	K	K	48.4	52	0		1127.5897	1,252.60	1,253.60	0	0.50	1142	1132	TRUE	
Cdh23	Cadherin-23 (Fragment) OS=Mus musculus GN=Cdh23	Q99PF4	114.1	0	0	0	0.00%	KTSGLGAFR	K	K	48.4	52	0		1127.5897	1,252.60	1,253.60	0	0.50	1142	1132	TRUE	
Cdh8	Cadherin, type 8	P55291|P55292	103915	0	0	0	0.00%	LTSSATVFR	K	K	42.1	54	0		1101.5551	1,268.60	1,269.60	0	0.25	1102	1118	TRUE	
Cdh4/Ncad	CDH2 (Rap-like-Rho-like-Ras-like polypeptide 1, X-linked	P15116|P18138	13130	11	11	100	90.90%	KVLDLDLNGR	K	M	47.1	57.9	0		1147.1853	1,266.54	1,265.55	0	0.21	1303	1311	TRUE	
Cpm5	Carboxypeptidase M	P16150|P15.1	115656	122	106	107	87.00%	LTVTVR	K	R	19.7	25.6	0		850.4537	704.5118	703.4705	0	0.28	71	57	TRUE	
Myo1d	Myosin-Id	P24330|P70469	110361	10	10	100	90.90%	RNDRRSFLK	K	K	28.1	27.9	0	MT: Oxidation (+15.99)	1034.7409	1,207.61	1,208.61	0	0.61	530	573	TRUE	
Myo1d	Myosin-Id	P24330|P70469	110361	10	10	100	90.90%	RNDRRSFLK	K	K	28.1	27.9	0	MT: Oxidation (+15.99)	1034.7409	1,207.61	1,208.61	0	0.61	530	573	TRUE	
Myo1c	Myosin-Ic	P23397|P70460	117757	10	10	100	90.90%	RNDRLQCDR	K	K	23.5	27.9	0	MT: Oxidation (+15.99)	1051.7487	1,207.57	1,208.56	0	0.60	530	573	TRUE	
Myo1c	Myosin-Ic	P23397|P70460	117757	10	10	100	90.90%	RNDRLQCDR	K	K	23.5	27.9	0	MT: Oxidation (+15.99)	1051.7487	1,207.57	1,208.56	0	0.60	530	573	TRUE	
Gnao12	G-protein O	P46087|P59073	110.1512	11	11	100	90.90%	VNDLLQQR	K	K	41.7	47.2	0	MT: Oxidation (+15.99)	1042.7282	1,014.6948	1,015.6921	0	0.39	489	496	TRUE	
Ptprd	Protein tyrosine phosphatase, receptor type, D	P26.0|P80.0	11.5.9	0	0	0	0.00%	VNFGSLVTR	K	K	51.4	55.7	0		1044.5116	1,197.62	1,197.62	0	0.07	1169	1176	TRUE	
Prmt8	Protein arginine methyltransferase 8	P70120|Q9ER.0	51.9.9	0	0	0	0.00%	VNFGSLVTR	K	K	51.4	55.7	0		1044.5116	1,197.62	1,197.62	0	0.07	1169	1176	TRUE	
Prmt8	PRT-10	P70120|Q9ER.0|P60606|P63.7	51.7.5	0	0	0	0.00%	ENLLETNTRGR	K	M	38.1	18.9	0	MT: Oxidation (+15.99); MS: Phosphorylation (+79.97)	1249.6519	1,167.69	1,168.69	0	0.47	1309	1312	TRUE	
Myo1b	Isoform 2 of Myosin-Ib	P24331|Q61939|P70570|P70571|P70572|Q61938	110808	0	0	0	0.00%	VNTLLDSAA	K	K	45.9	55.5	0		1047.2761	1,173.57	1,172.58	0	0.07	1122	1121	TRUE	
Ppp2r5b	Serine/threonine-protein phosphatase PP2 beta catalytic subunit	P63.0|Q63.0	117.7.5	0	0	0	0.00%	VPGNIELLK	K	K	51.4	57	0		1009.6219	1,167.63	1,168.63	0	0.09	1115	1121	TRUE	
Kcnk9	Potassium channel subfamily K member 9	P56550|Q8BX.0	117.7.5	0	0	0	0.00%	SPGNIELLK	K	K	51.4	57	0		1009.6219	1,167.63	1,168.63	0	0.09	1115	1121	TRUE	
Kcnk9	Acidic, alpha-dentinal-matrix	P56550|Q8BX.0	111.9.0	0	0	0	0.00%	KYNLNGTRGNDMDR	K	K	27.4	33.1	0	MT: Oxidation (+15.99)	1666.7825	1,975.90	1,976.91	0	0.38	73	90	TRUE	P35234|Q8K7
Dmp1	Acidic, alpha-dentinal-matrix	P70349|Q8K1.0	11.9.9.4	0	0	0	0.00%	KYNLNGTRGNDMDR	K	K	27.4	33.1	0		1662.7827	1,969.91	1,969.91	0	0.00	71	88	TRUE	P35234|Q8K7
Ppp2r5	Isoform 2 of Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform	P30154|P63.0	11.9.9.9.3	0	0	0	0.00%	VGLLQEFDNR	K	K	42.7	49.5	0	MT: Oxidation (+15.99)	1242.6211	1,383.69	1,384.69	0	0.03	1171	1181	TRUE	
Pdzk1	Isoform pdz1-alpha of Phosphodiesterase 4 DHHC-type containing protein 3	P70157|Q7.0.0	119.1.0	13	13	13	1.17%	VGLDCVVVRSTRERVVSR	K	K	35.1	19.5	0		1914.999	1,961.97	1,962.98	0	0.96	431	477	TRUE	
Pdzk1	Phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1 (p85 alpha) OS=Mus musculus GN=p_d	P60.0|Q3.0.0.0	11.1.7.1	10	10	11	0.90%	VGDDCVVVRSTRERVAVGEA	K	F	35.8	28.6	0		1935.384	1,243.19	1,243.19	0	0.00	427	451	TRUE	
Cnnm3	Cyclin-M3 OS=Mus musculus GN=Cnnm3	P70.0|Q8.0.0.7.1|P60.0|Q8.0.0.8	11.9.0.0	0	0	0	0.00%	VRGVRDSLGALTRDGLR	K	F	35.5	50.2	0		1962.9766	2,278.11	2,279.12	0	0.14	18	35	TRUE	
Gpr1	Sequestosome-1, alpha-endocrine	P70.0|Q3.0.0.0	11.9.1	11	11	11	0.90%	VRVLAEEAQDR	K	F	37.5	28.8	0		1211.6272	1,260.63	1,261.63	0	0.28	50	70	TRUE	P35234|Q8K
Gpr1	Sequestosome-1, alpha-endocrine	P70.0|Q3.0.0.0	11.9.1	11	11	11	0.90%	VRVLAEEAQDRLAGR	K	K	37.5	27.7	0		1414.2379	1,564.82	1,565.82	0	0.38	53	71	TRUE	P35234|Q8K
Tpm2	Isoform 2 of Tropomyosin beta chain	P70.0|Q8.7.7.0	11.9.1.1	0	0	0	0.00%	VRVVAEQDR	K	K	44	19.6	0		1011.5151	1,262.60	1,