SUPPORTING INFORMATION

Supplemental Figure 1. Validation of valosin-containing protein (VCP) as a nonspecifically cross-reacting protein. VCP-directed IP from wild-type and DJ-1 knockout mice followed by Western blotting with a DJ-1-directed antibody unequivocally establishes nonspecific crossreactivity of the DJ-1-directed antibody with VCP. A VCP-directed polyclonal antibody was used to capture VCP side-by-side from tissue extracts of DJ-1-/- mice and wild-type mice which had been subjected to the tcTPC procedure. A subsequent Western blotting analysis in which the blotting membrane was probed with the DJ-1 antibody we had used for the DJ-1 interactome investigation (i) established that the Dj-1 antibody can cross-react with a 97 kDa band present in both DJ-1 knockout and wild-type mice, (ii) documented that this cross-reactive band is strongly enriched in the VCP directed immunoprecipitation eluate, and (iii) showed complete absence of DJ-1 in the same VCP immunoprecipitation eluate. Thus, the presence of DJ-1 in the interactome list could be explained by an apparent cross-reactivity of the commercial DJ-1 antibody we had employed for the generation of the interactome dataset. Extracts before co-IP (lanes 1 and 4), unbound co-IP material (lanes 2 and 5) and co-IP eluate fractions (lanes 3 and 6). Please note the increase in DJ-1 antibody signal for a band of ~95 kDa (VCP has apparent MW of 97kDa) following VCP directed co-IP from DJ-1 knockout mouse extracts (lanes 4 and 6).

Supplemental Figure 2. Determination of specific candidate DJ-1 interactors based on iTRAQ ratio comparisons. The WT:KO iTRAQ ratios of brain (115:114) (A) and liver (117:116) (B) DJ-1 interactomes and the HZ:KO iTRAQ ratios obtained for the DJ-1 interactome analysis in mouse embryonic stem cell lines (115:114) (**C**) are depicted graphically. A solid line indicates a baseline iTRAQ ratio of 1.0 (assuming no DJ-1-specific enrichment in a comparison of specific versus control) and dashed lines represent thresholds of one and two standard deviations (SD) above the baseline calculated from the iTRAQ ratios observed in the individual subdatasets. Note that in addition to the bait protein (DJ-1), the iTRAQ ratios of two outliers in each graph were removed from the calculation of the standard deviations. Proteins which possessed ratios above the threshold of two SD are bolded.

Supplemental Figure 3. Significant correlation of brain and liver DJ-1 interactome data. (**A**) Graph depicting the correlation between brain and liver iTRAQ ratios including the line of best fit (solid line) and 95% confidence intervals (dashed lines). A Pearson correlation coefficient of 0.857 was significant at a two-tailed $P = 0.01$ level (SPSS ver. 18, IBM Corporation). (**B**) The theoretical relation between sample size and the Pearson correlation coefficient at six different powers and at a two-sided 0.01 significance level is depicted based on R statistical modeling source code (Quick-R, Robert I. Kabacoff, and ‘pwr’ code library, Stéphane Champely). As demonstrated by the intersection of the dashed lines, the brain and liver iTRAQ ratio sample size of 37 at a correlation coefficient of 0.857 is appropriate.

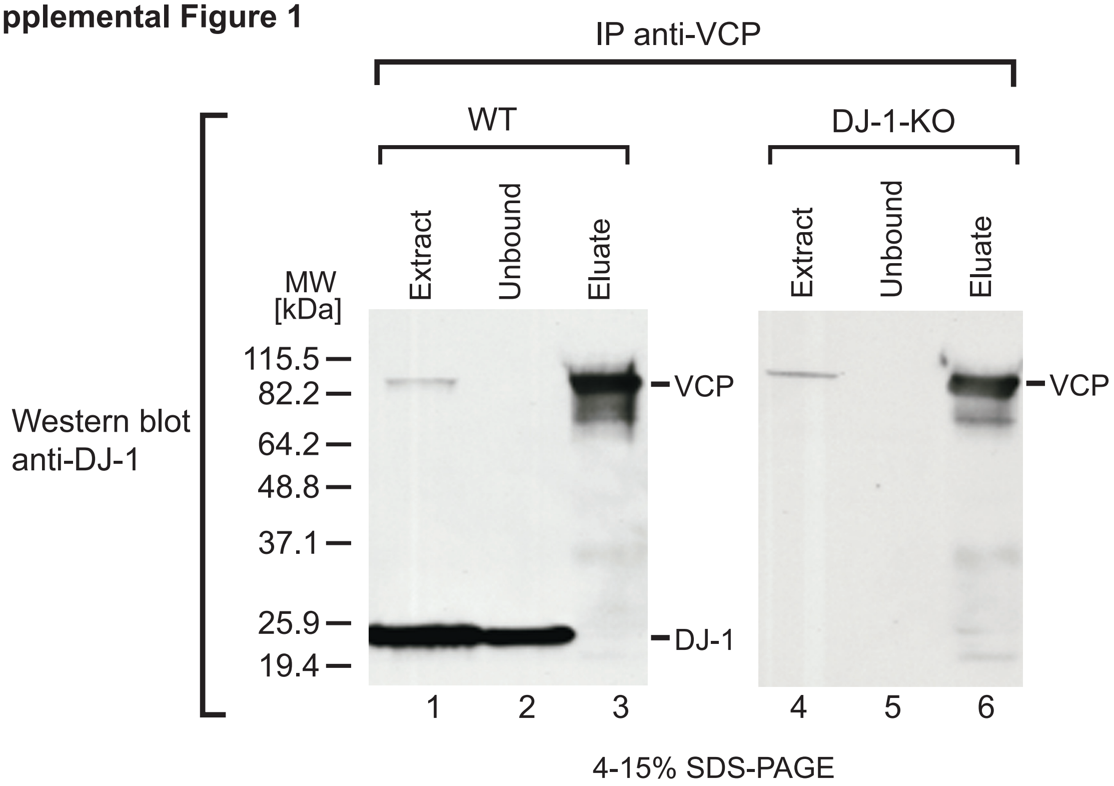
Supplemental Tables. Please refer to **Supplemental Tables 1, 2 or 3** for details of analyses summarized in **Tables 1, 2 or 3**, respectively. Depicted in these Supplemental Tables are information on proteins and peptides observed, including information on masses, percent sequence coverage, confidence scores, iTRAQ ratios, the calculation of average reporter ion intensities and the corresponding standard deviations of this calculation. Note that **Supplemental Tables 1, 2 or 3** depict analyses conducted with ProteinPilot, ProteinProspector and Mascot, respectively, and therefore the formats of the tables (and confidence scores) reflect the different designs of these search algorithms.

Supplemental Table 1. Details of DJ-1 candidate interactors in spectral counting-based comparison of formaldehyde crosslinked DJ-1 KO, HZ or WT ES cells +/- H_2O_2.

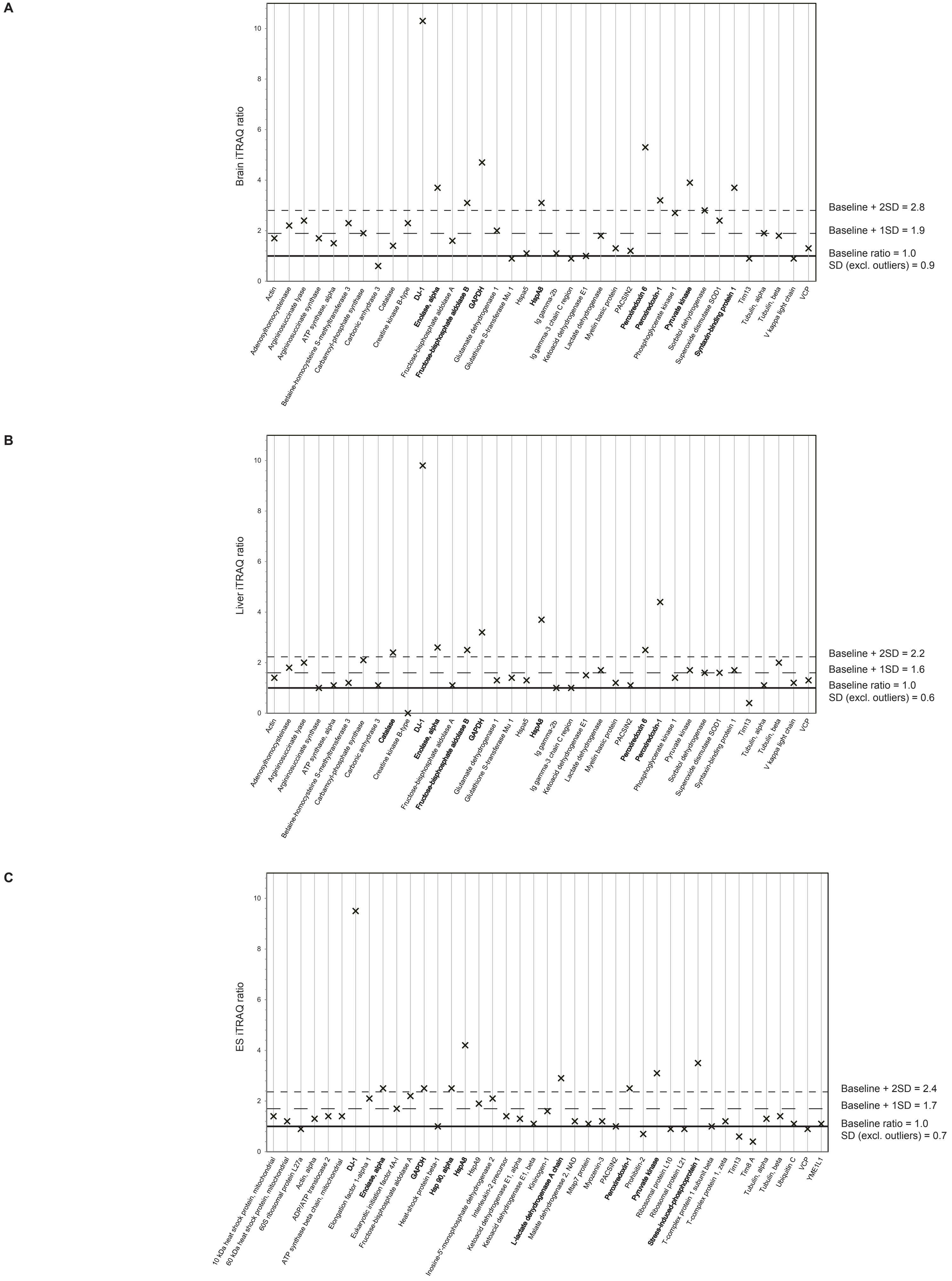
Supplemental Table 2. DJ-1 candidate interactors in spectral counting-based comparison of formaldehyde crosslinked DJ-1 KO, HZ or WT ES cells +/- H_2O_2.

Supplemental Table 3. DJ-1 candidate interactors in four-plex iTRAQ-based comparison of formaldehyde crosslinked DJ-1 KO, HZ or WT ES cells +/- H2O2

Supplemental Figure 1

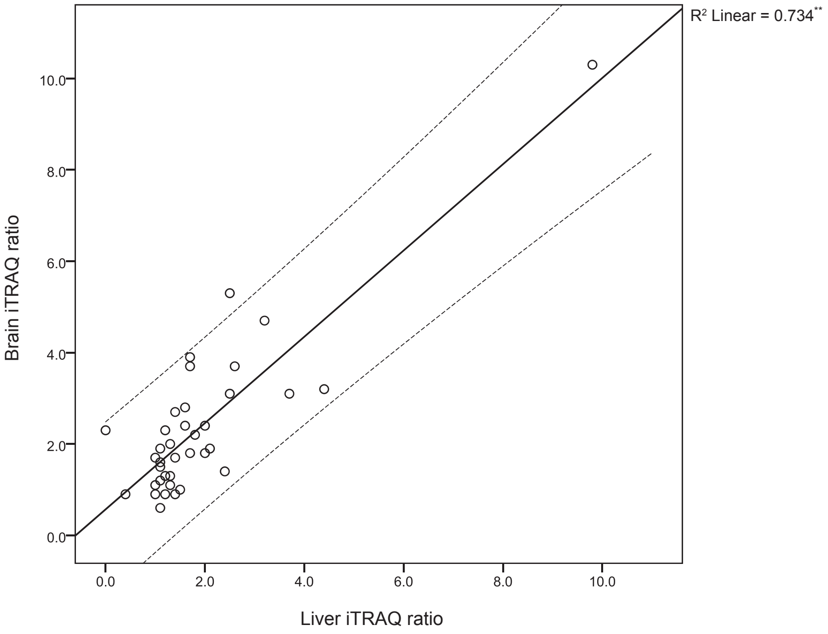


Supplemental Figure 2



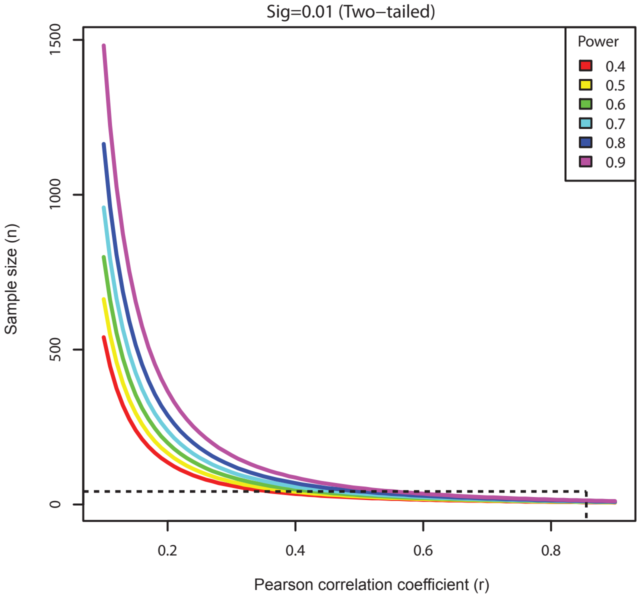
Supplemental Figure 3

A



** Pearson correlation coefficient = 0.857 (significant at the 0.01 level, 2-tailed)

B



Supplemental Table 1

												Peptide information				Quantitation		
														% Conf.	Brain		Liver	
Protein Name	Accession #	MW	Unique	%Cov	z	dMass	Prec MW	Prec m/z	Theor MW	Theor m/z	Peptide	Modifications	Cleavages	Score	114.0	115.0	116.0	117.0
DJ-1	IPI00117264.1	20,022	34	83.6	4	-0.03	1993.07	499.28	1993.10	499.28	VTVAGLAGKDPVQCSR	iTRAQ; iTRAQ(K)@9; Pyridylethyl(C)@14		99	16.5	34.6	13.6	35.3
					3	0.03	1888.08	630.37	1888.04	630.36	VTVAGLAGKDPVQCSR	iTRAQ; iTRAQ(K)@9; No Pyridylethyl(C)@14		82	0.0	37.2	9.5	53.3
					2	0.00	958.56	480.29	958.56	480.29	VTVAGLAGK	iTRAQ; Lys->Gln@9		99	0.1	17.2	0.0	82.8
					2	-0.02	1102.67	552.34	1102.70	552.35	VTVAGLAGK	iTRAQ; iTRAQ(K)@9		99	3.8	46.6	2.9	46.6
					2	0.00	958.59	480.30	958.59	480.30	VTVAGLAGK	No iTRAQ; iTRAQ(K)@9		85	4.8	18.5	5.8	70.8
					2	-0.01	1001.59	501.80	1001.60	501.81	VTVAGLAGK	Carbamyl@N-term; iTRAQ(K)@9		85	0.0	65.9	8.1	26.0
					3	-0.09	1517.81	506.94	1517.90	506.97	VEKDGLILTSR	iTRAQ; iTRAQ(K)@3		99	9.2	40.7	8.9	41.1
					4	-0.09	3057.51	765.39	3057.60	765.41	TQGPYDVVVLPGGNLGAQNLSESPMVK	iTRAQ; iTRAQ(K)@27		99	11.7	44.2	6.6	37.5
					4	-0.05	3073.55	769.39	3073.60	769.41	TQGPYDVVVLPGGNLGAQNLSESPMVK	iTRAQ; Oxidation(M)@25; iTRAQ(K)@27		99	0.0	55.0	0.0	45.0
					3	-0.02	3073.58	1025.53	3073.60	1025.54	TQGPYDVVVLPGGNLGAQNLSESPMVK	iTRAQ; Oxidation(M)@25; iTRAQ(K)@27		99	0.0	52.8	0.0	47.2
					3	0.00	2913.47	972.16	2913.47	972.16	TQGPYDVVVLPGGNLGAQNLSESPMVK	iTRAQ; Lys->Gln@27		86	0.0	20.1	0.0	79.9
					3	-0.05	1707.66	570.23	1707.71	570.24	MMNGSHYSYSESR	iTRAQ; Oxidation(M)@1		99	6.4	36.1	5.9	51.6
					3	0.02	1691.73	564.92	1691.72	564.91	MMNGSHYSYSESR	iTRAQ		99	4.6	33.1	4.3	58.0
					3	-0.02	1723.68	575.57	1723.71	575.58	MMNGSHYSYSESR	iTRAQ; Oxidation(M)@1; Oxidation(M)@2		99	13.8	46.3	8.7	31.2
					3	0.00	1708.69	570.57	1708.69	570.57	MMNGSHYSYSESR	iTRAQ; Oxidation(M)@1; Deamidated(N)@3		99	5.7	63.9	2.0	28.4
					3	0.00	1719.71	574.24	1719.71	574.24	MMNGSHYSYSESR	iTRAQ; Ser->Asp@12		99	0.0	47.1	5.9	47.0
					3	0.01	1673.71	558.91	1673.70	558.91	MMNGSHYSYSESR	iTRAQ; Dehydrated(S)@12		83	10.6	43.1	9.7	36.6
					3	-0.01	1660.89	554.64	1660.91	554.64	LGAQNLSESPMVK	iTRAQ; iTRAQ(K)@13	cleaved N-L@N-term	99	0.0	66.6	0.0	33.4
					3	-0.07	2193.16	732.06	2193.23	732.08	GPGTSFEFALAIVEALVGK	iTRAQ; iTRAQ(K)@19		99	2.4	56.2	0.0	41.5
					3	-0.10	1818.80	607.27	1818.90	607.31	GAEEMETVIPVDVMR	iTRAQ		99	4.3	32.4	13.5	49.8
					3	-0.04	1928.91	643.98	1928.95	643.99	DVMICPDTSLEDAK	iTRAQ; Pyridylethyl(C)@5; iTRAQ(K)@14		99	3.1	54.5	1.4	40.9
					3	0.04	1944.98	649.33	1944.94	649.32	DVMICPDTSLEDAK	iTRAQ; Oxidation(M)@3; Pyridylethyl(C)@5; iTRAQ(K)@14		99	9.2	43.6	0.4	46.8
					3	0.06	1784.91	595.98	1784.84	595.96	DVMICPDTSLEDAK	iTRAQ; Pyridylethyl(C)@5; No iTRAQ(K)@14		99	9.8	26.7	2.2	61.2
					3	-0.01	1956.97	653.33	1956.98	653.33	DVMICPDTSLEDAK	iTRAQ; Pyridylethyl(C)@5; Ala->Val@13; iTRAQ(K)@14		99	0.0	42.4	8.8	48.8
					3	0.05	1800.86	601.29	1800.80	601.28	DVMICPDTSLEDAK	iTRAQ; Oxidation(M)@3; Pyridylethyl(C)@5; Lys->Gln@14		99	9.3	32.4	13.7	44.6
					3	0.02	1784.83	595.95	1784.81	595.94	DVMICPDTSLEDAK	iTRAQ; Pyridylethyl(C)@5; Lys->Gln@14		99	0.0	40.5	0.0	59.4
					3	0.03	1973.00	658.68	1972.97	658.66	DVMICPDTSLEDAK	iTRAQ; Oxidation(M)@3; Pyridylethyl(C)@5; Ala->Val@13; iTRAQ(K)@14		99	0.0	44.3	2.2	53.5
					2	-0.01	1108.56	555.29	1108.58	555.30	DMANQVK	iTRAQ; Oxidation(M)@2; iTRAQ(K)@7		98	0.0	56.7	8.6	34.7
					2	-0.05	1092.53	547.27	1092.58	547.30	DMANQVK	iTRAQ; iTRAQ(K)@7		97	5.7	48.8	3.3	42.2
					2	0.00	1017.60	509.80	1017.59	509.80	DGLILTSR	iTRAQ		99	3.0	49.4	6.9	40.7
					2	-0.01	1031.60	516.81	1031.61	516.81	DGLILTSR	iTRAQ; Methyl(S)@7		93	3.5	47.0	3.0	46.6
					2	0.00	1045.59	523.80	1045.59	523.80	DGLILTSR	iTRAQ; Ser->Asp@7		83	3.6	45.3	1.2	49.8
					3	0.00	1490.80	497.94	1490.80	497.94	AQNLSESPMVK	iTRAQ; iTRAQ(K)@11	cleaved G-A@N-term	84	3.4	81.2	6.8	8.7
					2	0.00	1014.70	508.36	1014.70	508.36	ALVILAK	iTRAQ; iTRAQ(K)@7		94	1.7	35.0	0.5	62.7
														Average	4.3	44.3	4.8	46.6
														STDEV	4.5	13.9	4.3	14.7
PACSIN2	IPI00125880.1	55,833	18	56.2	3	0.00	1340.79	447.94	1340.79	447.94	VSELHLEVK	iTRAQ; iTRAQ(K)@9		99	22.2	30.5	20.2	27.1
					2	0.00	1085.56	543.79	1085.56	543.79	QMMGGFK	iTRAQ; iTRAQ(K)@7		92	24.6	26.2	23.4	25.8
					3	-0.04	1533.80	512.27	1533.84	512.29	HLDLSNVASYK	iTRAQ; iTRAQ(K)@11		88	29.3	29.3	17.2	24.2
					2	-0.08	1244.68	623.35	1244.76	623.39	EVLLEVQK	iTRAQ; iTRAQ(K)@8		79	17.4	28.4	28.7	25.5
					2	-0.01	1133.65	567.83	1133.65	567.83	ELEQSIK	iTRAQ; iTRAQ(K)@7		97	19.1	24.9	25.9	30.1
					3	0.01	1238.66	413.90	1238.65	413.89	EAEDGFRK	iTRAQ; iTRAQ(K)@8	missed R-K@7	76	19.4	34.3	23.4	22.9
					2	0.02	966.47	484.24	966.45	484.23	EAEDGFR	iTRAQ		94	22.4	27.5	23.8	26.3
					2	-0.02	1511.73	756.87	1511.75	756.88	AYAQQLTEWAR	iTRAQ; Dioxidation(W)@9		99	25.0	23.9	25.7	25.4
					2	0.02	1479.78	740.90	1479.76	740.89	AYAQQLTEWAR	iTRAQ		99	27.4	27.5	21.2	23.9
					2	0.02	1481.75	741.88	1481.73	741.87	AYAQQLTEWAR	iTRAQ; Deamidated(Q)@4; Deamidated(Q)@5		99	25.8	32.0	20.6	21.7
					2	0.02	1405.73	703.87	1405.71	703.86	AWIAVMSEAER	iTRAQ		99	18.4	23.1	27.9	30.6
					4	0.05	3468.81	868.21	3468.76	868.20	AVDGVTLTGINQTGDQSGQNKPGSNLSVPSNP	iTRAQ; iTRAQ(K)@21; Deamidated(N)@25; Methyl(S)@30; Methyl(N)@31	cleaved P-A@C-term	99	30.8	40.3	14.5	14.4
					3	0.00	1470.73	491.25	1470.73	491.25	ASLMNEDFEK	iTRAQ; iTRAQ(K)@10		98	22.0	25.9	22.6	29.5
					3	-0.01	2231.05	744.69	2231.06	744.69	ALYDYEGQEHDELSFK	iTRAQ; iTRAQ(K)@16		99	33.0	31.2	17.0	18.8
					2	-0.02	1020.55	511.28	1020.57	511.29	AGDELTK	iTRAQ; iTRAQ(K)@7		94	29.5	27.6	20.8	22.0
					3	-0.02	1498.81	500.61	1498.82	500.62	ADPSLNPEQLK	iTRAQ; iTRAQ(K)@11		99	28.2	27.7	21.7	22.4
					2	0.01	1102.58	552.30	1102.57	552.29	AADAVEDLR	iTRAQ		99	24.7	24.3	25.6	25.4
					2	0.00	1130.60	566.31	1130.61	566.31	AADAVEDLR	iTRAQ; Dimethyl(R)@9		99	18.9	24.1	27.8	29.3
														Average	24.3	28.3	22.7	24.7
														STDEV	4.7	4.3	4.0	4.1
Actin	IPI00110850.1	41,947	11	54.4	4	0.06	2438.37	610.60	2438.30	610.58	VAPEEHPVLLTEAPLNPKANR	iTRAQ; Lys->Gln@18	missed K-A@18	91	12.8	17.6	24.7	44.9
					4	0.05	2241.31	561.33	2241.26	561.32	VAPEEHPVLLTEAPLNPK	iTRAQ; iTRAQ(K)@18		99	12.2	63.8	10.9	13.1
					3	0.01	1659.81	554.28	1659.80	554.27	QEYDESGPSIVHR	iTRAQ		99	16.4	36.5	22.3	24.8
					2	-0.02	1275.60	638.81	1275.62	638.82	GYSFTTTAER	iTRAQ		99	26.4	46.6	11.9	15.1
					2	0.06	1304.74	653.38	1304.68	653.35	EITALAPSTMK	iTRAQ; Lys->Gln@11		89	17.4	11.3	26.1	45.2
					3	-0.01	1448.81	483.94	1448.82	483.95	EITALAPSTMK	iTRAQ; iTRAQ(K)@11		86	24.5	35.9	19.3	20.3
					3	0.03	1464.84	489.29	1464.81	489.28	EITALAPSTMK	iTRAQ; Oxidation(M)@10; iTRAQ(K)@11		78	13.3	33.3	23.4	30.0
					3	-0.01	1485.71	496.25	1485.72	496.25	DSYVGDEAQSK	iTRAQ; iTRAQ(K)@11		99	28.2	42.3	13.0	16.6
					2	0.00	1285.68	643.85	1285.68	643.85	DLTDYLMK	iTRAQ; iTRAQ(K)@8		99	27.8	47.5	9.7	15.1
					3	-0.02	1341.78	448.27	1341.80	448.27	AVFPSIVGRPR	iTRAQ		99	19.8	10.2	27.2	42.8
					2	-0.01	1119.53	560.77	1119.54	560.78	AGFAGDDAPR	iTRAQ		99	29.7	41.4	13.2	15.6
														Average	20.8	35.1	18.3	25.8
														STDEV	6.7	16.4	6.7	12.9
Myelin basic protein	IPI00223593.1		4	51.8	2	0.00	1189.65	595.83	1189.64	595.83	DTGILDSIGR	iTRAQ		99	34.6	49.7	9.7	6.0
					3	-0.01	1479.71	494.25	1479.73	494.25	YLATASTMDHAR	iTRAQ		99	37.5	45.9	4.7	11.8
					2	0.06	1217.70	609.86	1217.64	609.83	DTGILDSIGR	iTRAQ; Ser->Asp@7		92	44.8	55.2	0.0	0.0
					3	0.02	1495.74	499.59	1495.72	499.58	YLATASTMDHAR	iTRAQ; Oxidation(M)@8		81	43.8	56.2	0.0	0.0
														Average	40.2	51.7	3.6	4.5
														STDEV	4.9	4.8	4.6	5.7
Argininosuccinate synthase	IPI00134746.5	46,813	5	44.2	3	0.00	1745.94	582.99	1745.94	582.99	APNSPDVLEIEFK	iTRAQ; iTRAQ(K)@13		99	6.2	10.6	43.6	39.5
					2	0.01	1048.63	525.32	1048.62	525.31	GQVYILGR	iTRAQ		99	6.0	12.6	38.6	42.9
					2	0.00	1136.67	569.34	1136.67	569.34	YLLGTSLAR	iTRAQ	cleaved R-P@C-term	99	2.2	4.1	43.2	50.6
					2	0.02	1223.72	612.87	1223.70	612.86	VFIEDVSK	iTRAQ; iTRAQ(K)@8		99	2.6	4.8	47.8	44.8
					2	0.01	1038.48	520.25	1038.47	520.24	EDFEEAR	iTRAQ		99	5.5	6.2	47.9	40.3
														Average	4.5	7.7	44.2	43.6
														STDEV	2.0	3.7	3.9	4.4
Tim13	IPI00134484.1	10,458	2	42.1	2	-0.01	1385.65	693.83	1385.65	693.83	YMDAWNTVSR	iTRAQ		99	23.2	27.2	36.5	13.1
					3	-0.02	1695.96	566.33	1695.98	566.33	VQIAVANAQELLQR	iTRAQ		91	33.8	25.3	26.6	14.3
														Average	28.5	26.2	31.6	13.7
														STDEV	7.5	1.3	7.0	0.8
ATP synthase, alpha	IPI00130280.1		4	41.8	2	0.02	1169.71	585.86	1169.69	585.85	AVDSLVPIGR	iTRAQ		99	14.6	26.9	25.3	33.2
					2	0.00	1190.65	596.33	1190.66	596.34	EPMQTGIK	iTRAQ; iTRAQ(K)@8		99	16.9	26.2	27.3	29.6
					2	-0.01	1164.61	583.31	1164.62	583.32	ISEQSDAK	iTRAQ; iTRAQ(K)@8		99	23.7	29.3	22.1	24.9
					3	0.00	1458.83	487.28	1458.83	487.28	VVDALGNAIDGK	iTRAQ; iTRAQ(K)@12		85	18.7	28.1	26.7	26.4
														Average	18.5	27.7	25.3	28.5
														STDEV	3.9	1.4	2.3	3.7
GAPDH	IPI00849530.1	35,679	6	38.1	3	-0.03	1656.91	553.31	1656.94	553.32	GAAQNIIPASTGAAK	iTRAQ; iTRAQ(K)@15		99	2.3	83.3	3.5	10.8
					3	-0.09	1991.00	664.67	1991.10	664.71	IVSNASCTTNCLAPLAK	iTRAQ; No Pyridylethyl(C)@7; Cys->Thr@11; iTRAQ(K)@17		99	6.6	52.0	11.0	30.4
					2	-0.01	948.52	475.27	948.53	475.27	VGVNGFGR	iTRAQ		99	7.7	41.6	11.3	39.5
					2	-0.02	938.50	470.26	938.51	470.26	LTGMAFR	iTRAQ		94	10.1	40.1	13.2	36.6
					3	-0.06	1656.88	553.30	1656.94	553.32	GAAQNIIPASTGAAK	iTRAQ; iTRAQ(K)@15		91	24.0	35.8	8.3	31.9
					2	0.01	1156.71	579.36	1156.71	579.36	VIPELNGK	iTRAQ; iTRAQ(K)@8		71	10.7	34.7	12.6	42.0
														Average	10.2	47.9	10.0	31.9
														STDEV	7.4	18.4	3.6	11.2
Fructose-bisphosphate aldolase B	IPI00127206.6	39,225	8	37.4	3	-0.01	1530.87	511.30	1530.88	511.30	ALQASALAAWGGK	iTRAQ; iTRAQ(K)@13		99	7.5	21.7	16.5	54.3
					2	-0.01	1212.63	607.32	1212.64	607.33	ATQEAFMK	iTRAQ; iTRAQ(K)@8		99	2.7	8.3	21.5	67.5
					2	0.00	1088.59	545.30	1088.59	545.30	ELSEIAQR	iTRAQ		99	2.3	7.8	27.1	62.8
					3	-0.01	1633.82	545.61	1633.82	545.61	GILAADESVGTMGNR	iTRAQ		99	0.0	66.8	9.0	24.2
					3	0.02	1528.86	510.63	1528.85	510.62	LDQGGAPLAGTNK	iTRAQ; iTRAQ(K)@13		99	14.7	25.1	22.3	37.9
					2	0.00	1024.55	513.28	1024.54	513.28	DGVDFGK	iTRAQ; iTRAQ(K)@7		94	6.5	8.8	28.1	56.6
					2	0.00	972.52	487.27	972.52	487.26	LSFSYGR	iTRAQ		94	1.7	3.7	28.7	65.9
					2	-0.02	1050.65	526.33	1050.67	526.34	VLAAVYK	iTRAQ; iTRAQ(K)@7		75	18.2	21.9	14.9	45.0
														Average	6.7	20.5	21.0	51.8
														STDEV	6.6	20.4	7.1	15.1
Tubulin, beta	IPI00169463.1	49,832	7	36.6	3	-0.02	1763.91	588.98	1763.93	588.98	LHFFMPGFAPLTSR	iTRAQ		99	26.9	46.7	11.3	15.2
					2	0.03	1286.76	644.39	1286.73	644.37	LAVNMVPFPR	iTRAQ		99	35.1	57.1	0.0	7.7
					3	0.04	1615.88	539.63	1615.84	539.62	INVYYNEATGGK	iTRAQ; iTRAQ(K)@12		99	21.8	46.9	6.2	25.1
					2	0.01	1273.70	637.86	1273.69	637.85	FPGQLNADLR	iTRAQ		99	27.5	45.2	9.3	18.1
					3	-0.02	1733.86	578.96	1733.89	578.97	EVDEQMLNVQNK	iTRAQ; iTRAQ(K)@12		99	32.0	49.5	6.9	11.6
					3	-0.01	1749.87	584.30	1749.88	584.30	EVDEQMLNVQNK	iTRAQ; Oxidation(M)@6; iTRAQ(K)@12		94	23.5	41.9	17.3	17.2
					3	0.03	1979.10	660.71	1979.06	660.70	ALTVPELTQQMFDAK	iTRAQ; iTRAQ(K)@15		89	28.7	56.3	2.4	12.6
														Average	27.9	49.1	7.6	15.4
														STDEV	4.6	5.7	5.8	5.6
Tubulin, alpha	IPI00117350.1		6	36.2	3	0.00	2112.18	705.07	2112.18	705.07	VGINYQPPTVVPGGDLAK	iTRAQ; iTRAQ(K)@18		99	27.8	60.8	5.4	5.9
					3	0.01	1861.98	621.67	1861.98	621.67	NLDIERPTYTNLNR	iTRAQ		99	30.5	57.0	4.9	7.6
					2	-0.02	1068.58	535.30	1068.61	535.31	LSVDYGK	iTRAQ; iTRAQ(K)@7		99	33.1	47.2	12.1	7.7
					2	0.00	1212.69	607.35	1212.68	607.35	EIIDPVLDR	iTRAQ		97	30.2	54.6	6.2	8.9
					2	0.02	1166.56	584.29	1166.54	584.28	EDAANNYAR	iTRAQ		88	24.5	56.1	7.7	11.7
					2	-0.03	1258.54	630.28	1258.57	630.29	EDAANNYAR	iTRAQ; Ala->Tyr@8		77	22.3	42.1	17.2	18.4
														Average	28.1	53.0	8.9	10.0
														STDEV	4.0	7.0	4.8	4.5
VCP	IPI00676914.1	88,852	7	35.6	4	0.02	2111.13	528.79	2111.11	528.79	ELQELVQYPVEHPDK	iTRAQ; iTRAQ(K)@15		99	19.1	55.0	15.1	10.8
					2	-0.03	1105.55	553.78	1105.57	553.79	ESIESEIR	iTRAQ		99	14.9	23.4	26.8	34.9
					2	0.00	1385.73	693.87	1385.73	693.87	EVDIGIPDATGR	iTRAQ		99	26.9	25.5	20.6	26.9
					2	0.04	1259.64	630.83	1259.60	630.81	GGNIGDGGGAADR	iTRAQ		99	23.8	21.7	26.0	28.4
					2	0.00	1194.62	598.32	1194.62	598.32	MDELQLFR	iTRAQ		99	28.3	25.3	18.3	28.1
					2	0.00	1110.58	556.30	1110.58	556.30	AFEEAEK	iTRAQ; iTRAQ(K)@7		92	25.8	25.6	19.0	29.6
					2	-0.01	962.56	482.29	962.57	482.29	GDIFLVR	iTRAQ		85	23.2	28.4	18.8	29.6
														Average	23.2	29.3	20.7	26.9
														STDEV	4.7	11.5	4.3	7.5
Ig gamma-3 chain C region	IPI00117022.2		5	34.9	3	-0.15	1777.84	593.62	1778.00	593.67	VVSALPIQHQDWMR	iTRAQ; Gln->Thr@8; Met->Leu@13		99	30.9	25.3	21.4	22.4
					3	0.00	1838.96	613.99	1838.96	613.99	VVSALPIQHQDWMR	iTRAQ; Oxidation(M)@13		95	15.4	16.8	33.3	34.5
					3	-0.03	1367.68	456.90	1367.71	456.91	EVHTAWTQPR	iTRAQ		99	16.8	18.8	29.6	34.8
					2	0.98	1035.60	518.81	1034.62	518.32	ATLTVDK	iTRAQ; iTRAQ(K)@7		86	13.4	15.5	35.5	35.5
					2	0.00	1125.70	563.86	1125.70	563.86	ALPAPIER	iTRAQ; Arg->Lys@8; iTRAQ(K)@8		98	33.7	23.3	22.6	20.4
														Average	22.1	19.9	28.5	29.5
														STDEV	9.5	4.2	6.3	7.5
Fructose-bisphosphate aldolase A	IPI00856379.1	39,225	3	33.0	3	-0.03	1619.87	540.96	1619.90	540.97	GILAADESTGSIAK	iTRAQ; iTRAQ(K)@14		99	29.6	34.0	19.8	16.7
					3	0.00	1789.91	597.64	1789.90	597.64	LQSIGTENTEENRR	iTRAQ	missed R-R@13	99	25.0	55.8	8.1	11.1
					2	0.00	1010.53	506.27	1010.53	506.27	DGADFAK	iTRAQ; iTRAQ(K)@7		81	29.7	47.5	9.1	13.8
														Average	28.1	45.7	12.3	13.8
														STDEV	2.6	11.0	6.4	2.8
Sorbitol dehydrogenase	IPI00753038.1		3	31.1	3	0.00	1705.93	569.65	1705.92	569.65	GENLSLVVHGPGDIR	iTRAQ		99	7.8	23.8	23.7	44.7
					2	0.01	1064.65	533.33	1064.65	533.33	IGDFVVK	iTRAQ; iTRAQ(K)@7		97	2.0	9.5	35.5	52.9
					2	0.00	1080.65	541.33	1080.64	541.33	VAIEPGVPR	iTRAQ		92	6.4	12.7	31.7	49.1
														Average	5.4	15.3	30.3	48.9
														STDEV	3.0	7.5	6.0	4.1
Glutathione S-transferase Mu 1	IPI00649450.1		2	30.4	2	0.03	1243.74	622.88	1243.71	622.86	LYSEFLGK	iTRAQ; iTRAQ(K)@8		96	13.3	16.0	26.2	44.6
					3	-0.13	1779.73	594.25	1779.86	594.29	HHLDGETEEERIR	iTRAQ; Oxidation(R)@11	missed R-I@11	93	33.5	25.1	20.6	20.8
														Average	23.4	20.5	23.4	32.7
														STDEV	14.3	6.4	3.9	16.8
V kappa light chain	IPI00123576.4		5	30.3	3	-0.01	1860.06	621.03	1860.07	621.03	LLIYRTSNLASGVPAR	iTRAQ; Thr->Ala@6; Oxidation(P)@14	missed R-T@5	99	28.9	19.9	22.8	28.4
					2	-0.02	1201.64	601.83	1201.65	601.83	TSNLASGVPAR	iTRAQ; Thr->Ala@1; Oxidation(P)@9		99	22.3	22.0	25.8	29.9
					3	0.02	1875.09	626.04	1875.07	626.03	LLIYRTSNLASGVPAR	iTRAQ; Tyr->Phe@4; Deamidated(N)@8; Oxidation(P)@14	missed R-T@5	99	22.2	20.5	23.5	33.8
					2	-0.03	1215.64	608.83	1215.67	608.84	TSNLASGVPAR	iTRAQ		99	15.9	19.9	29.5	34.7
					2	-0.03	1218.64	610.33	1218.67	610.34	TSNLASGVPAR	iTRAQ; Asn->Thr@3; Oxidation(P)@9		99	33.7	23.7	18.9	23.7
														Average	24.6	21.2	24.1	30.1
														STDEV	6.9	1.6	3.9	4.4
Peroxiredoxin 6	IPI00758024.1		2	29.9	2	0.01	1231.62	616.82	1231.61	616.81	DANNMPVTAR	iTRAQ		99	4.9	36.3	11.7	47.2
					2	-1.07	1333.70	667.85	1334.77	668.39	LSILYPATTGR	iTRAQ		93	8.6	35.0	21.0	35.4
														Average	6.8	35.6	16.3	41.3
														STDEV	2.7	0.9	6.6	8.3
Pyruvate kinase	IPI00775829.1		4	29.8	2	-0.02	1220.68	611.35	1220.70	611.36	GSFPVEAVK	iTRAQ; iTRAQ(K)@9		99	2.6	9.0	29.2	59.1
					3	0.03	1929.09	644.04	1929.07	644.03	TGVLQGGPESEVEIVK	iTRAQ; iTRAQ(K)@16		99	0.0	20.7	31.1	48.2
					2	0.02	943.61	472.81	943.59	472.80	AAVIAVTR	iTRAQ		95	7.4	14.5	29.2	48.9
					2	0.04	875.52	438.77	875.48	438.75	AGMNIAR	iTRAQ		72	6.1	17.9	28.1	47.9
														Average	4.0	15.5	29.4	51.0
														STDEV	3.3	5.0	1.3	5.4
Betaine-homocysteine S-methyltransferase 3	IPI00130950.1		7	29.2	2	-0.03	1218.60	610.31	1218.63	610.32	EATTEQQLR	iTRAQ		99	0.3	0.7	49.7	49.3
					3	0.02	1309.67	437.57	1309.66	437.56	VNEAACDIAR	iTRAQ; Pyridylethyl(C)@6		99	5.9	12.7	37.3	44.0
					2	-0.02	1241.65	621.83	1241.67	621.84	AIAEELAPER	iTRAQ		99	2.0	6.1	42.4	49.5

					2	0.02	1218.65	610.33	1218.63	610.32	EATTEQQLR	iTRAQ		99	0.0	0.0	48.5	51.5
					2	-0.02	1067.57	534.79	1067.59	534.80	GNYVAEK	iTRAQ; iTRAQ(K)@7		96	0.8	2.7	43.3	53.2
					2	0.02	1151.60	576.81	1151.58	576.80	EYWQNLR	iTRAQ		94	1.8	3.9	41.6	52.7
					2	0.06	1118.61	560.31	1118.55	560.28	GAAELMQQK	iTRAQ; Lys->Gln@9		90	3.7	7.5	38.4	50.4
														Average	2.1	4.8	43.0	50.1
														STDEV	2.1	4.4	4.7	3.1
Enolase, alpha	IPI00756027.1		4	28.6	3	-0.93	2247.19	750.07	2248.12	750.38	DATNVGDEGGFAPNILENK	iTRAQ; iTRAQ(K)@19		99	12.8	52.4	8.4	26.4
					2	-0.03	1191.63	596.82	1191.66	596.84	IEEELGSK	iTRAQ; iTRAQ(K)@8		99	12.0	45.2	9.8	33.0
					3	-0.01	1567.77	523.60	1567.78	523.60	LMIEMDGTENK	iTRAQ; iTRAQ(K)@11		98	14.6	41.7	14.9	28.8
					2	0.00	1102.68	552.35	1102.68	552.35	EALELLK	iTRAQ; iTRAQ(K)@7		85	11.7	49.4	11.2	27.6
														Average	12.8	47.2	11.1	29.0
														STDEV	1.3	4.7	2.8	2.8
HspA8	IPI00480560.1		6	28.3	3	-0.03	1936.96	646.66	1936.99	646.67	NQVAMNPTNTVFDAK	iTRAQ; iTRAQ(K)@15		99	12.7	42.0	9.5	35.8
					2	-0.02	1121.58	561.80	1121.60	561.81	MVQEAEK	iTRAQ; iTRAQ(K)@7		95	13.4	41.7	5.7	39.2
					3	-0.02	1952.97	652.00	1952.99	652.00	NQVAMNPTNTVFDAK	iTRAQ; Oxidation(M)@5; iTRAQ(K)@15		94	17.9	62.6	0.0	19.5
					3	-0.02	1590.77	531.26	1590.80	531.27	NSLESYAFNMK	iTRAQ; iTRAQ(K)@11		90	10.4	41.0	10.2	38.3
					2	0.01	1091.65	546.83	1091.64	546.83	ITITNDK	iTRAQ; iTRAQ(K)@7		89	10.6	46.1	4.8	38.4
					3	0.00	1371.72	458.25	1371.72	458.25	VEIIANDQGNR	iTRAQ		84	20.5	30.9	23.4	25.2
														Average	14.2	44.1	8.9	32.8
														STDEV	4.1	10.4	8.0	8.3
Superoxide dismutase SOD1	IPI00130589.7		2	28.3	2	0.02	1317.68	659.85	1317.66	659.84	DGVANVSIEDR	iTRAQ		99	9.4	14.3	31.8	44.5
					3	1.00	1511.86	504.96	1510.86	504.63	VISLSGEHSIIGR	iTRAQ		99	5.8	22.0	25.0	47.2
														Average	7.6	18.1	28.4	45.8
														STDEV	2.5	5.4	4.8	1.9
Peroxiredoxin-1	IPI00848536.1	18,927	4	26.8	2	0.00	1037.53	519.77	1037.53	519.77	ADEGISFR	iTRAQ		99	7.1	17.5	12.9	62.4
					2	0.02	1368.81	685.41	1368.78	685.40	QITINDLPVGR	iTRAQ	cleaved Q-Q@N-term	99	6.3	27.2	12.4	54.1
					2	0.03	1207.74	604.88	1207.71	604.86	GLFIIDDK	iTRAQ; iTRAQ(K)@8		98	4.4	12.7	16.5	66.4
														Average	6.0	19.1	13.9	61.0
														STDEV	1.4	7.4	2.2	6.3
Carbonic anhydrase 3	IPI00221890.6		4	26.2	3	0.02	1625.88	542.97	1625.86	542.96	GDNQSPIELHTK	iTRAQ; iTRAQ(K)@12		99	22.9	32.8	11.4	32.8
					2	0.00	1046.57	524.29	1046.56	524.29	GGPLSGPYR	iTRAQ		99	12.7	33.9	12.3	41.1
					2	0.00	1272.61	637.31	1272.61	637.31	VVFDDTYDR	iTRAQ		97	0.0	0.0	19.6	80.4
														Average	11.8	22.2	14.4	51.5
														STDEV	11.5	19.3	4.5	25.4
Hspa5	IPI00319992.1		3	26.0	3	0.01	2124.14	709.06	2124.13	709.05	SQIFSTASDNQPTVTIK	iTRAQ; iTRAQ(K)@17		99	13.6	7.7	39.2	39.5
					3	-0.03	2031.03	678.02	2031.07	678.03	VTHAVVTVPAYFNDAQR	iTRAQ		99	26.0	24.4	18.5	31.1
					3	0.00	1965.00	656.01	1965.00	656.01	NQLTSNPENTVFDAK	iTRAQ; iTRAQ(K)@15		93	3.9	16.6	34.0	45.5
														Average	14.5	16.2	30.6	38.7
														STDEV	11.1	8.4	10.8	7.2
Glutamate dehydrogenase 1	IPI00114209.1		3	25.6	3	-0.01	1634.81	545.94	1634.82	545.95	DIVHSGLAYTMER	iTRAQ		99	12.1	20.2	28.3	39.5
					3	0.02	1866.99	623.34	1866.97	623.33	HGGTIPVVPTAEFQDR	iTRAQ		97	19.9	32.6	21.0	26.5
					2	-0.01	1126.62	564.32	1126.63	564.32	FTMELAK	iTRAQ; iTRAQ(K)@7		95	4.8	21.9	30.9	42.3
														Average	12.3	24.9	26.7	36.1
														STDEV	7.5	6.7	5.2	8.4
Syntaxin-binding protein 1	IPI00415403.1		4	22.7	3	-0.01	1519.70	507.57	1519.71	507.58	ADDPTMGEGPDK	iTRAQ; iTRAQ(K)@12		99	18.8	55.6	9.3	16.3
					2	-0.02	1367.70	684.86	1367.72	684.87	ISEQTYQLSR	iTRAQ		99	17.8	70.6	6.3	5.3
					2	-0.01	1100.65	551.33	1100.67	551.34	SQLLILDR	iTRAQ		98	20.5	71.9	2.4	5.2
					2	0.02	1121.66	561.84	1121.64	561.83	DLSQMLK	iTRAQ; iTRAQ(K)@7		74	15.5	71.3	3.4	9.8
														Average	18.2	67.3	5.4	9.1
														STDEV	2.1	7.8	3.1	5.2
Lactate dehydrogenase	IPI00869393.1	36,368	2	22.7	2	0.01	1287.69	644.85	1287.68	644.85	VTLTPEEEAR	iTRAQ		99	6.7	13.4	28.6	51.3
					2	0.03	1393.75	697.88	1393.72	697.87	QVVDSAYEVIK	iTRAQ; Lys->Gln@11		95	12.5	20.2	26.5	40.8
														Average	9.6	16.8	27.5	46.1
														STDEV	4.1	4.8	1.4	7.4
Ketoacid dehydrogenase E1	IPI00331555.2	50,774	2	21.7	3	0.02	1799.95	600.99	1799.93	600.98	VDGNDVFAVYNATK	iTRAQ; iTRAQ(K)@14		99	19.5	20.2	25.1	35.3
					2	-0.01	1352.65	677.33	1352.65	677.33	VMEAFEQAER	iTRAQ		99	35.3	33.4	12.0	19.4
														Average	27.4	26.8	18.5	27.3
														STDEV	11.2	9.3	9.3	11.2
Creatine kinase B-type	IPI00136703.1		2	21.0	2	-0.03	1174.62	588.32	1174.65	588.33	LLIEMEQR	iTRAQ		99	28.6	68.8	2.5	0.0
					3	-0.01	1944.01	649.01	1944.02	649.01	LEQGQAIDDLMPAQK	iTRAQ; iTRAQ(K)@15		97	30.6	69.4	0.0	0.0
														Average	29.6	69.1	1.3	0.0
														STDEV	1.4	0.4	1.8	0.0
Ig gamma-2b	IPI00754836.2		8	19.3	3	0.03	1793.98	599.00	1793.96	598.99	VVSTLPIQHQDWM	iTRAQ; iTRAQ(H)@9; Deamidated(Q)@10; Dethiomethyl(M)@13	cleaved M-S@C-term	99	25.2	17.8	24.1	32.9
					2	-0.03	1079.62	540.82	1079.65	540.83	VVSTLPIQH	iTRAQ; Gln->Ala@8	cleaved H-Q@C-term	72	19.6	43.5	25.8	11.1
					4	0.02	3054.52	764.64	3054.50	764.63	TEENYKDTAPVLDSDGSYFIYSK	iTRAQ; Tyr->Gln@5; iTRAQ(K)@6; Oxidation(P)@10; iTRAQ(K)@23	cleaved H-T@N-term	99	24.2	25.1	20.9	29.8
					4	0.06	3040.53	761.14	3040.48	761.13	TEENYKDTAPVLDSDGSYFIYSK	iTRAQ; Deamidated(N)@4; Tyr->Glu@5; iTRAQ(K)@6; iTRAQ(K)@23	cleaved H-T@N-term	99	27.1	30.2	21.5	21.2
					4	-0.12	3010.24	753.57	3010.36	753.60	TEENYKDTAPVLDSDGSYFIYSK	No iTRAQ; Deamidated(N)@4; iTRAQ(K)@6; Phospho(T)@8; iTRAQ(K)@23	cleaved H-T@N-term	97	30.2	29.2	19.1	21.5
					3	0.04	2181.11	728.05	2181.07	728.03	DTAPVLDSDGSYFIYSK	iTRAQ; Oxidation(P)@4; iTRAQ(K)@17		99	25.5	30.1	26.8	17.6
					3	-0.06	2151.00	718.01	2151.06	718.03	DTAPVLDSDGSYFIYSK	iTRAQ; Thr->Ser@2; iTRAQ(K)@17		99	27.3	26.8	22.8	23.0
					2	0.01	1069.59	535.80	1069.59	535.80	DLPSPIER	iTRAQ		96	20.8	15.2	26.9	37.1
														Average	25.0	27.2	23.5	24.3
														STDEV	3.5	8.6	2.9	8.5
Phosphoglycerate kinase 1	IPI00555069.3		3	19.2	3	0.02	1777.91	593.64	1777.89	593.64	LGDVYVNDAFGTAHR	iTRAQ		99	12.5	11.6	31.3	44.6
					2	0.03	1171.67	586.84	1171.65	586.83	ELNYFAK	iTRAQ; iTRAQ(K)@7		92	8.5	33.9	24.1	33.5
					2	0.01	908.49	455.25	908.48	455.25	YAEAVGR	iTRAQ		81	9.3	36.4	24.0	30.3
														Average	10.1	27.3	26.5	36.1
														STDEV	2.1	13.6	4.2	7.5
Adenosylhomocysteinase	IPI00605533.1		3	19.0	3	-0.01	1936.00	646.34	1936.01	646.35	GISEETTTGVHNLYK	iTRAQ; iTRAQ(K)@15		99	9.8	16.2	24.5	49.5
					2	0.02	1027.67	514.84	1027.65	514.83	IILLAEGR	iTRAQ		96	0.0	0.0	34.7	65.3
					2	0.01	1027.66	514.84	1027.65	514.83	IILLAEGR	iTRAQ		85	3.9	13.4	32.9	49.8
														Average	4.6	9.9	30.7	54.9
														STDEV	4.9	8.7	5.4	9.1
Catalase	IPI00869393.1		3	16.9	3	0.00	1534.73	512.58	1534.73	512.58	NFTDVHPDYGAR	iTRAQ		99	18.9	15.1	18.0	48.0
					2	0.00	1055.59	528.80	1055.58	528.80	NLPVGEAGR	iTRAQ		88	6.0	16.5	25.4	52.1
					3	-0.03	1636.76	546.59	1636.79	546.60	FNSANEDNVTQVR	iTRAQ		79	3.5	8.2	24.5	63.8
														Average	9.5	13.3	22.6	54.6
														STDEV	8.3	4.5	4.0	8.2
Argininosuccinate lyase	IPI00314788.5		2	13.4	3	0.03	1660.94	554.65	1660.91	554.64	AEMQQILQGLDK	iTRAQ; iTRAQ(K)@12		99	5.1	8.4	26.0	60.5
					2	0.00	1231.59	616.80	1231.60	616.81	FNSSISYDR	iTRAQ		98	1.2	6.6	33.2	59.1
														Average	3.2	7.5	29.6	59.8
														STDEV	2.8	1.2	5.1	1.0
Carbamoyl-phosphate synthase	IPI00111908.8	166,495	4	12.9	2	0.02	1233.71	617.86	1233.68	617.85	VPAIYGVDTR	iTRAQ		97	4.3	9.7	24.3	61.7
					2	-0.02	1373.72	687.87	1373.75	687.88	IMGTSPLQIDR	iTRAQ		96	0.0	0.0	31.0	69.0
					2	-0.02	1082.57	542.29	1082.59	542.30	EIGFSDK	iTRAQ; iTRAQ(K)@7		93	4.7	7.0	37.6	50.7
					2	0.02	1075.63	538.82	1075.61	538.81	DELGLNK	iTRAQ; iTRAQ(K)@7		81	3.0	6.5	25.9	64.6
														Average	3.0	5.8	29.7	61.5
														STDEV	2.1	4.1	6.0	7.8

Supplemental Table 2

Protein Name	Accession #	MW	KO Score	Unique	% Cov	M+H	m/z	z	ppm	Peptide	Start	End	Score	HZ Score	Unique	% Cov	M+H	m/z	z	ppm	Peptide	Start	End	Score	H202- Score	Unique	% Cov	M+H	m/z	z	ppm	Peptide	Start	End	Score	H202+ Score	Unique	% Cov	M+H	m/z	z	ppm	Peptide	Start	End	Score
DJ-1	IPI00117264.1	20,022	93.0	4	18.5									838.7	21	88.9	2422.24	606.32	4	-15	GLIAAICAGPTALLAHEVGFGCK	100	122	63	708.2	23	88.9	2422.25	606.32	4	-9.8	GLIAAICAGPTALLAHEVGFGCK	100	122	20.1	424.1	16	50.8								
			93.0	4	18.5									838.7	21	88.9	2786.38	929.47	3	-6.9	TQGPYDVVVLPGGNLGAQNLSESPmVK	63	89	54.1	708.2	23	88.9	2786.41	929.47	3	1.3	TQGPYDVVVLPGGNLGAQNLSESPmVK	63	89	56	424.1	16	50.8								
			93.0	4	18.5									838.7	21	88.9	1675.70	838.36	2	-59	GAEEMETVIPVDVMR	13	27	50.5	708.2	23	88.9	1675.81	838.41	2	4.6	GAEEMETVIPVDVMR	13	27	38.5	424.1	16	50.8	1675.79	838.40	2	-6.1	GAEEMETVIPVDVMR	13	27	48.4
			93.0	4	18.5									838.7	21	88.9	1705.91	569.31	3	2.9	VTVAGLAGKDPVQCSR	33	48	30.6	708.2	23	88.9	1705.89	569.30	3	-9.4	VTVAGLAGKDPVQCSR	33	48	39.7	424.1	16	50.8	1705.89	569.30	3	-12	VTVAGLAGKDPVQCSR	33	48	40.5
			93.0	4	18.5									838.7	21	88.9	1657.79	553.27	3	28	DVmICPDTSLEDAK	49	62	42.6	708.2	23	88.9	1657.74	553.25	3	-0.42	DVmICPDTSLEDAK	49	62	28.6	424.1	16	50.8	1657.59	553.20	3	-96	DVmICPDTSLEDAK	49	62	22.6
			93.0	4	18.5									838.7	21	88.9	2692.34	898.12	3	-24	GPGTSFEFALAIVEALVGKDMANQVK	157	182	42.3	708.2	23	88.9	2692.32	898.11	3	-30	GPGTSFEFALAIVEALVGKDMANQVK	157	182	39.5	424.1	16	50.8								
			93.0	4	18.5									838.7	21	88.9	2770.40	924.14	3	-2.2	TQGPYDVVVLPGGNLGAQNLSESPMVK	63	89	46.4	708.2	23	88.9	2770.39	924.14	3	-5	TQGPYDVVVLPGGNLGAQNLSESPMVK	63	89	34.1	424.1	16	50.8								
			93.0	4	18.5	1641.69	547.90	3	-39	DVMICPDTSLEDAK	49	62	20.8	838.7	21	88.9	1641.69	547.90	3	-39	DVMICPDTSLEDAK	49	62	38.4	708.2	23	88.9	1641.75	547.92	3	-0.37	DVMICPDTSLEDAK	49	62	16.1	424.1	16	50.8	1641.69	547.90	3	-39	DVMICPDTSLEDAK	49	62	19
			93.0	4	18.5									838.7	21	88.9	1691.81	846.41	2	8.1	GAEEMETVIPVDVmR	13	27	44	708.2	23	88.9									424.1	16	50.8	1691.79	846.40	2	-3.1	GAEEMETVIPVDVmR	13	27	34.9
			93.0	4	18.5									838.7	21	88.9	1548.63	516.88	3	3.5	MMNGSHYSYSESR	133	145	38.5	708.2	23	88.9	1548.58	516.86	3	-29	MMNGSHYSYSESR	133	145	34.2	424.1	16	50.8	1548.69	516.90	3	42	MMNGSHYSYSESR	133	145	19.1
			93.0	4	18.5									838.7	21	88.9	1230.71	410.91	3	2.8	VEKDGLILTSR	146	156	39	708.2	23	88.9	1230.68	410.90	3	-22	VEKDGLILTSR	146	156	22.6	424.1	16	50.8	1273.59	425.20	3	-99	Carbamyl-VEKDGLILTSR	146	156	11.8
			93.0	4	18.5									838.7	21	88.9	1564.65	522.22	3	22	MmNGSHYSYSESR	133	145	36.9	708.2	23	88.9	1564.64	522.22	3	15	MmNGSHYSYSESR	133	145	26.6	424.1	16	50.8								
			93.0	4	18.5	755.59	378.30	2	168	APLVLKD	183	189	30.9	838.7	21	88.9	755.46	378.23	2	-14	APLVLKD	183	189	36	708.2	23	88.9	755.43	378.22	2	-43	APLVLKD	183	189	36.5	424.1	16	50.8	755.39	378.20	2	-97	APLVLKD	183	189	28.4
			93.0	4	18.5									838.7	21	88.9	815.46	408.24	2	-41	VTVAGLAGK	33	41	42.3	708.2	23	88.9	815.44	408.22	2	-76	VTVAGLAGK	33	41	43.9	424.1	16	50.8	815.39	408.20	2	-130	VTVAGLAGK	33	41	41.8
			93.0	4	18.5									838.7	21	88.9									708.2	23	88.9	883.54	442.27	2	-81	RALVILAK	5	12	25.1	424.1	16	50.8	883.59	442.30	2	-18	RALVILAK	5	12	33.6
			93.0	4	18.5									838.7	21	88.9	866.52	433.76	2	8.2	VTTHPLAK	123	130	29.9	708.2	23	88.9	866.49	433.75	2	-21	VTTHPLAK	123	130	30.3	424.1	16	50.8	866.39	433.70	2	-135	VTTHPLAK	123	130	13.6
			93.0	4	18.5									838.7	21	88.9									708.2	23	88.9	1707.80	854.40	2	5.6	GAEEmETVIPVDVmR	13	27	33	424.1	16	50.8								
			93.0	4	18.5									838.7	21	88.9	2550.36	510.88	5	-3.7	KGLIAAICAGPTALLAHEVGFGCK	99	122	33.5	708.2	23	88.9									424.1	16	50.8								
			93.0	4	18.5									838.7	21	88.9	1580.62	527.55	3	8.9	mmNGSHYSYSESR	133	145	28.1	708.2	23	88.9									424.1	16	50.8	1580.49	527.50	3	-79	mmNGSHYSYSESR	133	145	18.6
			93.0	4	18.5									838.7	21	88.9									708.2	23	88.9	1691.82	846.41	2	13	GAEEmETVIPVDVMR	13	27	33	424.1	16	50.8								
			93.0	4	18.5									838.7	21	88.9	874.51	437.76	2	7.3	DGLILTSR	149	156	31.4	708.2	23	88.9	874.48	437.74	2	-20	DGLILTSR	149	156	36.3	424.1	16	50.8	874.39	437.70	2	-122	DGLILTSR	149	156	21.7
			93.0	4	18.5									838.7	21	88.9	3547.81	887.71	4	-20	DGLILTSRGPGTSFEFALAIVEALVGKDMANQVK	149	182	28.3	708.2	23	88.9	3547.76	887.70	4	-34	DGLILTSRGPGTSFEFALAIVEALVGKDMANQVK	149	182	24.1	424.1	16	50.8								
			93.0	4	18.5									838.7	21	88.9									708.2	23	88.9									424.1	16	50.8	1342.59	448.20	3	-178	Acetyl-MASKRALVILAK	1	12	21.1
			93.0	4	18.5									838.7	21	88.9									708.2	23	88.9									424.1	16	50.8	1564.59	522.20	3	-19	mMNGSHYSYSESR	133	145	21.9
			93.0	4	18.5	727.59	364.30	2	117	ALVILAK	6	12	27.6	838.7	21	88.9	727.50	364.25	2	-9.8	ALVILAK	6	12	29.9	708.2	23	88.9	727.49	364.25	2	-21	ALVILAK	6	12	24.7	424.1	16	50.8	727.39	364.20	2	-158	ALVILAK	6	12	27.1
			93.0	4	18.5									838.7	21	88.9									708.2	23	88.9	909.43	455.22	2	0.5	DPVQCSR	42	48	16.5	424.1	16	50.8								
			93.0	4	18.5									838.7	21	88.9									708.2	23	88.9	805.39	403.20	2	7.1	DMANQVK	176	182	9.3	424.1	16	50.8								
			93.0	4	18.5	1557.98	390.25	4	96	DmANQVKAPLVLKD	176	189	13.7	838.7	21	88.9									708.2	23	88.9									424.1	16	50.8								
Tim8A	IPI00125776.1	11,043	124.4	3	52.6	3106.59	1036.20	3	39	Carbamyl-MESSTSSSGSALGAVDPQLQHFIEVETQK	1	29	48.8	114.6	3	52.6	3105.45	1035.82	3	-6.4	Acetyl-MESSTSSSGSALGAVDPQLQHFIEVETQK	1	29	49.3	51.9	2	22.7									42.0	1	11.3								
			124.4	3	52.6	1353.79	677.40	2	57	FIDTSQFILNR	70	80	51.8	114.6	3	52.6	1353.72	677.36	2	-0.27	FIDTSQFILNR	70	80	41.2	51.9	2	22.7	1353.72	677.36	2	-0.76	FIDTSQFILNR	70	80	38	42.0	1	11.3	1353.59	677.30	2	-91	FIDTSQFILNR	70	80	42
			124.4	3	52.6	1195.59	598.30	2	7.2	SKPVFSESLSD	87	97	23.8	114.6	3	52.6	1195.60	598.30	2	9.2	SKPVFSESLSD	87	97	24.1	51.9	2	22.7	1195.59	598.30	2	9	SKPVFSESLSD	87	97	13.9	42.0	1	11.3								
Tim13	IPI00134484.1	10,458	133.4	3	43.2	1552.99	777.00	2	72	VQIAVANAQELLQR	28	41	51.4	144.7	3	43.2	1552.88	776.95	2	1.8	VQIAVANAQELLQR	28	41	52.2	66.7	2	26.3	1552.90	776.95	2	14	VQIAVANAQELLQR	28	41	26.7	53.2	2	28.4								
			133.4	3	43.2	1518.59	759.80	2	-16	Acetyl-MDSGFGSDFGGTGGGK	1	16	44.7	144.7	3	43.2	1518.62	759.82	2	4.7	Acetyl-MDSGFGSDFGGTGGGK	1	16	45.9	66.7	2	26.3									53.2	2	28.4	1518.59	759.80	2	-16	Acetyl-MDSGFGSDFGGTGGGK	1	16	30.8
			133.4	3	43.2	1200.59	600.80	2	-30	LDPGAIMEQVK	17	27	37.3	144.7	3	43.2	1200.65	600.83	2	14	LDPGAIMEQVK	17	27	46.6	66.7	2	26.3	1200.63	600.82	2	4	LDPGAIMEQVK	17	27	40	53.2	2	28.4	1200.59	600.80	2	-30	LDPGAIMEQVK	17	27	22.4
10 kDa heat shock protein, mitochondrial	IPI00263863.7	10,832	111.2	4	38.6	1529.79	510.60	3	-9.4	VVLDDKDYFLFR	80	91	28.1	131.7	4	38.6	1529.81	510.61	3	4.9	VVLDDKDYFLFR	80	91	44.3	42.4	2	16.8									83.6	3	26.7								
			111.2	4	38.6	1076.59	538.80	2	-5.5	VLLPEYGGTK	70	79	26.6	131.7	4	38.6	1076.61	538.81	2	8.4	VLLPEYGGTK	70	79	34.9	42.4	2	16.8	1076.62	538.81	2	17	VLLPEYGGTK	70	79	24.1	83.6	3	26.7	1076.59	538.80	2	-5.5	VLLPEYGGTK	70	79	34
			111.2	4	38.6	907.59	454.30	2	98	FLPLFDR	8	14	28.9	131.7	4	38.6	907.51	454.26	2	11	FLPLFDR	8	14	26.6	42.4	2	16.8	907.49	454.25	2	-14	FLPLFDR	8	14	18.3	83.6	3	26.7	907.39	454.20	2	-122	FLPLFDR	8	14	19.1
			111.2	4	38.6	1044.59	522.80	2	34	SGEIEPVSVK	56	65	27.6	131.7	4	38.6	1044.58	522.79	2	20	SGEIEPVSVK	56	65	25.9	42.4	2	16.8									83.6	3	26.7	1044.59	522.80	2	34	SGEIEPVSVK	56	65	30.5
Tubulin beta	IPI00117352.1	49,671	192.4	5	13.7									370.9	11	32.9	2798.33	933.45	3	-4.6	SGPFGQIFRPDNFVFGQSGAGNNWAK	78	103	48	82.7	3	9.0									145.6	6	17.8								
			192.4	5	13.7									370.9	11	32.9	1301.66	651.33	2	14	ISVYYNEATGGK	47	58	39.3	82.7	3	9.0									145.6	6	17.8								
			192.4	5	13.7	1615.79	808.40	2	-27	AILVDLEPGTMDSVR	63	77	42.1	370.9	11	32.9	1615.84	808.43	2	4.7	AILVDLEPGTMDSVR	63	77	42.4	82.7	3	9.0									145.6	6	17.8	1615.79	808.40	2	-27	AILVDLEPGTMDSVR	63	77	30.6
			192.4	5	13.7	1319.79	660.40	2	68	IMNTFSVVPSPK	163	174	42	370.9	11	32.9	1319.72	660.36	2	11	IMNTFSVVPSPK	163	174	39.6	82.7	3	9.0	1319.69	660.35	2	-6	IMNTFSVVPSPK	163	174	22.4	145.6	6	17.8	1319.59	660.30	2	-83	IMNTFSVVPSPK	163	174	32.4
			192.4	5	13.7	1130.59	565.80	2	-2.3	FPGQLNADLR	242	251	36.6	370.9	11	32.9	1130.61	565.81	2	13	FPGQLNADLR	242	251	35.4	82.7	3	9.0									145.6	6	17.8	1130.59	565.80	2	-2.3	FPGQLNADLR	242	251	28.4
			192.4	5	13.7	1696.79	848.90	2	-24	NSSYFVEWIPNNVK	337	350	33.9	370.9	11	32.9	1696.84	848.92	2	3.3	NSSYFVEWIPNNVK	337	350	31.5	82.7	3	9.0									145.6	6	17.8								
			192.4	5	13.7	1143.59	572.30	2	-36	LAVNMVPFPR	253	262	37.8	370.9	11	32.9	1143.64	572.32	2	5.3	LAVNMVPFPR	253	262	34.7	82.7	3	9.0	1143.63	572.32	2	-0.34	LAVNMVPFPR	253	262	24.3	145.6	6	17.8	1143.59	572.30	2	-36	LAVNMVPFPR	253	262	21.2
			192.4	5	13.7									370.9	11	32.9	1620.83	540.95	3	-1.3	LHFFMPGFAPLTSR	263	276	30.1	82.7	3	9.0									145.6	6	17.8	1620.69	540.90	3	-93	LHFFMPGFAPLTSR	263	276	20.4
			192.4	5	13.7									370.9	11	32.9	1229.61	615.31	2	12	ISEQFTAMFR	381	390	37.1	82.7	3	9.0									145.6	6	17.8								
			192.4	5	13.7									370.9	11	32.9									82.7	3	9.0	1958.93	653.65	3	-26	GHYTEGAELVDSVLDVVR	104	121	36	145.6	6	17.8	1958.79	653.60	3	-100	GHYTEGAELVDSVLDVVR	104	121	12.6
			192.4	5	13.7									370.9	11	32.9	1659.91	830.46	2	10	ALTVPELTQQVFDAK	283	297	17.3	82.7	3	9.0									145.6	6	17.8								
			192.4	5	13.7									370.9	11	32.9	2393.82	798.61	3	-164	IREEYPDRImNTFSVVPSPK	155	174	15.5	82.7	3	9.0									145.6	6	17.8								
CPN10-like protein	IPI00120045.1	10,978	82.3	3	31.4	1529.79	510.60	3	-9.4	VVLDDKDYFLFR	81	92	28.1	105.1	3	31.4	1529.81	510.61	3	4.9	VVLDDKDYFLFR	81	92	44.3	24.1	1	9.8									64.5	2	19.6								
			82.3	3	31.4	1076.59	538.80	2	-5.5	VLLPEYGGTK	71	80	26.6	105.1	3	31.4	1076.61	538.81	2	8.4	VLLPEYGGTK	71	80	34.9	24.1	1	9.8	1076.62	538.81	2	17	VLLPEYGGTK	71	80	24.1	64.5	2	19.6	1076.59	538.80	2	-5.5	VLLPEYGGTK	71	80	34
			82.3	3	31.4	1044.59	522.80	2	34	SGEIEPVSVK	57	66	27.6	105.1	3	31.4	1044.58	522.79	2	20	SGEIEPVSVK	57	66	25.9	24.1	1	9.8									64.5	2	19.6	1044.59	522.80	2	34	SGEIEPVSVK	57	66	30.5
60S ribosomal protein P2	IPI00139795.2	11,651	89.5	3	31.3	1773.09	591.70	3	103	ILDSVGIEADDDRLNK	26	41	39.3																																	
			89.5	3	31.3	1242.79	621.90	2	100	NIEDVIAQGVGK	50	61	23.6																																	
			89.5	3	31.3	859.59	430.30	2	121	VISELNGK	42	49	26.6																																	
GAPDH	IPI00463022.1	35,762	85.6	3	7.8									256.2	7	30.0	2213.09	738.37	3	-6.6	VIISAPSADAPMFVMGVNHEK	117	137	63.9	83.3	4	13.2									117.7	5	24.9	2212.89	738.30	3	-101	VIISAPSADAPMFVMGVNHEK	117	137	40.3
			85.6	3	7.8									256.2	7	30.0	1604.85	535.62	3	1.6	VPTPNVSVVDLTCR	233	246	43.8	83.3	4	13.2	1604.84	535.62	3	-4.9	VPTPNVSVVDLTCR	233	246	22.8	117.7	5	24.9								
			85.6	3	7.8	1227.59	614.30	2	-15	VVDLMAYMASK	322	332	35.1	256.2	7	30.0	1227.62	614.32	2	10	VVDLMAYMASK	322	332	36.4	83.3	4	13.2									117.7	5	24.9								
			85.6	3	7.8									256.2	7	30.0	1369.76	685.38	2	11	GAAQNIIPASTGAAK	199	213	39.9	83.3	4	13.2	1369.75	685.38	2	7.8	GAAQNIIPASTGAAK	199	213	25.5	117.7	5	24.9	1369.79	685.40	2	36	GAAQNIIPASTGAAK	199	213	32.7
			85.6	3	7.8	805.39	403.20	2	-48	VGVNGFGR	4	11	29.9	256.2	7	30.0	805.44	403.22	2	9.3	VGVNGFGR	4	11	23.6	83.3	4	13.2	805.43	403.22	2	-0.33	VGVNGFGR	4	11	16.9	117.7	5	24.9								
			85.6	3	7.8									256.2	7	30.0	2595.32	649.58	4	-17	VIHDNFGIVEGLMTTVHAITATQK	161	184	27.2	83.3	4	13.2									117.7	5	24.9								
			85.6	3	7.8	795.39	398.20	2	-32	LTGMAFR	226	232	20.6	256.2	7	30.0	795.44	398.22	2	25	LTGMAFR	226	232	21.4	83.3	4	13.2	795.42	398.21	2	-1.8	LTGMAFR	226	232	18.1	117.7	5	24.9	795.39	398.20	2	-32	LTGMAFR	226	232	16.1
			85.6	3	7.8									256.2	7	30.0									83.3	4	13.2									117.7	5	24.9	3395.47	679.90	5	-75	Carbamyl-VIHDNFGIVEGLmTTVHAITATQKTVDGPSGK	161	192	19.9
			85.6	3	7.8									256.2	7	30.0									83.3	4	13.2									117.7	5	24.9	869.39	435.20	2	-134	VIPELNGK	218	225	8.7
HspA8	IPI00323357.3	70,872												249.3	9	21.5	1659.88	830.45	2	-7	IINEPTAAAIAYGLDK	172	187	39.3	277.2	13	23.1									307.6	14	26.2	1659.79	830.40	2	-62	IINEPTAAAIAYGLDK	172	187	27.9
														249.3	9	21.5	1649.81	825.41	2	8.8	NQVAMNPTNTVFDAK	57	71	35.2	277.2	13	23.1	1649.82	825.42	2	18	NQVAMNPTNTVFDAK	57	71	15.4	307.6	14	26.2	1649.79	825.40	2	-1.5	NQVAMNPTNTVFDAK	57	71	32
														249.3	9	21.5	1653.87	551.96	3	22	HWPFMVVNDAGRPK	89	102	34.6	277.2	13	23.1	1653.83	551.95	3	0.33	HWPFMVVNDAGRPK	89	102	38.4	307.6	14	26.2								
														249.3	9	21.5	1691.75	564.59	3	14	STAGDTHLGGEDFDNR	221	236	31.6	277.2	13	23.1	1691.73	564.58	3	-0.06	STAGDTHLGGEDFDNR	221	236	35.5	307.6	14	26.2	1691.79	564.60	3	35	STAGDTHLGGEDFDNR	221	236	19.4
														249.3	9	21.5									277.2	13	23.1	1788.00	596.67	3	3.2	IINEPTAAAIAYGLDKK	172	188	29.2	307.6	14	26.2								
														249.3	9	21.5	1982.03	661.35	3	17	TVTNAVVTVPAYFNDSQR	138	155	28.1	277.2	13	23.1									307.6	14	26.2	1981.89	661.30	3	-57	TVTNAVVTVPAYFNDSQR	138	155	30.3
														249.3	9	21.5									277.2	13	23.1	858.46	429.73	2	4.4	GTLDPVEK	312	319	26.7	307.6	14	26.2	858.39	429.70	2	-75	GTLDPVEK	312	319	18.4
														249.3	9	21.5	992.57	496.79	2	6.7	VCNPIITK	602	609	28.1	277.2	13	23.1									307.6	14	26.2	992.59	496.80	2	33	VCNPIITK	602	609	19.6
														249.3	9	21.5									277.2	13	23.1	1199.69	600.35	2	9.9	DAGTIAGLNVLR	160	171	25.8	307.6	14	26.2								
														249.3	9	21.5									277.2	13	23.1	1303.63	652.32	2	26	NSLESYAFNMK	540	550	21.9	307.6	14	26.2	1303.59	652.30	2	-4.6	NSLESYAFNMK	540	550	27
														249.3	9	21.5									277.2	13	23.1	993.53	497.27	2	3.2	EIAEAYLGK	129	137	18.4	307.6	14	26.2	993.59	497.30	2	68	EIAEAYLGK	129	137	26.8
														249.3	9	21.5									277.2	13	23.1									307.6	14	26.2	1253.59	627.30	2	-19	FEELNADLFR	302	311	28.7
														249.3	9	21.5									277.2	13	23.1	1228.64	614.83	2	14	VEIIANDQGNR	26	36	21.9	307.6	14	26.2								
														249.3	9	21.5	1481.83	494.61	3	14	SQIHDIVLVGGSTR	329	342	18.8	277.2	13	23.1	1481.81	494.61	3	-0.16	SQIHDIVLVGGSTR	329	342	11.8	307.6	14	26.2	1481.79	494.60	3	-15	SQIHDIVLVGGSTR	329	342	11.6
														249.3	9	21.5									277.2	13	23.1	1081.59	541.30	2	23	LLQDFFNGK	349	357	14.1	307.6	14	26.2								
														249.3	9	21.5	3378.69	676.54	5	60	LYQSAGGmPGGmPGGFPGGGAPPSGGASSGPTIEEVD	610	646	14.2	277.2	13	23.1									307.6	14	26.2								
														249.3	9	21.5									277.2	13	23.1									307.6	14	26.2	1616.79	808.90	2	3.1	SFYPEEVSSMVLTK	113	126	20.1
														249.3	9	21.5									277.2	13	23.1	765.41	383.21	2	-1.6	VQVEYK	103	108	9.3	307.6	14	26.2	765.39	383.20	2	-28	VQVEYK	103	108	8.9
														249.3	9	21.5	1864.89	622.30	3	-6.2	Carbamyl-NQVAmNPTNTVFDAKR	57	72	19.4	277.2	13	23.1									307.6	14	26.2								
														249.3	9	21.5									277.2	13	23.1	804.44	402.73	2	-1.9	ITITNDK	501	507	8.8	307.6	14	26.2								
														249.3	9	21.5									277.2	13	23.1									307.6	14	26.2	1325.59	663.30	2	-48	CNEIISWLDK	574	583	19.8
														249.3	9	21.5									277.2	13	23.1									307.6	14	26.2	2442.98	611.50	4	-105	Carbamyl-HWPFMVVNDAGRPKVQVEYK	89	108	17.1
60 kDa heat shock protein, mitochondrial precurs	IPI00308885.5	60,956	258.6	7	13.3									351.6	9	23.4	2560.28	854.10	3	14	LVQDVANNTNEEAGDGTTTATVLAR	97	121	55.9	128.7	7	13.1									127.6	6	8.7								
			258.6	7	13.3									351.6	9	23.4	1905.04	635.68	3	-8.3	ISSVQSIVPALEIANAHR	251	268	47.5	128.7	7	13.1									127.6	6	8.7								
			258.6	7	13.3	2113.29	705.10	3	69	ALMLQGVDLLADAVAVTMGPK	38	58	46.5	351.6	9	23.4	2113.08	705.03	3	-27	ALMLQGVDLLADAVAVTMGPK	38	58	47.5	128.7	7	13.1	2113.12	705.04	3	-11	ALMLQGVDLLADAVAVTMGPK	38	58	35.9	127.6	6	8.7								
			258.6	7	13.3	1344.79	672.90	2	57	TVIIEQSWGSPK	61	72	44.8	351.6	9	23.4	1344.72	672.86	2	5	TVIIEQSWGSPK	61	72	35.3	128.7	7	13.1									127.6	6	8.7								
			258.6	7	13.3	1176.59	588.80	2	-0.15	DIGNIISDAMK	181	191	37.6	351.6	9	23.4	1176.60	588.81	2	9.2	DIGNIISDAMK	181	191	36.9	128.7	7	13.1									127.6	6	8.7								
			258.6	7	13.3									351.6	9	23.4	2532.17	844.73	3	-13	ILQSSSEVGYDAMLGDFVNMVEK	494	516	33.5	128.7	7	13.1									127.6	6	8.7								
			258.6	7	13.3	912.59	456.80	2	5.5	VGLQVVAVK	293	301	38.9	351.6	9	23.4	912.59	456.80	2	6.7	VGLQVVAVK	293	301	39.6	128.7	7	13.1									127.6	6	8.7	912.59	456.80	2	5.5	VGLQVVAVK	293	301	25.9
			258.6	7	13.3	855.59	428.30	2	145	GANPVEIR	134	141	31.8	351.6	9	23.4									128.7	7	13.1									127.6	6	8.7	855.39	428.20	2	-88	GANPVEIR	134	141	25.1
			258.6	7	13.3	844.59	422.80	2	93	VGEVIVTK	345	352	29.9	351.6	9	23.4	844.52	422.77	2	13	VGEVIVTK	345	352	32	128.7	7	13.1	844.51	422.76	2	-9.3	VGEVIVTK	345	352	18.9	127.6	6	8.7	844.39	422.70	2	-143	VGEVIVTK	345	352	29.9
			258.6	7	13.3	785.59	393.30	2	101	IGIEIIK	463	469	29.1	351.6	9	23.4	785.52	393.27	2	13	IGIEIIK	463	469	23.4	128.7	7	13.1	785.50	393.25	2	-16	IGIEIIK	463	469	12.9	127.6	6	8.7	785.39	393.20	2	-153	IGIEIIK	463	469	17.4
			258.6	7	13.3									351.6	9	23.4									128.7	7	13.1	805.43	403.22	2	25	DDAMLLK	353	359	19.8	127.6	6	8.7								
			258.6	7	13.3									351.6	9	23.4									128.7	7	13.1	743.42	372.22	2	-9.5	GIIDPTK	517	523	15.9	127.6	6	8.7								
			258.6	7	13.3									351.6	9	23.4									128.7	7	13.1	833.41	417.21	2	26	APGFGDNR	302	309	10.1	127.6	6	8.7								
			258.6	7	13.3									351.6	9	23.4									128.7	7	13.1	1732.89	578.30	3	-32	AAVEEGIVLGGGCALLR	430	446	15.2	127.6	6	8.7								
			258.6	7	13.3									351.6	9	23.4									128.7	7	13.1									127.6	6	8.7	960.39	480.70	2	-123	VTDALNATR	421	429	17.9
			258.6	7	13.3									351.6	9	23.4									128.7	7	13.1									127.6	6	8.7	959.50	959.50	1	-54	Carbamyl-GVITVKDGK	197	205	11.4
Peroxiredoxin-1	IPI00121788.1	22,177												162.6	5	23.1	1196.64	598.82	2	8.2	LVQAFQFTDK	159	168	37.4	19.6	1	4.0																			
														162.6	5	23.1	1107.61	554.31	2	8.2	TIAQDYGVLK	111	120	38.1	19.6	1	4.0																			
														162.6	5	23.1	1225.70	613.35	2	7.1	QITINDLPVGR	141	151	34.1	19.6	1	4.0																			
														162.6	5	23.1	920.52	460.76	2	7.2	GLFIIDDK	129	136	27.8	19.6	1	4.0	920.50	460.76	2	-4.3	GLFIIDDK	129	136	19.6											
														162.6	5	23.1	831.48	416.24	2	28	SVDEIIR	152	158	25.2	19.6	1	4.0																			
PACSIN2	IPI00125880.1	55,833	308.7	9	18.9	1943.79	648.60	3	-41	ALYDYEGQEHDELSFK	433	448	54.1	310.8	9	19.8	1943.89	648.64	3	13	ALYDYEGQEHDELSFK	433	448	44.5	224.5	10	22.8	1943.86	648.63	3	-0.44	ALYDYEGQEHDELSFK	433	448	29.3	161.7	7	14.2								
			308.7	9	18.9	1336.59	668.80	2	-54	AYAQQLTEWAR	54	64	50.3	310.8	9	19.8	1336.66	668.84	2	0.33	AYAQQLTEWAR	54	64	46	224.5	10	22.8	1336.68	668.84	2	10	AYAQQLTEWAR	54	64	35.3	161.7	7	14.2	1336.59	668.80	2	-54	AYAQQLTEWAR	54	64	35.8
			308.7	9	18.9									310.8	9	19.8	1211.64	606.32	2	8.8	ADPSLNPEQLK	178	188	43.9	224.5	10	22.8									161.7	7	14.2								
			308.7	9	18.9	1183.59	592.30	2	53	ASLMNEDFEK	102	111	34.5	310.8	9	19.8	1183.54	592.27	2	7.5	ASLMNEDFEK	102	111	41.6	224.5	10	22.8	1183.53	592.27	2	1.4	ASLMNEDFEK	102	111	17.1	161.7	7	14.2	1183.39	592.20	2	-116	ASLMNEDFEK	102	111	34.5
			308.7	9	18.9	1246.59	416.20	3	-46	HLDLSNVASYK	254	264	40.1	310.8	9	19.8	1246.65	416.22	3	3.3	HLDLSNVASYK	254	264	28.4	224.5	10	22.8	1246.63	623.82	2	-7.9	HLDLSNVASYK	254	264	28.1	161.7	7	14.2								
			308.7	9	18.9									310.8	9	19.8	1936.96	968.99	2	-0.99	LDSGQVGLYPANYVEAIQ	469	486	33.5	224.5	10	22.8	1936.97	968.99	2	3.1	LDSGQVGLYPANYVEAIQ	469	486	29.9	161.7	7	14.2								
			308.7	9	18.9	1613.79	538.60	3	29	LCGDLMNCLHER	37	48	32.4	310.8	9	19.8									224.5	10	22.8									161.7	7	14.2								
			308.7	9	18.9	959.59	480.30	2	118	AADAVEDLR	276	284	25.6	310.8	9	19.8	959.51	480.26	2	27	AADAVEDLR	276	284	22.6	224.5	10	22.8	959.48	480.25	2	3.9	AADAVEDLR	276	284	24.8	161.7	7	14.2	959.39	480.20	2	-90	AADAVEDLR	276	284	30.4
			308.7	9	18.9	957.59	479.30	2	33	EVLLEVQK	246	253	27.2	310.8	9	19.8	957.57	479.29	2	4.3	EVLLEVQK	246	253	30.9	224.5	10	22.8	957.55	479.28	2	-7.7	EVLLEVQK	246	253	17.6	161.7	7	14.2	957.59	479.30	2	33	EVLLEVQK	246	253	30.4
			308.7	9	18.9	1339.89	447.30	3	122	ADPSLNPEQLKK	178	189	23.1	310.8	9	19.8									224.5	10	22.8	1339.73	447.25	3	6.3	ADPSLNPEQLKK	178	189	15.1	161.7	7	14.2								
			308.7	9	18.9									310.8	9	19.8	2150.09	717.37	3	1	GRLDSGQVGLYPANYVEAIQ	467	486	19.4	224.5	10	22.8									161.7	7	14.2								
			308.7	9	18.9	2634.97	527.80	5	-172	FFREVLLEVQKHLDLSNVASYK	243	264	21.4	310.8	9	19.8									224.5	10	22.8									161.7	7	14.2								
			308.7	9	18.9									310.8	9	19.8									224.5	10	22.8	978.50	489.75	2	6.9	GPQYGTVEK	73	81	13.9	161.7	7	14.2								
			308.7	9	18.9									310.8	9	19.8									224.5	10	22.8	798.38	399.69	2	16	QMMGGFK	123	129	13.4	161.7	7	14.2	798.39	399.70	2	36	QMMGGFK	123	129	12.6
			308.7	9	18.9									310.8	9	19.8									224.5	10	22.8									161.7	7	14.2	1618.89	540.30	3	26	Carbamyl-QLVEKGPQYGTVEK	68	81	11.4
			308.7	9	18.9									310.8	9	19.8									224.5	10	22.8									161.7	7	14.2	1181.49	394.50	3	-49	ETKEAEDGFR	130	139	6.6
Actin, cytoplasmic 1	IPI00110850.1	41,737	33.1	1	2.9									139.1	5	12.5									119.8	5	14.1									159.6	7	20.0	1869.79	935.40	2	-23	Acetyl-DDDIAALVVDNGSGMCK	1	18	42.1
			33.1	1	2.9									139.1	5	12.5									119.8	5	14.1	1954.07	652.03	3	4.4	VAPEEHPVLLTEAPLNPK	96	113	41	159.6	7	20.0								
			33.1	1	2.9									139.1	5	12.5	976.47	488.74	2	22	AGFAGDDAPR	19	28	31.9	119.8	5	14.1	976.44	488.72	2	-7.8	AGFAGDDAPR	19	28	31.6	159.6	7	20.0	976.39	488.70	2	-57	AGFAGDDAPR	19	28	36
			33.1	1	2.9	1161.59	581.30	2	-22	EITALAPSTMK	316	326	33.1	139.1	5	12.5	1161.62	581.31	2	2.6	EITALAPSTMK	316	326	35	119.8	5	14.1									159.6	7	20.0								
			33.1	1	2.9									139.1	5	12.5									119.8	5	14.1	1132.54	566.77	2	14	GYSFTTTAER	197	206	17.1	159.6	7	20.0	1132.39	566.70	2	-119	GYSFTTTAER	197	206	26.1
			33.1	1	2.9									139.1	5	12.5	1171.60	391.21	3	28	HQGVMVGMGQK	40	50	26.4	119.8	5	14.1									159.6	7	20.0	1171.59	391.20	3	12	HQGVMVGMGQK	40	50	16.8
			33.1	1	2.9									139.1	5	12.5	998.49	499.75	2	2.9	DLTDYLMK	184	191	24.5	119.8	5	14.1	998.48	499.74	2	-11	DLTDYLMK	184	191	14.9	159.6	7	20.0	998.39	499.70	2	-94	DLTDYLMK	184	191	18.1
			33.1	1	2.9									139.1	5	12.5	795.49	398.25	2	17	IIAPPER	329	335	21.3	119.8	5	14.1	795.47	398.24	2	-3.6	IIAPPER	329	335	15.2	159.6	7	20.0	795.39	398.20	2	-100	IIAPPER	329	335	12.6
			33.1	1	2.9									139.1	5	12.5									119.8	5	14.1									159.6	7	20.0	1198.59	400.20	3	-100	AVFPSIVGRPR	29	39	7.9
ADP/ATP translocase 2	IPI00127841.2	32,800	50.4	2	5.7	1121.59	561.30	2	17	EQGVLSFWR	63	71	27.8	85.6	4	12.1	1121.58	561.30	2	9.6	EQGVLSFWR	63	71	32	99.1	5	15.2	1121.60	561.31	2	27	EQGVLSFWR	63	71	17.8	86.8	4	19.9	1121.59	561.30	2	17	EQGVLSFWR	63	71	27.7
			50.4	2	5.7									85.6	4	12.1									99.1	5	15.2	951.50	476.25	2	19	Acetyl-TDAAVSFAK	1	9	25.9	86.8	4	19.9								
			50.4	2	5.7	856.59	428.80	2	108	GNLANVIR	72	79	22.6	85.6	4	12.1	856.51	428.76	2	9.7	GNLANVIR	72	79	24.5	99.1	5	15.2									86.8	4	19.9	856.39	428.70	2	-125	GNLANVIR	72	79	22.5
			50.4	2	5.7									85.6	4	12.1									99.1	5	15.2	1446.75	723.88	2	4.5	YFPTQALNFAFK	80	91	23.2	86.8	4	19.9	1446.79	723.90	2	35	YFPTQALNFAFK	80	91	18.7
			50.4	2	5.7									85.6	4	12.1	856.50	428.76	2	18	TAVAPIER	23	30	16.3	99.1	5	15.2	856.49	428.75	2	-1.3	TAVAPIER	23	30	20.6	86.8	4	19.9								
			50.4	2	5.7									85.6	4	12.1	1219.59	610.30	2	-5.4	AAYFGIYDTAK	188	198	12.8	99.1	5	15.2									86.8	4	19.9								
			50.4	2	5.7									85.6	4	12.1									99.1	5	15.2									86.8	4	19.9	2989.97	598.80	5	124	Acetyl-TDAAVSFAKDFLAGGVAAAISKTAVAPIER	1	30	17.9
			50.4	2	5.7									85.6	4	12.1									99.1	5	15.2	840.35	420.68	2	1.7	MMMQSGR	237	243	11.6	86.8	4	19.9								
60S ribosomal protein L12	IPI00338838.3	17,793	86.5	2	15.2	1723.89	575.30	3	25	EILGTAQSVGCNVDGR	131	146	50												21.1	1	5.5																			
			86.5	2	15.2	881.59	441.30	2	54	IGPLGLSPK	32	40	36.5												21.1	1	5.5	881.51	441.26	2	-39	IGPLGLSPK	32	40	21.1											
Tubulin alpha	IPI00403810.2	49,910	183.5	5	13.4	1410.69	470.90	3	-63	QLFHPEQLITGK	85	96	45	75.0	3	7.8	1410.80	470.94	3	20	QLFHPEQLITGK	85	96	22.9	119.6	5	13.4	1410.77	470.93	3	-3.5	QLFHPEQLITGK	85	96	24.1	122.4	5	13.8	1410.69	470.90	3	-63	QLFHPEQLITGK	85	96	20.3
			183.5	5	13.4	1701.99	851.50	2	51	AVFVDLEPTVIDEVR	65	79	39.5	75.0	3	7.8									119.6	5	13.4	1701.93	851.47	2	12	AVFVDLEPTVIDEVR	65	79	36.8	122.4	5	13.8	1701.79	851.40	2	-66	AVFVDLEPTVIDEVR	65	79	30.3
			183.5	5	13.4	1756.89	586.30	3	-44	IHFPLATYAPVISAEK	265	280	41.5	75.0	3	7.8	1756.96	586.32	3	-2.4	IHFPLATYAPVISAEK	265	280	35.5	119.6	5	13.4	1756.95	586.32	3	-5.3	IHFPLATYAPVISAEK	265	280	18.2	122.4	5	13.8	1756.89	586.30	3	-44	IHFPLATYAPVISAEK	265	280	19.1
			183.5	5	13.4	1015.59	508.30	2	14	DVNAAIATIK	327	336	29.7	75.0	3	7.8									119.6	5	13.4	1015.58	508.29	2	2	DVNAAIATIK	327	336	21.1	122.4	5	13.8	1015.59	508.30	2	14	DVNAAIATIK	327	336	32.3
			183.5	5	13.4	887.39	444.20	2	-46	FDLMYAK	395	401	27.8	75.0	3	7.8	887.45	444.23	2	17	FDLMYAK	395	401	16.6	119.6	5	13.4									122.4	5	13.8								
			183.5	5	13.4									75.0	3	7.8									119.6	5	13.4	781.41	391.21	2	4	LSVDYGK	157	163	19.4	122.4	5	13.8								
			183.5	5	13.4									75.0	3	7.8									119.6	5	13.4									122.4	5	13.8	1085.59	543.30	2	-25	EIIDLVLDR	113	121	20.4
Elongation factor 1-alpha 1	IPI00307837.4	50,314	39.5	1	2.4									177.8	6	13.8	2515.36	839.13	3	-7.9	VETGVLKPGMVVTFAPVNVTTEVK	269	292	48	99.9	5	9.5									112.5	4	10.3	2515.29	839.10	3	-39	VETGVLKPGMVVTFAPVNVTTEVK	269	292	34.5
			39.5	1	2.4	1025.59	513.30	2	-17	IGGIGTVPVGR	258	268	39.5	177.8	6	13.8	1025.63	513.32	2	15	IGGIGTVPVGR	258	268	37.7	99.9	5	9.5	1025.60	513.30	2	-12	IGGIGTVPVGR	258	268	18.1	112.5	4	10.3								
			39.5	1	2.4									177.8	6	13.8	975.54	488.28	2	-8	LPLQDVYK	250	257	29.8	99.9	5	9.5	975.55	488.28	2	-3.9	LPLQDVYK	250	257	31.1	112.5	4	10.3	975.59	488.30	2	43	LPLQDVYK	250	257	29.6
			39.5	1	2.4									177.8	6	13.8	839.47	420.24	2	24	EVSTYIK	175	181	26.2	99.9	5	9.5	839.46	420.23	2	9.6	EVSTYIK	175	181	13.3	112.5	4	10.3	839.39	420.20	2	-69	EVSTYIK	175	181	20
			39.5	1	2.4									177.8	6	13.8	914.56	457.78	2	-6.6	QTVAVGVIK	433	441	25.9	99.9	5	9.5									112.5	4	10.3	914.59	457.80	2	28	QTVAVGVIK	433	441	28.4
			39.5	1	2.4									177.8	6	13.8									99.9	5	9.5	1120.61	560.81	2	11	STTTGHLIYK	21	30	23.1	112.5	4	10.3								
			39.5	1	2.4									177.8	6	13.8	1455.91	364.73	4	11	QTVAVGVIKAVDKK	433	446	10.2	99.9	5	9.5									112.5	4	10.3								
			39.5	1	2.4									177.8	6	13.8									99.9	5	9.5	870.53	435.77	2	-8.8	QLIVGVNK	149	156	14.3	112.5	4	10.3								
YME1L1	IPI00136555.1	80,029	205.7	8	12.2									239.2	8	11.5	1531.81	511.28	3	13	FDMQVTVPRPDVK	440	452	38.1	133.1	7	9.0									79.1	4	5.6								
			205.7	8	12.2	1108.79	554.90	2	108	GILLVGPPGTGK	316	327	35.9	239.2	8	11.5	1108.79	554.90	2	2.5	GILLVGPPGTGK	316	327	28.3	133.1	7	9.0	1108.67	554.84	2	-2.7	GILLVGPPGTGK	316	327	27.3	79.1	4	5.6	1108.59	554.80	2	-72	GILLVGPPGTGK	316	327	23.4
			205.7	8	12.2	1415.79	708.40	2	2.4	LVEAQNIAPSFVK	167	179	40.6	239.2	8	11.5	1415.78	708.39	2	-4.9	LVEAQNIAPSFVK	167	179	37.5	133.1	7	9.0	1415.81	708.41	2	16	LVEAQNIAPSFVK	167	179	25.6	79.1	4	5.6								
			205.7	8	12.2	999.59	500.30	2	46	SVDPEIIAR	470	478	31.6	239.2	8	11.5	999.56	500.28	2	13	SVDPEIIAR	470	478	35.9	133.1	7	9.0	999.55	500.28	2	7	SVDPEIIAR	470	478	21.2	79.1	4	5.6	999.59	500.30	2	46	SVDPEIIAR	470	478	30.5
			205.7	8	12.2									239.2	8	11.5	969.51	485.26	2	4.2	TGFAEGFLK	212	220	35.9	133.1	7	9.0									79.1	4	5.6								
			205.7	8	12.2	1269.69	423.90	3	50	NIPEAHQDAFK	201	211	32	239.2	8	11.5									133.1	7	9.0									79.1	4	5.6								
			205.7	8	12.2	977.59	489.30	2	117	GTDLESLDK	187	195	27.9	239.2	8	11.5	977.50	489.25	2	20	GTDLESLDK	187	195	28.3	133.1	7	9.0	977.50	489.25	2	18	GTDLESLDK	187	195	17.6	79.1	4	5.6								
			205.7	8	12.2									239.2	8	11.5	1171.59	586.30	2	17	LGVMTYSDTGK	640	650	20.8	133.1	7	9.0									79.1	4	5.6								
			205.7	8	12.2	1489.89	497.30	3	91	DAmPINKATImPR	554	566	13.8	239.2	8	11.5									133.1	7	9.0									79.1	4	5.6								
			205.7	8	12.2									239.2	8	11.5	755.45	378.23	2	112	Carbamyl-SSSLYR	120	125	14.4	133.1	7	9.0	755.44	378.22	2	91	Carbamyl-SSSLYR	120	125	8.8	79.1	4	5.6	755.39	378.20	2	32	Carbamyl-SSSLYR	120	125	11
			205.7	8	12.2	863.39	432.20	2	-34	Carbamyl-LQSTSER	160	166	8.9	239.2	8	11.5									133.1	7	9.0									79.1	4	5.6								
			205.7	8	12.2	1488.98	373.00	4	135	Carbamyl-AQALTQKTNDSLR	221	233	15	239.2	8	11.5									133.1	7	9.0									79.1	4	5.6	1488.98	373.00	4	135	Carbamyl-AQALTQKTNDSLR	221	233	14.2
			205.7	8	12.2									239.2	8	11.5									133.1	7	9.0	815.44	408.23	2	0.07	ILMGPER	519	525	14.5	79.1	4	5.6								
			205.7	8	12.2									239.2	8	11.5									133.1	7	9.0	1808.00	603.34	3	40	ELEFSKDKILmGPER	511	525	18.1	79.1	4	5.6								
Prohibitin	IPI00133440.1	29,820	116.7	3	12.1	1396.89	466.30	3	31	ILFRPVASQLPR	94	105	45.6	26.9	1	4.4	1396.85	466.29	3	3.5	ILFRPVASQLPR	94	105	26.9	19.4	1	3.7									20.2	1	5.9								
			116.7	3	12.1	1185.79	593.40	2	113	DLQNVNITLR	84	93	38.7	26.9	1	4.4									19.4	1	3.7									20.2	1	5.9								
			116.7	3	12.1	1213.79	607.40	2	43	VLPSITTEILK	118	128	32.4	26.9	1	4.4									19.4	1	3.7									20.2	1	5.9								
			116.7	3	12.1									26.9	1	4.4									19.4	1	3.7									20.2	1	5.9	1849.78	463.20	4	-107	KLEAAEDIAYQLSRSR	240	255	20.2
			116.7	3	12.1									26.9	1	4.4									19.4	1	3.7	1149.59	575.30	2	-0.17	FDAGELITQR	134	143	19.4	20.2	1	5.9								
Hsp90, beta	IPI00554929.1	83,195												231.2	7	11.5	1513.80	757.40	2	8.4	GVVDSEDLPLNISR	378	391	43.2	69.0	3	4.0	1513.81	757.41	2	17	GVVDSEDLPLNISR	378	391	25.2	97.2	4	5.8	1513.79	757.40	2	4.7	GVVDSEDLPLNISR	378	391	35.3
														231.2	7	11.5	1275.65	638.33	2	5.8	ELISNASDALDK	41	52	39.5	69.0	3	4.0									97.2	4	5.8	1275.59	638.30	2	-39	ELISNASDALDK	41	52	33.7
														231.2	7	11.5	1242.71	621.86	2	3.3	ADLINNLGTIAK	95	106	36.1	69.0	3	4.0									97.2	4	5.8								
														231.2	7	11.5	2422.15	808.05	3	-15	VFIMDSCDELIPEYLNFIR	359	377	32.9	69.0	3	4.0									97.2	4	5.8								
														231.2	7	11.5	1151.58	576.29	2	19	YIDQEELNK	275	283	26.8	69.0	3	4.0									97.2	4	5.8	1151.59	576.30	2	30	YIDQEELNK	275	283	19.4
														231.2	7	11.5	1194.66	597.83	2	12	IDILPNPQER	72	81	25.3	69.0	3	4.0									97.2	4	5.8								
														231.2	7	11.5	733.46	367.23	2	20	SLVSVTK	531	537	27.4	69.0	3	4.0									97.2	4	5.8	733.39	367.20	2	-72	SLVSVTK	531	537	8.8
														231.2	7	11.5									69.0	3	4.0	1039.52	520.26	2	21	YESLTDPSK	55	63	22.4	97.2	4	5.8								
														231.2	7	11.5									69.0	3	4.0	730.44	365.73	2	-4.3	LSELLR	450	455	21.4	97.2	4	5.8								
Peptidyl-prolyl cis-trans isomerase A	IPI00554989.1	17,840												68.7	2	11.0	1055.55	528.28	2	5.9	VSFELFADK	19	27	37.8	21.9	1	5.5									43.7	2	11.0	1055.59	528.30	2	49	VSFELFADK	19	27	22.3
														68.7	2	11.0	1154.58	577.79	2	6.7	FEDENFILK	82	90	30.9	21.9	1	5.5	1154.58	577.79	2	7.9	FEDENFILK	82	90	21.9	43.7	2	11.0	1154.59	577.80	2	17	FEDENFILK	82	90	21.4
Pyruvate kinase	IPI00407130.3	58,004	49.3	2	7.7									108.4	5	10.3	1171.64	586.32	2	4.4	LDIDSAPITAR	33	43	33.1												43.2	2	4.1	1171.59	586.30	2	-33	LDIDSAPITAR	33	43	20.9
			49.3	2	7.7									108.4	5	10.3	946.52	473.76	2	13	VNLAMDVGK	492	500	33.1												43.2	2	4.1								
			49.3	2	7.7	1019.59	510.30	2	76	GDYPLEAVR	370	378	26.7	108.4	5	10.3																				43.2	2	4.1								
			49.3	2	7.7									108.4	5	10.3	705.43	353.22	2	3.1	VFLAQK	306	311	22.4												43.2	2	4.1								
			49.3	2	7.7									108.4	5	10.3	2301.22	767.74	3	2.9	RLAPITSDPTEAAAVGAVEASFK	402	424	14.3												43.2	2	4.1								
			49.3	2	7.7									108.4	5	10.3	725.47	363.24	2	82	ARGFFK	501	506	5.5												43.2	2	4.1								
			49.3	2	7.7									108.4	5	10.3																				43.2	2	4.1	1141.59	571.30	2	-15	GDLGIEIPAEK	295	305	22.3
			49.3	2	7.7	4408.47	882.50	5	76	AEGSDVANAVLDGADCImLSGETAKGDYPLEAVRMQHLIAR	345	385	22.6	108.4	5	10.3																				43.2	2	4.1								
Actin, gamma	IPI00266875.5	42,880												82.8	3	7.4	976.47	488.74	2	22	AGFAGDDAPR	20	29	31.9	46.5	2	4.6	976.44	488.72	2	-7.8	AGFAGDDAPR	20	29	31.6	78.8	4	10.2	976.39	488.70	2	-57	AGFAGDDAPR	20	29	36
														82.8	3	7.4	1171.60	391.21	3	28	HQGVMVGMGQK	41	51	26.4	46.5	2	4.6									78.8	4	10.2	1171.59	391.20	3	12	HQGVMVGMGQK	41	51	16.8
														82.8	3	7.4	998.49	499.75	2	2.9	DLTDYLMK	185	192	24.5	46.5	2	4.6	998.48	499.74	2	-11	DLTDYLMK	185	192	14.9	78.8	4	10.2	998.39	499.70	2	-94	DLTDYLMK	185	192	18.1
														82.8	3	7.4									46.5	2	4.6									78.8	4	10.2	1198.59	400.20	3	-100	AVFPSIVGRPR	30	40	7.9
Ketoacid dehydrogenase E1, alpha	IPI00331555.2	50,774												82.3	3	9.6	2446.28	816.10	3	0.088	LKPNPSLLFSDVYQEMPAQLR	402	422	47.4																						
														82.3	3	9.6	1627.87	814.44	2	-23	Acetyl-AIVMSAAKIWRPSR	1	15	19.7																						
														82.3	3	9.6	835.45	418.23	2	49	qDHPISR	358	364	15.2																						
Eukaryotic initiation factor 4A-I	IPI00118676.3	46,154	26.8	1	3.9									123.1	4	8.6	1618.88	540.30	3	4.1	LQMEAPHIIVGTPGR	147	161	42.3																						
			26.8	1	3.9									123.1	4	8.6	1555.73	778.37	2	7.9	MFVLDEADEMLSR	178	190	35.1																						
			26.8	1	3.9									123.1	4	8.6	894.46	447.73	2	8.5	VFDMLNR	162	168	27.8																						
			26.8	1	3.9									123.1	4	8.6	1677.90	839.45	2	15	Carbamyl-LQmEAPHIIVGTPGR	147	161	17.9																						
			26.8	1	3.9	1832.19	611.40	3	118	GVAINMVTEEDKRTLR	370	385	26.8	123.1	4	8.6																															
Peroxiredoxin-4	IPI00116254.1	31,053	23.0	1	5.5									61.9	2	6.9	1225.70	613.35	2	7.1	QITLNDLPVGR	216	226	34.1	19.6	1	2.9																			
			23.0	1	5.5									61.9	2	6.9	920.52	460.76	2	7.2	GLFIIDDK	204	211	27.8	19.6	1	2.9	920.50	460.76	2	-4.3	GLFIIDDK	204	211	19.6											
			23.0	1	5.5	1546.89	516.30	3	43	Acetyl-EARSKLLDGTTASR	1	15	23	61.9	2	6.9									19.6	1	2.9																			
Fructose-bisphosphate aldolase A	IPI00221402.6	39,225												41.8	1	3.9	1332.72	666.86	2	13	GILAADESTGSIAK	28	41	41.8	18.4	1	2.5									53.1	2	6.3	1332.59	666.80	2	-81	GILAADESTGSIAK	28	41	29
														41.8	1	3.9									18.4	1	2.5	1044.57	522.79	2	-0.38	QLLLTADDR	60	68	18.4	53.1	2	6.3	1044.59	522.80	2	23	QLLLTADDR	60	68	24.1
HspA9	IPI00133903.1	73,529												120.9	3	5.9	1856.93	619.65	3	14	VEAVNMAEGIIHDTETK	579	595	48.5	47.2	2	3.5																			
														120.9	3	5.9	1290.69	645.85	2	9.9	VQQTVQDLFGR	395	405	35.7	47.2	2	3.5																			
														120.9	3	5.9	1333.74	667.37	2	2.6	AQFEGIVTDLIK	349	360	36.7	47.2	2	3.5	1333.73	667.37	2	-2.3	AQFEGIVTDLIK	349	360	15.6											
														120.9	3	5.9									47.2	2	3.5	1242.68	621.84	2	1.8	DAGQISGLNVLR	207	218	31.6											
ATP synthase, alpha	IPI00130280.1	59,753	34.4	1	1.8									73.4	2	4.0	1171.65	586.33	2	12	VVDALGNAIDGK	150	161	44.1	71.7	3	5.2	1171.63	586.32	2	-4.2	VVDALGNAIDGK	150	161	25	67.1	2	4.0	1171.59	586.30	2	-33	VVDALGNAIDGK	150	161	40.4
			34.4	1	1.8	1026.59	513.80	2	-1.5	AVDSLVPIGR	195	204	34.4	73.4	2	4.0	1026.62	513.81	2	25	AVDSLVPIGR	195	204	29.3	71.7	3	5.2	1026.60	513.81	2	9.4	AVDSLVPIGR	195	204	27.1	67.1	2	4.0	1026.59	513.80	2	-1.5	AVDSLVPIGR	195	204	26.7
			34.4	1	1.8									73.4	2	4.0									71.7	3	5.2	723.45	362.23	2	-4.1	APGIIPR	176	182	19.6	67.1	2	4.0								
Hsp90, alpha	IPI00330804.3	84,657												106.1	3	4.8	1513.80	757.40	2	8.4	GVVDSEDLPLNISR	387	400	43.2	69.0	3	4.0	1513.81	757.41	2	17	GVVDSEDLPLNISR	387	400	25.2	54.7	2	3.1	1513.79	757.40	2	4.7	GVVDSEDLPLNISR	387	400	35.3
														106.1	3	4.8	1242.71	621.86	2	3.3	ADLINNLGTIAK	100	111	36.1	69.0	3	4.0									54.7	2	3.1								
														106.1	3	4.8	1151.58	576.29	2	19	YIDQEELNK	284	292	26.8	69.0	3	4.0									54.7	2	3.1	1151.59	576.30	2	30	YIDQEELNK	284	292	19.4
														106.1	3	4.8									69.0	3	4.0	1039.52	520.26	2	21	YESLTDPSK	60	68	22.4	54.7	2	3.1								
														106.1	3	4.8									69.0	3	4.0	730.44	365.73	2	-4.3	LSELLR	459	464	21.4	54.7	2	3.1								
Enolase 1, alpha non-neuron	IPI00756027.1	47,125												68.1	2	4.1	1439.73	720.37	2	-6.2	YITPDQLADLYK	270	281	48												28.6	1	2.8	1439.79	720.40	2	35	YITPDQLADLYK	270	281	28.6
														68.1	2	4.1	806.47	403.74	2	28	YNQILR	407	412	20.1												28.6	1	2.8								

Supplemental Table 3

	Protein information									Peptide information							
Protein Name	Accession #	MW	Mascot Score	Unique	% Cov	z	M+H	m/z	M+H Calc	Peptide	Start	End	Mascot Score	114.0	115.0	116.0	117.0
DJ-1	IPI00117264.1	20,022	676.2	24	54.0	3	1929.93	643.98	1929.98	iTRAQ-DVMICPDTSLEDAK(iTRAQ K)	49	62	38.3	5.7	26.9	29.7	37.8
					54.0	3	1692.64	564.88	1692.72	iTRAQ-MMNGSHYSYSESR	133	145	30.4	1.3	25.2	38.4	35.1
					54.0	3	1819.85	607.29	1819.91	iTRAQ-GAEEMETVIPVDVMR	13	27	40.3	7.0	25.2	31.2	36.6
					54.0	2	1043.64	522.33	1043.69	iTRAQ-APLVLK(iTRAQ K)D	183	189	29.6	1.1	37.3	27.0	34.6
					54.0	2	1043.64	522.32	1043.69	iTRAQ-APLVLK(iTRAQ K)D	183	189	28.6	3.0	34.5	32.5	30.0
					54.0	2	1103.70	552.35	1103.73	iTRAQ-VTVAGLAGK(iTRAQ K)	33	41	70.0	0.9	32.5	33.1	33.5
					54.0	2	1043.64	522.32	1043.69	iTRAQ-APLVLK(iTRAQ K)D	183	189	24.9	3.2	22.0	37.4	37.4
					54.0	2	1043.67	522.34	1043.69	iTRAQ-APLVLK(iTRAQ K)D	183	189	22.6	0.6	34.3	28.9	36.2
					54.0	3	1692.75	564.92	1692.72	iTRAQ-MMNGSHYSYSESR	133	145	19.6	6.4	37.9	31.0	24.7
					54.0	2	1015.64	508.32	1015.74	iTRAQ-ALVILAK(iTRAQ K)	6	12	24.6	2.1	19.9	37.1	40.9
					54.0	2	1015.71	508.36	1015.74	iTRAQ-ALVILAK(iTRAQ K)	6	12	22.8	0.6	30.8	33.0	35.6
					54.0	2	928.55	464.78	928.67	iTRAQ-APLVLK(iTRAQ K)	183	188	23.3	0.7	28.4	32.9	37.9
					54.0	2	1015.73	508.37	1015.74	iTRAQ-ALVILAK(iTRAQ K)	6	12	19.7	4.8	30.9	30.0	34.4
					54.0	2	928.57	464.79	928.67	iTRAQ-APLVLK(iTRAQ K)	183	188	22.9	0.6	30.3	33.8	35.2
					54.0	3	1154.67	385.56	1154.74	iTRAQ-VTTHPLAK(iTRAQ K)	123	130	17.9	2.9	30.6	27.6	38.9
					54.0	4	1836.81	459.96	1836.85	iTRAQ-MMNGSHYSY(iTRAQ Y)SESR	133	145	11.9	2.6	27.4	23.2	46.8
					54.0	2	1018.60	509.80	1018.60	iTRAQ-DGLILTSR	149	156	19.3	4.7	21.4	31.0	42.9
					54.0	2	1043.68	522.35	1043.69	iTRAQ-APLVLK(iTRAQ K)D	183	189	17.9	9.0	30.6	24.6	35.8
					54.0	3	1518.88	506.96	1518.93	iTRAQ-VEK(iTRAQ K)DGLILTSR	146	156	9.0	9.0	19.5	52.3	19.2
					54.0	3	1154.69	385.57	1154.74	iTRAQ-VTTHPLAK(iTRAQ K)	123	130	14.9	0.9	49.5	10.2	39.3
					54.0	2	1093.56	547.29	1093.62	iTRAQ-DMANQVK(iTRAQ K)	176	182	9.9	0.8	22.4	34.9	41.9
					54.0	2	790.51	395.76	790.55	iTRAQ-EILK(iTRAQ K)	90	93	10.6	4.5	34.3	32.3	28.8
					54.0	2	790.50	395.76	790.55	iTRAQ-EILK(iTRAQ K)	90	93	11.4	0.4	33.2	30.4	36.0
					54.0	2	790.49	395.75	790.55	iTRAQ-EILK(iTRAQ K)	90	93	11.2	1.0	21.8	34.6	42.5
													Average	3.1	29.4	31.5	35.9
													STDEV	2.7	6.9	7.2	5.9
10 kDa heat shock protein, mitochondrial	IPI00263863.7	10,832	152.8	5	50.5	3	1574.01	525.34	1573.98	iTRAQ-VLQATVVAVGSGGK(iTRAQ K)	40	53	50.3	25.4	31.0	23.4	20.3
					50.5	3	1332.76	444.93	1332.79	iTRAQ-SGEIEPVSVK(iTRAQ K)	56	65	31.9	20.2	30.4	27.4	21.9
					50.5	2	1051.66	526.33	1051.61	iTRAQ-FLPLFDR	8	14	25.4	17.8	40.7	20.0	21.4
					50.5	2	1132.71	566.86	1132.69	iTRAQ-GGIMLPEK(iTRAQ K)	28	35	23.6	22.6	33.2	19.8	24.4
					50.5	3	1817.97	606.66	1818.03	iTRAQ-VVLDDK(iTRAQ K)DYFLFR	80	91	19.9	24.2	22.7	28.9	24.2
													Average	22.0	31.6	23.9	22.4
													STDEV	3.1	6.5	4.2	1.8
Tim13	IPI00134484.1	10,458	122.2	3	36.8	3	1697.01	566.34	1696.98	iTRAQ-VQIAVANAQELLQR	28	41	51.8	42.6	32.5	20.8	4.1
					36.8	3	1488.83	496.95	1488.86	iTRAQ-LDPGAIMEQVK(iTRAQ K)	17	27	39.3	40.2	27.8	21.8	10.2
					36.8	2	1386.66	693.83	1386.66	iTRAQ-YMDAWNTVSR	73	82	31.1	48.9	21.6	15.3	14.1
					36.8	3	1488.91	496.97	1488.86	iTRAQ-LDPGAIMEQVK(iTRAQ K)	17	27	32.3				
													Average	43.9	27.3	19.3	9.5
													STDEV	4.5	5.4	3.5	5.1
GAPDH	IPI00474610.3	35,679	329.1	11	27.1	3	1748.91	583.64	1748.95	iTRAQ-VPTPNVSVVDLTCR	232	245	42.5	19.0	28.8	31.1	21.0
					27.1	3	1748.91	583.64	1748.95	iTRAQ-VPTPNVSVVDLTCR	232	245	44.6	12.6	33.2	23.3	30.9
					27.1	3	1658.02	553.34	1657.97	iTRAQ-GAAQNIIPASTGAAK(iTRAQ K)	198	212	34.4	14.6	20.7	26.6	38.1
					27.1	2	1157.67	579.34	1157.74	iTRAQ-VIPELNGK(iTRAQ K)	217	224	34.3	8.5	37.7	27.3	26.5
					27.1	3	1515.88	505.96	1515.84	iTRAQ-VVDLMAYMASK(iTRAQ K)	321	331	23.4				
					27.1	2	1157.67	579.34	1157.74	iTRAQ-VIPELNGK(iTRAQ K)	217	224	31.8	11.0	36.0	24.3	28.7
					27.1	2	1157.74	579.37	1157.74	iTRAQ-VIPELNGK(iTRAQ K)	217	224	30.1	12.2	34.0	24.9	28.8
					27.1	2	939.49	470.25	939.52	iTRAQ-LTGMAFR	225	231	16.6	11.2	25.7	30.6	32.5
					27.1	2	953.54	477.27	953.59	iTRAQ-FNGTVK(iTRAQ K)	53	58	11.7	13.4	34.8	29.6	22.2
					27.1	2	949.53	475.27	949.53	iTRAQ-VGVNGFGR	4	11	13.8	11.5	25.2	31.8	31.5
					27.1	2	949.55	475.28	949.53	iTRAQ-VGVNGFGR	4	11	11.2	11.6	33.9	27.3	27.2
													Average	12.5	31.0	27.7	28.8
													STDEV	2.8	5.6	3.0	5.0
Prohibitin-2	IPI00321718.4	33,297	213.4	9	26.8	3	1503.81	501.94	1503.85	iTRAQ-IVQAEGEAEAAK(iTRAQ K)	225	236	41.8	32.7	22.5	22.9	21.9
					26.8	3	1499.03	500.35	1498.97	iTRAQ-VLPSIVNEVLK(iTRAQ K)	132	142	43.0				
					26.8	2	1321.77	661.39	1321.73	iTRAQ-FNASQLITQR	148	157	24.9	31.9	19.5	37.3	11.2
					26.8	2	1136.70	568.85	1136.68	iTRAQ-MLGEALSK(iTRAQ K)	237	244	21.7	33.6	21.4	27.0	18.1
					26.8	2	911.56	456.28	911.52	iTRAQ-AIFFNR	49	54	21.5	38.5	22.8	23.9	14.7
					26.8	2	1122.73	561.87	1122.70	iTRAQ-AQFLVEK(iTRAQ K)	210	216	20.9	35.8	23.5	21.5	19.2
					26.8	2	1138.58	569.79	1138.59	iTRAQ-LGLDYEER	124	131	18.9	26.4	23.5	29.3	20.8
					26.8	2	863.56	432.28	863.52	GSDSLIK(iTRAQ K)	290	296	11.9	27.6	30.6	20.7	21.1
					26.8	3	1360.60	454.20	1360.77	MAQNLK(iTRAQ K)DLAGR	1	11	8.8				
													Average	32.3	23.4	26.1	18.1
													STDEV	4.3	3.5	5.8	3.9
Tubulin, beta	IPI00169463.1	49,832	379.4	11	26.7	3	1734.87	578.96	1734.92	iTRAQ-EVDEQMLNVQNK(iTRAQ K)	325	336	40.1	14.8	29.2	28.0	28.0
					26.7	2	1287.73	644.37	1287.74	iTRAQ-LAVNMVPFPR	253	262	35.0	23.2	18.2	32.3	26.3
					26.7	3	1607.89	536.64	1607.93	iTRAQ-IMNTFSVVPSPK(iTRAQ K)	163	174	31.1				
					26.7	3	1607.86	536.63	1607.93	iTRAQ-IMNTFSVVPSPK(iTRAQ K)	163	174	31.9	17.2	23.0	25.5	34.3
					26.7	3	1616.91	539.64	1616.88	iTRAQ-INVYYNEATGGK(iTRAQ K)	47	58	24.4	13.9	32.7	28.9	24.5
					26.7	2	1183.71	592.36	1183.70	iTRAQ-YLTVAAVFR	310	318	27.3	16.8	31.7	29.7	21.9
					26.7	2	1373.69	687.35	1373.70	iTRAQ-ISEQFTAMFR	381	390	21.7	18.3	18.3	30.7	32.7
					26.7	3	1988.14	663.39	1988.04	iTRAQ-INVYYNEATGGKYVPR	47	62	17.9	36.1	34.6	8.9	20.4
					26.7	3	1559.98	520.67	1559.96	iTRAQ-K(iTRAQ K)LAVNMVPFPR	252	262	14.6	31.5	34.9	14.4	19.2
					26.7	3	1220.63	407.55	1220.66	iTRAQ-TAVCDIPPR	351	359	16.8	22.1	44.5	16.8	16.6
					26.7	3	1257.54	419.85	1257.57	iTRAQ-NMMAACDPR	298	306	13.7	17.7	31.2	30.4	20.7
													Average	21.2	29.8	24.6	24.5
													STDEV	7.3	8.1	8.1	5.8
Tim8 A	IPI00125776.1	11,043	67.4	2	22.7	2	1483.81	742.41	1483.81	iTRAQ-SK(iTRAQ K)PVFSESLSD	87	97	31.4	51.7	19.6	13.5	15.2
					22.7	3	1497.84	499.95	1497.82	iTRAQ-FIDTSQFILNR	70	80	36.0				
													Average	51.7	19.6	13.5	15.2
													STDEV	nd	nd	nd	nd
Ribosomal protein L21	IPI00378437.3	18,503	76	4	22.5	3	1387.73	463.25	1387.76	iTRAQ-HGVVPLATYMR	22	32	40.1	27.8	25.7	32.8	13.7
					22.5	3	1387.73	463.25	1387.76	iTRAQ-HGVVPLATYMR	22	32	39.0	27.1	23.1	29.4	20.4
					22.5	3	1731.28	577.76	1731.07	GDIVDIK(iTRAQ K)GIGTVQK(iTRAQ K)	37	50	19.4				
					22.5	2	923.61	462.31	923.53	MTNTKGK(iTRAQ K)	1	7	8.3				
					22.5	2	732.50	366.75	732.55	iTRAQ-ILAK(iTRAQ K)	84	87	8.2				
													Average	27.5	24.4	31.1	17.1
													STDEV	0.5	1.8	2.4	4.7
ADP/ATP translocase 2	IPI00127841.2	32,800	192.4	10	21.5	2	1265.65	633.33	1265.68	iTRAQ-EQGVLSFWR	63	71	34.1	13.5	21.9	32.3	32.3
					21.5	3	1735.05	579.02	1734.97	iTRAQ-YFPTQALNFAFK(iTRAQ K)	80	91	27.8				
					21.5	3	1734.91	578.97	1734.97	iTRAQ-YFPTQALNFAFK(iTRAQ K)	80	91	26.9				
					21.5	2	961.57	481.29	961.62	iTRAQ-LAADVGK(iTRAQ K)	140	146	24.1	15.3	35.5	23.8	25.4
					21.5	2	1046.57	523.79	1046.59	iTRAQ-GAWSNVLR	272	279	17.6	13.8	19.5	29.8	36.8
					21.5	2	1000.59	500.80	1000.59	iTRAQ-TAVAPIER	23	30	15.9	9.4	25.2	36.2	29.2
					21.5	2	1000.57	500.79	1000.60	iTRAQ-GNLANVIR	72	79	20.2	11.8	20.7	29.7	37.8
					21.5	2	875.55	438.28	875.46	IARDEGSK	260	267	8.4				
					21.5	2	961.60	481.30	961.62	iTRAQ-LAADVGK(iTRAQ K)	140	146	8.3	42.4	26.8	13.8	16.9
					21.5	2	800.52	400.76	800.52	iTRAQ-AFFK(iTRAQ K)	268	271	8.2				
													Average	17.7	24.9	27.6	29.7
													STDEV	12.3	5.9	7.9	7.8
PACSIN2	IPI00125880.1	55,833	410.8	17	21.2	2	1480.77	740.89	1480.77	iTRAQ-AYAQQLTEWAR	54	64	43.1	21.3	23.7	29.2	25.8
					21.2	3	1534.91	512.31	1534.87	iTRAQ-HLDLSNVASYK(iTRAQ K)	254	264	43.0	26.1	24.3	24.1	25.6
					21.2	2	1471.76	736.38	1471.76	iTRAQ-ASLMNEDFEK(iTRAQ K)	102	111	34.0	28.6	28.4	21.5	21.5
					21.2	3	1534.83	512.28	1534.87	iTRAQ-HLDLSNVASYK(iTRAQ K)	254	264	32.7	23.3	32.5	26.7	17.5
					21.2	2	1406.75	703.88	1406.72	iTRAQ-AWIAVMSEAER	82	92	31.4	21.4	21.4	33.1	24.1
					21.2	3	1534.81	512.28	1534.87	iTRAQ-HLDLSNVASYK(iTRAQ K)	254	264	34.4	20.8	35.0	21.0	23.2
					21.2	3	1499.88	500.63	1499.86	iTRAQ-ADPSLNPEQLK(iTRAQ K)	178	188	32.0	28.7	19.5	26.1	25.7
					21.2	3	1499.82	500.61	1499.85	iTRAQ-ADPSLNPEQLK(iTRAQ K)	178	188	30.3	17.3	21.8	36.4	24.6
					21.2	2	1086.49	543.75	1086.59	iTRAQ-QMMGGFK(iTRAQ K)	123	129	18.4	24.4	27.7	25.4	22.5
					21.2	2	1114.59	557.80	1114.62	iTRAQ-NVSSYEK(iTRAQ K)	384	390	18.4	18.8	21.0	32.8	27.4
					21.2	2	1086.55	543.78	1086.59	iTRAQ-QMMGGFK(iTRAQ K)	123	129	19.4	27.5	27.7	23.9	20.8
					21.2	2	1134.68	567.84	1134.69	iTRAQ-ELEQSIK(iTRAQ K)	269	275	16.1	27.5	26.1	23.2	23.2
					21.2	2	967.48	484.24	967.46	iTRAQ-EAEDGFR	133	139	15.3	30.6	21.7	26.7	21.0
					21.2	2	904.60	452.80	904.59	iTRAQ-QLVEK(iTRAQ K)	68	72	11.4	26.1	25.7	27.2	21.1
					21.2	2	1266.69	633.85	1266.72	iTRAQ-GPQYGTVEK(iTRAQ K)	73	81	12.1	25.8	28.1	25.0	21.2
					21.2	2	1114.63	557.82	1114.62	iTRAQ-NVSSYEK(iTRAQ K)	384	390	9.9	28.0	23.1	24.4	24.5
					21.2	2	1021.61	511.31	1021.60	iTRAQ-AGDELTK(iTRAQ K)	449	455	8.9	26.5	24.5	28.2	20.8
													Average	24.9	25.4	26.8	23.0
													STDEV	3.8	4.2	4.2	2.5
Actin, alpha	IPI00480406.1	41,947	210.1	9	21.2	3	1449.87	483.96	1449.85	iTRAQ-EITALAPSTMK(iTRAQ K)	318	328	34.2	14.3	24.7	34.5	26.6
					21.2	3	2249.06	750.36	2249.14	iTRAQ-YPIEHGIITNWDDMEK(iTRAQ K)	71	86	29.8	20.2	29.3	29.8	20.6
					21.2	3	1486.71	496.24	1486.75	iTRAQ-DSYVGDEAQSK(iTRAQ K)	53	63	36.7	13.0	17.2	39.1	30.7
					21.2	3	1459.82	487.28	1459.80	iTRAQ-HQGVMVGMGQK(iTRAQ K)	42	52	21.3	20.3	20.0	22.9	36.9
					21.2	4	1659.90	415.73	1659.85	iTRAQ-IWHHTFYNELR	87	97	26.9				
					21.2	2	932.62	466.81	932.66	iTRAQ-GILTLK(iTRAQ K)	65	70	15.7				
					21.2	2	932.62	466.81	932.66	iTRAQ-GILTLK(iTRAQ K)	65	70	15.9				
					21.2	2	788.48	394.74	788.47	iTRAQ-LDLAGR	180	185	12.7				
					21.2	2	1286.76	643.88	1286.71	iTRAQ-DLTDYLMK(iTRAQ K)	186	193	16.9				
													Average	16.9	22.8	31.6	28.7
													STDEV	3.9	5.3	6.9	6.8
Enolase, alpha	IPI00462072.2	47,010	177.8	9	20.8	3	1727.93	576.65	1727.97	iTRAQ-YITPDQLADLYK(iTRAQ K)	269	280	34.9	7.9	36.2	28.4	27.5
					20.8	2	1187.80	594.40	1187.78	iTRAQ-TIAPALVSK(iTRAQ K)	71	79	23.9	19.0	34.6	18.2	28.2
					20.8	3	1949.11	650.38	1949.05	iTRAQ-AAVPSGASTGIYEALELR	32	49	28.9				
					20.8	2	1192.71	596.86	1192.69	iTRAQ-IEEELGSK(iTRAQ K)	412	419	16.6	16.1	32.2	22.8	29.0
					20.8	2	950.57	475.79	950.55	iTRAQ-YNQILR	406	411	18.1	18.4	37.7	20.8	23.1
					20.8	2	1103.72	552.37	1103.72	iTRAQ-EALELLK(iTRAQ K)	221	227	20.8	18.1	35.5	18.2	28.3
					20.8	3	1469.79	490.60	1469.86	iTRAQ-GVSQAVEHINK(iTRAQ K)	60	70	10.4	11.6	47.1	19.2	22.1
					20.8	2	830.53	415.77	830.56	iTRAQ-NPLAK(iTRAQ K)	429	433	11.1				
					20.8	2	1741.99	871.50	1742.03	IGAEVYHNLKNVIK(iTRAQ K)	183	196	13.1				
													Average	15.2	37.2	21.3	26.4
													STDEV	4.5	5.2	3.9	3.0
HspA8	IPI00753407.1	76,511	456.9	15	19.8	3	1904.96	635.66	1905.02	iTRAQ-SFYPEEVSSMVLTK(iTRAQ K)	176	189	39.0	4.1	16.4	32.4	47.2
					19.8	2	1372.71	686.86	1372.73	iTRAQ-VEIIANDQGNR	89	99	39.5	7.5	20.7	40.9	31.0
					19.8	2	1397.76	699.38	1397.72	iTRAQ-FEELNADLFR	365	374	35.1	6.0	26.9	38.5	28.6
					19.8	3	1613.91	538.64	1613.88	iTRAQ-CNEIISWLDK(iTRAQ K)	637	646	39.6	6.3	42.7	17.8	33.1
					19.8	3	1625.95	542.65	1625.91	iTRAQ-SQIHDIVLVGGSTR	392	405	30.8	3.0	37.1	24.8	35.0
					19.8	3	1369.78	457.26	1369.80	iTRAQ-LLQDFFNGK(iTRAQ K)	412	420	26.9	5.1	23.9	31.9	39.1
					19.8	3	1369.78	457.27	1369.80	iTRAQ-LLQDFFNGK(iTRAQ K)	412	420	23.9				
					19.8	2	1343.78	672.39	1343.78	iTRAQ-DAGTIAGLNVLR	223	234	25.6	5.6	24.0	34.0	36.4
					19.8	2	975.58	488.30	975.63	iTRAQ-LIGDAAK(iTRAQ K)	113	119	25.4	7.0	33.2	35.5	24.3
					19.8	2	975.56	488.28	975.63	iTRAQ-LIGDAAK(iTRAQ K)	113	119	21.9	5.2	29.1	37.1	28.6
					19.8	2	1146.67	573.84	1146.69	iTRAQ-GTLDPVEK(iTRAQ K)	375	382	18.7	9.1	29.0	28.5	33.4
					19.8	2	1092.66	546.83	1092.67	iTRAQ-ITITNDK(iTRAQ K)	564	570	17.8	7.0	32.1	28.3	32.5
					19.8	2	975.63	488.32	975.63	iTRAQ-LIGDAAK(iTRAQ K)	113	119	18.4	11.0	28.3	30.8	29.9
					19.8	3	1280.80	427.60	1280.79	iTRAQ-VCNPIITK(iTRAQ K)	665	672	15.4				
					19.8	2	1011.57	506.29	1011.61	iTRAQ-QFGLMK(iTRAQ K)	24	29	12.8	14.1	38.3	26.6	20.9
													Average	7.0	29.4	31.3	32.3
													STDEV	3.0	7.4	6.2	6.6
Fructose-bisphosphate aldolase A	IPI00221402.6	39,225	168.9	8	19.8	3	1634.82	545.61	1634.81	iTRAQ-LQSIGTENTEENR	43	55	30.1	13.9	35.2	26.3	24.6
					19.8	2	1188.69	594.85	1188.67	iTRAQ-QLLLTADDR	60	68	27.1	10.9	26.3	34.0	28.8
					19.8	2	917.57	459.29	917.63	iTRAQ-GGVVGIK(iTRAQ K)	101	107	17.8	13.3	35.8	28.0	22.9
					19.8	2	1051.70	526.35	1051.70	iTRAQ-VLAAVYK(iTRAQ K)	208	214	23.1	13.6	34.7	19.4	32.3
					19.8	2	872.57	436.79	872.60	iTRAQ-IVAPGK(iTRAQ K)	22	27	22.3	13.9	34.0	25.0	27.1
					19.8	3	1332.76	444.93	1332.70	GILAADESTGSIAK	28	41	22.2	20.2	30.4	27.4	21.9
					19.8	3	1084.63	362.21	1084.59	iTRAQ-ELSDIAHR	14	21	10.7	21.3	38.3	14.3	26.0
					19.8	2	1089.71	545.36	1089.71	iTRAQ-ALQASALK(iTRAQ K)	304	311	15.6	13.1	30.4	27.0	29.4
					19.8								Average	15.0	33.1	25.2	26.6
					19.8								STDEV	3.7	3.8	5.9	3.5
					19.8												
Ketoacid dehydrogenase E1, beta	IPI00115302.3	35,505	120	6	19.3	3	1631.80	544.61	1631.83	iTRAQ-SGDLFNCGSLTIR	101	113	31.6	21.7	17.8	23.9	36.6
					19.3	2	965.54	483.27	965.59	iTRAQ-SPFQAK(iTRAQ K)	147	152	17.8	21.8	31.4	27.7	19.0
					19.3	3	1807.01	603.01	1806.90	YRSGDLFNCGSLTIR	99	113	22.7	26.2	24.1	33.5	16.2
					19.3	3	1487.84	496.62	1487.82	iTRAQ-NPCIFFEPK(iTRAQ K)	163	171	18.8	24.8	32.1	16.1	27.0
					19.3	4	3045.59	762.15	3045.64	IPLSQAEVIQEGSDVTLVAWGTQVHVIR	188	215	18.4	19.6	21.8	36.1	22.5
					19.3	2	708.44	354.72	708.45	iTRAQ-ILYR	172	175	10.7	22.7	26.2	27.4	23.7
													Average	22.8	25.6	27.4	24.2
													STDEV	2.4	5.6	7.1	7.1
Heat-shock protein beta-1	IPI00128522.1	23,014	89.2	3	16.3	3	1215.74	405.92	1215.72	iTRAQ-AQIGGPEAGK(iTRAQ K)	193	202	28.6				
					16.3	3	2086.15	696.06	2086.17	iTRAQ-VSLDVNHFAPEELTVK(iTRAQ K)	101	116	31.3	22.2	28.5	19.8	29.6
					16.3	2	1149.57	575.29	1149.58	iTRAQ-SPSWEPFR	13	20	29.3	25.2	18.3	33.2	23.3
					16.3	4	2086.13	522.29	2086.17	iTRAQ-VSLDVNHFAPEELTVK(iTRAQ K)	101	116	23.9				
					16.3								Average	23.7	23.4	26.5	26.4
					16.3								STDEV	2.2	7.2	9.5	4.4
					16.3												
Ketoacid dehydrogenase E1, alpha	IPI00331555.2	50,774	162.7	6	15.7	3	1997.08	666.36	1997.03	iTRAQ-AVAENQPFLIEAMTYR	318	333	40.8				
					15.7	2	1325.71	663.36	1325.67	iTRAQ-SMTLLNTMDR	109	118	29.7	25.1	26.6	28.6	19.8
					15.7	2	1353.66	677.34	1353.66	iTRAQ-VMEAFEQAER	391	400	27.9	19.8	26.4	28.7	25.1
					15.7	2	1194.62	597.81	1194.64	iTRAQ-GPGYGIMSIR	289	298	23.1	21.5	23.2	31.3	24.0
					15.7	2	1242.69	621.85	1242.66	iTRAQ-TDLVFGQYR	152	160	21.9	18.4	31.0	27.1	23.5
					15.7	4	1860.98	466.00	1861.07	MAIVMSAAK(iTRAQ K)IWRPSR	1	15	19.3				
													Average	21.2	26.8	28.9	23.1
													STDEV	2.9	3.2	1.7	2.3
Peroxiredoxin-1	IPI00648105.1	18,927	95.1	3	14.7	3	1925.18	642.40	1925.10	iTRAQ-QGGLGPMNIPLISDPK(iTRAQ K)	94	109	41.3	24.9	38.5	19.0	17.5
					14.7	3	1294.72	432.25	1294.76	iTRAQ-IGYPAPNFK(iTRAQ K)	8	16	27.4	7.0	16.7	37.7	38.6
					14.7	2	1294.70	647.86	1294.76	iTRAQ-IGYPAPNFK(iTRAQ K)	8	16	13.7	5.1	37.5	28.6	28.9
					14.7								Average	12.3	30.9	28.5	28.3
					14.7								STDEV	11.0	12.3	9.3	10.5
					14.7												
Eukaryotic initiation factor 4A-I	IPI00118676.3	46,154	188	5	14.5	3	1762.98	588.33	1762.98	iTRAQ-LQMEAPHIIVGTPGR	147	161	54.2	17.5	34.8	24.4	23.3
					14.5	3	1762.94	588.32	1762.98	iTRAQ-LQMEAPHIIVGTPGR	147	161	43.5	20.2	38.0	23.2	18.6
					14.5	2	1699.85	850.43	1699.82	iTRAQ-MFVLDEADEMLSR	178	190	39.3	15.8	33.9	24.1	26.2
					14.5	3	1869.85	623.95	1869.90	iTRAQ-DFTVSAMHGDMDQK(iTRAQ K)	296	309	33.2	21.3	36.1	9.7	32.9
					14.5	2	1038.53	519.77	1038.55	iTRAQ-VFDMLNR	162	168	30.3	20.3	22.5	30.1	27.1
					14.5	2	1258.80	629.90	1258.79	iTRAQ-VLITTDLLAR	325	334	31.0	17.7	32.0	21.6	28.7
													Average	18.8	32.9	22.2	26.1
													STDEV	2.1	5.5	6.8	4.9

Interleukin-2 precursor	IPI00115183.1	19,400	168.7	6	14.2	4	2985.30	747.08	2985.41	iTRAQ-LKGSDNTFECQFDDESATVVDFLR	131	154	32.2	19.9	29.8	25.2	25.0
					14.2	4	2985.35	747.09	2985.41	iTRAQ-LKGSDNTFECQFDDESATVVDFLR	131	154	31.9	25.1	30.1	19.9	24.8
					14.2	4	2985.24	747.07	2985.41	iTRAQ-LKGSDNTFECQFDDESATVVDFLR	131	154	31.4	19.9	31.6	17.4	31.0
					14.2	4	2985.33	747.09	2985.41	iTRAQ-LKGSDNTFECQFDDESATVVDFLR	131	154	20.8				
					14.2	4	2985.42	747.11	2985.43	LK(iTRAQ K)GSDNTFECQFDDESATVVDFLR	131	154	21.8				
					14.2	4	2985.69	747.18	2985.41	iTRAQ-LKGSDNTFECQFDDESATVVDFLR	131	154	18.2				
													Average	21.7	30.5	20.8	27.0
													STDEV	3.0	1.0	4.0	3.5
Tubulin, alpha	IPI00117350.1	49,925	150.4	6	14.1	3	1860.08	620.70	1860.02	iTRAQ-AVFVDLEPTVIDEIR	65	79	39.1				
					14.1	2	1175.68	588.34	1175.66	iTRAQ-FDLMYAK(iTRAQ K)	395	401	22.6	23.9	28.9	23.1	24.1
					14.1	2	1194.59	597.80	1194.65	iTRAQ-EDMAALEK(iTRAQ K)	423	430	26.4	20.9	22.3	29.6	27.1
					14.1	3	2057.03	686.35	2057.04	iTRAQ-AVCMLSNTTAIAEAWAR	374	390	28.1				
					14.1	2	1069.64	535.32	1069.64	iTRAQ-LSVDYGK(iTRAQ K)	157	163	17.3	23.1	27.7	22.5	26.8
					14.1	2	1167.56	584.28	1167.55	iTRAQ-EDAANNYAR	97	105	16.9	19.2	17.4	31.2	32.2
					14.1	3	2057.05	686.36	2057.04	iTRAQ-AVCMLSNTTAIAEAWAR	374	390	16.0	19.4	44.2	16.9	19.6
													Average	21.3	28.1	24.7	26.0
													STDEV	2.1	10.1	5.8	4.6
YME1L1	IPI00136555.1	80,029	385.4	11	14.0	3	1396.83	466.28	1396.90	iTRAQ-GILLVGPPGTGK(iTRAQ K)	316	327	43.1	36.2	7.0	17.7	39.0
					14.0	3	1396.84	466.28	1396.90	iTRAQ-GILLVGPPGTGK(iTRAQ K)	316	327	36.0				
					14.0	3	1396.93	466.31	1396.90	iTRAQ-GILLVGPPGTGK(iTRAQ K)	316	327	36.5	13.7	37.3	25.9	23.1
					14.0	3	2306.24	769.42	2306.28	iTRAQ-GTVGFSGAELENLVNQAALK(iTRAQ K)	479	498	40.1				
					14.0	3	1557.79	519.94	1557.85	iTRAQ-NIPEAHQDAFK(iTRAQ K)	201	211	36.3	29.1	29.2	23.4	18.3
					14.0	3	1557.79	519.93	1557.85	iTRAQ-NIPEAHQDAFK(iTRAQ K)	201	211	34.7	24.7	32.3	25.9	17.1
					14.0	2	1265.65	633.33	1265.71	iTRAQ-GTDLESLDK(iTRAQ K)	187	195	28.5	23.5	22.8	32.7	21.0
					14.0	2	1009.65	505.33	1009.65	iTRAQ-FTVLGGK(iTRAQ K)	306	312	23.9	34.4	28.9	23.4	13.3
					14.0	3	1360.67	454.23	1360.68	iTRAQ-IESPMHPYSR	390	399	17.4	19.9	33.2	22.5	24.5
					14.0	2	959.54	480.27	959.55	iTRAQ-ILMGPER	519	525	19.9	26.2	24.9	27.3	21.6
					14.0	2	1018.60	509.80	1018.59	iTRAQ-DLGLSELK	62	69	14.5	4.7	21.4	31.0	42.9
													Average	23.6	26.3	25.5	24.5
													STDEV	9.9	8.9	4.5	9.9
T-complex protein 1 subunit beta	IPI00320217.8	57,347	159.1	7	13.7	3	1451.79	484.60	1451.82	iTRAQ-IHPQTIISGWR	120	130	34.5	44.4	19.0	20.6	15.9
					13.7	3	1525.85	509.29	1525.92	iTRAQ-GSGNLEAIHVIK(iTRAQ K)	191	202	31.2	18.8	37.5	23.0	20.7
					13.7	3	2385.31	795.78	2385.35	iTRAQ-LALVTGGEIASTFDHPELVK(iTRAQ K)	322	341	26.1	18.9	17.3	26.3	37.5
					13.7	2	1014.66	507.84	1014.64	iTRAQ-LAVEAVLR	181	188	24.9	25.3	19.3	27.5	27.8
					13.7	3	1525.85	509.29	1525.92	iTRAQ-GSGNLEAIHVIK(iTRAQ K)	191	202	23.3	16.5	35.7	27.3	20.4
					13.7	2	1656.48	828.74	1656.78	EALLSSAVDHGSDEAR	138	153	10.4				
					13.7	2	764.49	382.75	764.43	iTRAQ-VDSTAK	257	262	8.7				
													Average	24.8	25.8	25.0	24.5
													STDEV	11.5	9.9	3.0	8.4
60S ribosomal protein L27a	IPI00553612.2	16,458	54.5	2	12.9	2	1283.78	642.39	1283.78	iTRAQ-TGVAPIIDVVR	94	104	33.5	23.2	22.4	32.0	22.4
					12.9	3	1256.69	419.57	1256.69	iTRAQ-YHPGYFGK(iTRAQ K)	47	54	21.0	24.6	19.4	32.4	23.6
													Average	23.9	20.9	32.2	23.0
													STDEV	1.0	2.1	0.3	0.8
Hsp 90, alpha	IPI00330804.3	84,657	292.3	10	12.4	3	1638.01	546.68	1637.96	iTRAQ-TLTIVDTGIGMTK(iTRAQ K)	87	99	39.2	10.1	41.0	26.1	22.7
					12.4	3	1829.96	610.66	1829.99	iTRAQ-SLTNDWEEHLAVK(iTRAQ K)	315	327	39.3	14.0	38.0	23.4	24.6
					12.4	3	1829.95	610.65	1829.99	iTRAQ-SLTNDWEEHLAVK(iTRAQ K)	315	327	36.4	8.4	25.8	30.7	35.2
					12.4	2	1439.72	720.37	1439.79	iTRAQ-YIDQEELNK(iTRAQ K)	284	292	34.5	19.4	34.4	23.1	23.2
					12.4	2	1530.95	765.98	1530.93	iTRAQ-ADLINNLGTIAK(iTRAQ K)	100	111	31.4	7.8	23.7	37.7	30.7
					12.4	3	1312.66	438.23	1312.67	iTRAQ-LGIHEDSQNR	447	456	18.5				
					12.4	2	959.61	480.31	959.62	iTRAQ-ALLFVPR	339	345	27.1	10.7	29.1	30.2	30.0
					12.4	2	1560.72	780.87	1560.76	EGLELPEDEEEK(iTRAQ K)	547	558	20.1	14.7	23.6	27.5	34.2
					12.4	3	1451.90	484.64	1451.91	iTRAQ-ELHINLIPSK(iTRAQ K)	74	83	17.8				
					12.4	3	1312.65	438.22	1312.67	iTRAQ-LGIHEDSQNR	447	456	10.4				
					12.4	3	1807.98	603.33	1808.06	LDSGKELHINLIPSK(iTRAQ K)	69	83	11.9				
													Average	12.1	30.8	28.4	28.7
													STDEV	4.1	7.1	5.1	5.2
Myozenin-3	IPI00153879.1	26,982	158.1	7	11.8	3	2406.24	802.75	2406.33	EPVMAVPGDLAEPVPSLDLGK(iTRAQ K)K	8	29	29.6				
					11.8	2	936.58	468.79	936.59	GSLLFQK(iTRAQ K)	48	54	22.4	13.6	32.5	28.9	25.0
					11.8	3	2406.35	802.79	2406.33	EPVMAVPGDLAEPVPSLDLGKK(iTRAQ K)	8	29	24.1	31.3	36.8	20.5	11.5
					11.8	3	2406.20	802.74	2406.33	EPVMAVPGDLAEPVPSLDLGKK(iTRAQ K)	8	29	23.4	30.8	19.4	19.4	30.4
					11.8	3	2406.23	802.75	2406.33	EPVMAVPGDLAEPVPSLDLGKK(iTRAQ K)	8	29	19.8				
					11.8	3	2550.47	850.83	2550.46	EPVMAVPGDLAEPVPSLDLGK(iTRAQ K)K(iTRAQ K)	8	29	14.7	23.7	29.1	16.9	30.3
					11.8	3	2550.34	850.78	2550.46	EPVMAVPGDLAEPVPSLDLGK(iTRAQ K)K(iTRAQ K)	8	29	17.4	23.5	32.0	16.2	28.3
													Average	24.6	29.9	20.4	25.1
													STDEV	7.2	6.5	5.1	7.9
ATP synthase beta chain, mitochondrial	IPI00468481.2	56,301	134.1	5	11.3	3	2311.34	771.12	2311.24	iTRAQ-FLSQPFQVAEVFTGHMGK(iTRAQ K)	463	480	38.1	25.5	25.9	23.5	25.1
					11.3	2	1529.82	765.41	1529.81	iTRAQ-IMNVIGEPIDER	144	155	34.9	15.5	30.5	33.9	20.1
					11.3	3	1579.91	527.31	1579.86	iTRAQ-FTQAGSEVSALLGR	311	324	31.0				
					11.3	2	989.51	495.26	989.54	VASASASGALR	8	18	15.9				
					11.3	2	857.58	429.29	857.63	iTRAQ-LVPLK(iTRAQ K)	481	485	14.2				
													Average	20.5	28.2	28.7	22.6
													STDEV	7.1	3.3	7.3	3.6
HspA9	IPI00133903.1	73,529	222.1	10	10.9	2	1434.80	717.91	1434.78	iTRAQ-VQQTVQDLFGR	395	405	43.0	16.2	28.1	36.0	19.8
					10.9	3	1622.01	541.34	1621.96	iTRAQ-AQFEGIVTDLIK(iTRAQ K)	349	360	26.7				
					10.9	3	1590.89	530.97	1590.86	iTRAQ-SDIGEVILVGGMTR	378	391	33.5				
					10.9	3	1437.76	479.92	1437.78	iTRAQ-RYDDPEVQK(iTRAQ K)	127	135	21.9	14.7	28.4	43.7	13.2
					10.9	2	892.51	446.76	892.57	iTRAQ-NVPFK(iTRAQ K)	139	143	16.4	13.6	31.0	31.6	23.8
					10.9	2	991.50	496.25	991.51	iTRAQ-DNMALQR	301	307	17.6	15.0	22.4	46.1	16.4
					10.9	2	892.52	446.76	892.57	iTRAQ-NVPFK(iTRAQ K)	139	143	14.1	18.4	35.8	27.9	17.9
					10.9	4	2550.32	638.33	2550.33	AMQDAEVSK(iTRAQ K)SDIGEVILVGGMTR	369	391	23.1				
					10.9	2	908.16	454.58	908.45	EMAGDNK(iTRAQ K)	492	498	9.5				
					10.9	3	2550.31	850.78	2550.33	AMQDAEVSK(iTRAQ K)SDIGEVILVGGMTR	369	391	16.3				
					10.9								Average	15.6	29.1	37.1	18.2
					10.9								STDEV	1.8	4.9	7.8	3.9
					10.9												
Malate dehydrogenase 2, NAD	IPI00331590.1	35,612	73.2	3	10.7	3	1530.82	510.95	1530.86	iTRAQ-GCDVVVIPAGVPR	92	104	29.0	26.9	18.8	25.0	29.3
					10.7	3	1530.82	510.95	1530.86	iTRAQ-GCDVVVIPAGVPR	92	104	28.4	17.6	31.6	30.9	19.9
					10.7	2	889.54	445.27	889.60	iTRAQ-NLGIGK(iTRAQ K)	302	307	21.8	15.8	31.1	31.3	21.8
					10.7	3	2103.11	701.71	2103.18	ITPFEEK(iTRAQ K)MIAEAIPELK	308	324	22.4	28.8	23.2	23.3	24.7
													Average	22.3	26.2	27.6	23.9
													STDEV	6.5	6.2	4.1	4.1
L-lactate dehydrogenase A chain	IPI00319994.5	36,368	69.2	3	10.6	3	1964.04	655.35	1964.04	iTRAQ-DLADELALVDVMEDK(iTRAQ K)	42	56	30.7				
					10.6	3	1440.72	480.91	1440.74	iTRAQ-VIGSGCNLDSAR	157	168	20.6	13.4	37.6	29.0	20.0
					10.6	3	1440.67	480.90	1440.74	iTRAQ-VIGSGCNLDSAR	157	168	11.9	9.2	41.3	26.3	23.1
					10.6	2	1231.77	616.39	1231.83	iTRAQ-FIIPNIVK(iTRAQ K)	118	125	17.9	17.3	36.0	28.4	18.4
					10.6								Average	13.3	38.3	27.9	20.5
					10.6								STDEV	4.0	2.7	1.4	2.4
					10.6												
Elongation factor 1-alpha 1	IPI00307837.4	50,314	134.2	6	10.1	3	1603.01	535.01	1602.97	iTRAQ-EHALLAYTLGVK(iTRAQ K)	137	148	36.9	23.9	26.6	17.5	32.0
					10.1	2	1202.79	601.90	1202.80	iTRAQ-QTVAVGVIK(iTRAQ K)	433	441	23.2	11.2	33.2	23.2	32.3
					10.1	2	1263.80	632.41	1263.78	iTRAQ-LPLQDVYK(iTRAQ K)	250	257	22.4	12.8	34.2	22.3	30.7
					10.1	2	1127.63	564.32	1127.68	iTRAQ-EVSTYIK(iTRAQ K)	175	181	21.4	11.8	23.6	31.3	33.4
					10.1	2	1169.65	585.33	1169.71	iTRAQ-IGGIGTVPVGR	258	268	18.5	8.3	23.7	33.3	34.7
					10.1	2	914.62	457.81	914.57	QTVAVGVIK	433	441	11.8				
													Average	13.6	28.3	25.5	32.6
													STDEV	6.0	5.1	6.6	1.5
60 kDa heat shock protein, mitochondrial	IPI00461249.1	61,055	146.8	7	9.6	3	1938.09	646.70	1938.02	iTRAQ-CEFQDAYVLLSEK(iTRAQ K)	237	249	28.4	21.9	17.5	19.5	41.1
					9.6	2	1073.70	537.35	1073.74	iTRAQ-IGIEIIK(iTRAQ K)	463	469	29.3	25.7	29.9	27.2	17.2
					9.6	3	1632.98	545.00	1632.94	iTRAQ-TVIIEQSWGSPK(iTRAQ K)	61	72	24.4	25.1	20.9	32.0	22.0
					9.6	2	1073.70	537.35	1073.74	iTRAQ-IGIEIIK(iTRAQ K)	463	469	25.6	18.3	34.4	25.4	21.9
					9.6	2	1031.64	516.32	1031.66	iTRAQ-GIIDPTK(iTRAQ K)	517	523	17.4	27.7	30.4	21.7	20.2
					9.6	2	1104.60	552.80	1104.61	iTRAQ-VTDALNATR	421	429	13.2				
					9.6	2	1073.73	537.37	1073.74	iTRAQ-IGIEIIK(iTRAQ K)	463	469	19.7				
					9.6	2	1093.64	547.32	1093.64	iTRAQ-DDAMLLK(iTRAQ K)	353	359	14.4	25.4	34.7	18.9	21.0
													Average	24.0	28.0	24.1	23.9
													STDEV	3.4	7.1	5.1	8.6
Mtap7 protein	IPI00380510.1	82,840	55.1	3	9.6	4	2985.26	747.07	2985.51	TAPSRPTSTVSGQTSNHSGNKPDPPPVLR	34	62	31.9				
					9.6	4	2984.98	747.00	2985.51	TAPSRPTSTVSGQTSNHSGNKPDPPPVLR	34	62	26.9				
					9.6	4	2985.78	747.20	2985.51	TAPSRPTSTVSGQTSNHSGNKPDPPPVLR	34	62	27.7				
					9.6	4	2985.78	747.20	2985.51	TAPSRPTSTVSGQTSNHSGNKPDPPPVLR	34	62	20.4				
					9.6	3	1986.02	662.68	1986.08	iTRAQ-SVSTMNLSKHVDPVISK	181	197	8.8	26.5	28.7	25.3	19.5
					9.6	4	2985.38	747.10	2985.51	TAPSRPTSTVSGQTSNHSGNKPDPPPVLR	34	62	22.6				
					9.6	4	2985.78	747.20	2985.51	TAPSRPTSTVSGQTSNHSGNKPDPPPVLR	34	62	21.2				
					9.6	4	3075.67	769.67	3075.55	iTRAQ-QPNENGMSIQNENFEEVINLPVGSK(iTRAQ K)	669	693	14.4	21.6	24.3	28.3	25.8
					9.6								Average	24.1	26.5	26.8	22.7
					9.6								STDEV	3.5	3.1	2.1	4.4
					9.6												
Kininogen-1	IPI00114958.1	73,103	106.9	5	9.2	4	3458.83	865.46	3458.57	FPSLHGDCVALPNGDDGECRGNLFMDINNK	210	239	33.3				
					9.2	4	3458.88	865.48	3458.57	FPSLHGDCVALPNGDDGECRGNLFMDINNK	210	239	25.3				
					9.2	4	3014.42	754.36	3014.59	SAHRQVVAGLNFDITYTIVQTNCSK(iTRAQ K)	183	207	19.3	26.3	39.6	16.8	17.3
					9.2	4	3458.94	865.49	3458.57	FPSLHGDCVALPNGDDGECRGNLFMDINNK	210	239	23.1				
					9.2	2	834.50	417.75	834.50	DKNSVK(iTRAQ K)	530	535	13.8	21.8	32.5	22.7	23.0
					9.2	4	3014.47	754.37	3014.59	SAHRQVVAGLNFDITYTIVQTNCSK(iTRAQ K)	183	207	17.4	20.6	35.0	24.2	20.2
													Average	22.9	35.7	21.2	20.2
													STDEV	3.0	3.6	3.9	2.8
Pyruvate kinase	IPI00407130.3	58,004	94.8	6	9.2	2	1315.78	658.39	1315.73	iTRAQ-LDIDSAPITAR	33	43	29.6	12.3	30.4	26.5	30.8
					9.2	2	1163.60	582.31	1163.62	iTRAQ-GDYPLEAVR	370	378	16.3	14.0	30.4	25.8	29.7
					9.2	3	1551.81	517.94	1551.84	iTRAQ-NTGIICTIGPASR	44	56	12.3	10.0	55.1	18.4	16.5
					9.2	2	830.51	415.76	830.46	iTRAQ-NPQTAR	458	463	16.1	9.3	48.0	15.2	27.5
					9.2	2	833.51	417.26	833.56	iTRAQ-VLGEK(iTRAQ K)	257	261	9.8	13.1	22.7	32.8	31.3
					9.2	2	819.52	410.26	819.58	iTRAQ-TGLIK(iTRAQ K)	121	125	10.7	14.1	41.0	22.0	22.9
													Average	12.2	37.9	23.5	26.4
													STDEV	2.1	12.2	6.3	5.8
VCP	IPI00676914.1	88,852	169.2	6	8.9	3	1460.85	487.62	1460.90	iTRAQ-GILLYGPPGTGK(iTRAQ K)	240	251	39.7	36.6	35.8	11.2	16.4
					8.9	3	1968.17	656.73	1968.06	iTRAQ-VINQILTEMDGMSTK(iTRAQ K)	595	609	29.9				
					8.9	2	1130.66	565.83	1130.64	iTRAQ-EMVELPLR	218	225	27.8	21.4	15.5	31.9	31.2
					8.9	2	1195.65	598.33	1195.63	iTRAQ-MDELQLFR	46	53	26.8	18.3	17.2	34.6	29.9
					8.9	3	1845.19	615.73	1845.09	iTRAQ-LDQLIYIPLPDEK(iTRAQ K)	634	646	28.6				
					8.9	2	1343.79	672.40	1343.64	ARGGNIGDGGGAADR	580	594	16.4				
													Average	25.4	22.8	25.9	25.8
													STDEV	9.8	11.2	12.8	8.2
T-complex protein 1, zeta	IPI00116281.2	57,874	102.8	4	8.9	3	1534.95	512.32	1534.90	iTRAQ-GIDPFSLDALAK(iTRAQ K)	295	306	33.6				
					8.9	3	1363.79	455.27	1363.84	iTRAQ-ALQFLEQVK(iTRAQ K)	129	137	26.8				
					8.9	2	1242.69	621.85	1242.73	iTRAQ-TLNPKAEVAR	5	14	21.6	23.0	29.2	25.6	22.2
					8.9	3	1761.94	587.98	1761.94	VLAQNSGFDLQETLVK	449	464	20.8	21.2	23.9	27.9	27.0
													Average	22.1	26.6	26.7	24.6
													STDEV	1.3	3.8	1.6	3.4
Inosine-5'-monophosphate dehydrogenase 2	IPI00323971.2	55,816	65.8	3	8.2	2	1300.77	650.89	1300.73	iTRAQ-NLIDAGVDALR	312	322	37.0	11.4	36.1	22.8	29.8
					8.2	4	2831.57	708.65	2831.54	GSIHK(iTRAQ K)FVPYLIAGIQHSCQDIGAK	451	474	17.6				
					8.2	2	1024.57	512.79	1024.57	iTRAQ-VSEYARR	350	356	11.2	16.7	23.9	33.3	26.1
													Average	14.0	30.0	28.0	27.9
													STDEV	3.8	8.6	7.5	2.7
Ribosomal protein L10	IPI00340103.1	24,558	56	3	7.5	3	1396.81	466.27	1396.82	iTRAQ-VHIGQVIMSIR	129	139	35.7	22.8	15.9	40.0	21.3
					7.5	2	926.53	463.77	926.56	iTRAQ-WGFTK(iTRAQ K)	171	175	11.9	28.5	28.3	24.2	19.0
					7.5	2	782.50	391.75	782.43	iTRAQ-WGFTK	171	175	8.4				
													Average	25.7	22.1	32.1	20.2
													STDEV	4.0	8.8	11.2	1.7
Ubiquitin C	IPI00458995.2	99,577	134.8	6	7.4	3	2076.18	692.73	2076.16	iTRAQ-TITLEVEPSDTIENVK(iTRAQ K)	240	255	33.3	21.6	19.7	30.7	28.0
					7.4	2	1053.61	527.31	1053.66	iTRAQ-MQIFVK(iTRAQ K)	1	6	23.1	15.2	28.6	30.8	25.5
					7.4	2	1053.61	527.31	1053.66	iTRAQ-MQIFVK(iTRAQ K)	1	6	22.6	17.8	30.6	27.2	24.3
					7.4	2	1866.00	933.50	1865.98	iTRAQ-QLEGGRTLSDYNIQK	201	215	21.9				
					7.4	2	1183.62	592.31	1183.62	iTRAQ-EGIPPDQQR	262	270	16.6	28.0	11.5	26.2	34.3
					7.4	2	936.58	468.79	936.64	iTRAQ-LIFAGK(iTRAQ K)	575	580	19.6				
					7.4	3	1819.93	607.31	1820.09	iTRAQ-TITLDVEPSVTTKK(iTRAQ K)	848	861	20.3				
													Average	20.7	22.6	28.7	28.0
													STDEV	5.6	8.8	2.4	4.4
Stress-induced-phosphoprotein 1	IPI00121514.3	62,583	47.7	2	6.1	3	1913.97	638.66	1914.04	iTRAQ-FMNPFNLPNLYQK(iTRAQ K)	124	136	33.1	14.1	48.8	13.7	21.9
					6.1	4	2610.36	653.34	2610.34	iTRAQ-ELDPTNMTY(iTRAQ Y)ITNQAAVHFEK	253	272	14.6	14.3	50.6	19.3	17.3
													Average	14.2	49.7	16.5	19.6
													STDEV	0.1	1.3	4.0	3.3