

Supplemental table 1 - Details about identified proteins

Treatment	Spot n°	ID by www.ncbi.nlm.nih.gov		ID by www.dictybase.org			UniPROT ID	MW(Da)/pI expected	MW(Da)/pI observed	n° matches	n° sequences	% coverage	mass					peptide				
		gi	accession number	DDB	protein ID	gene name							observed	Mr(expt)	charge	Mr(calc)	delta	miss	score	ion score (identity)	sequence	modifications
Ni EC25	0013	133059	P22683	DDB0191484	60S acidic ribosomal protein P2	rplP2	P22683	10559/4.90	10270/4.91	3 (3)	3 (3)	58%	1049.5668	2097.1140	2	2097.1098	0.0042	0	54	47	K.YLAAYLLASLSGNANAASVT K.I	
													687.0397	2058.0954	3	2058.0796	0.0158	1	56	45	K.ILQSVGVEVDAARVESVCK.E	
													726.0988	2175.2582	3	2175.1579	0.1003	0	51	45	K.VGSVAAAAAPAAATSAAPAA AAAAK.K	
Ni EC25	0106	7107412	AAF36404	DDB0201567	LIM-type zinc finger-containing protein	limD	Q54EY5	22386/4.70	26720/4.98	4 (4)	4 (4)	27%	602.2880	1202.5615	2	1202.6118	-0.0503	0	56	45	K.VQLFPTNCPK.C	Carbamidomethyl (C)
													603.7979	1205.5812	2	1205.6404	-0.0592	0	64	45	K.ILQLGQYSER.D	
													501.9145	1502.7217	3	1502.7517	-0.0301	1	53	47	K.AYFNELKVYNSR.D	
													704.9841	2111.9306	3	2112.0310	-0.1004	1	82	47	K.NLVSGQYSEKEGLIYCPR.C	Carbamidomethyl (C)
Ni EC25	1108	66803106	XP_635396	DDB0216235	rho GDP-dissociation inhibitor	rdiA	Q95UQ1	22383/6.00	21500/5.63	6 (3)	5 (3)	39%	600.3016	1797.8831	3	1797.9989	-0.1158	0	57	55	K.ITLTFNIQHDIVSGLK.Q	
													620.3040	1857.8902	3	1857.9836	-0.0934	0	44	55	K.IQIEGRPDTIYPLDTK.E	
													678.6590	2032.9551	3	2033.0265	-0.0714	0	39	53	K.HMLGSFAPQALAHSVTNPR.H	
													683.9389	2048.7950	3	2049.0214	-0.2265	0	55	55	K.HMLGSFAPQALAHSVTNPR.H	Oxidation (M)
													819.6792	2456.0159	3	2456.1384	-0.1225	0	57	53	K.VVFTDDDNEEHL SVEYAFSIK. S	
													649.2804	2593.0925	4	2593.3071	-0.2146	1	36	54	K.VSTEKHMLGSFAPQALAHSVTN PR.H	Oxidation (M)
Ni EC25	1115	66806101	XP_636772	DDB0191138	actin related protein 2/3 complex, subunit 5	arcE	O96626	15128/5.05	18180/5.27	6 (4)	5 (3)	42%	690.8199	1379.6252	2	1379.7085	-0.0833	0	59	57	R.GLATGENSPIFFK.W	
													816.8947	1631.7749	2	1631.8883	-0.1133	0	45	56	K.DQNATIVLNLLGSFK.D	
													626.0003	1874.9792	3	1875.0102	-0.0310	1	32	56	K.DQNATIVLNLLGSFKDK.D	
													701.7081	2102.1024	3	2102.1735	-0.0712	1	59	57	K.TGAIKDQNATIVLNLLGSFK. D	
													702.7105	2105.1096	3	2105.1256	-0.0159	1	55	53	K.TGAIKDQNATIVLNLLGSFK. D	3 Deamidated (NQ)
													794.0671	2379.1795	3	2379.2798	-0.1003	0	56	53	K.ALNAGKPQDALNVALADPPI YTK.T	
Ni EC25	3711	60469746	EAL67734	DDB0231551	glutamate-ammonia ligase	glnA3	Q54WR9	83077/5.80	76430/6.23	8 (5)	8 (5)	13%	462.7477	923.4809	2	923.5804	-0.0994	0	23	43	R.TLIGAKPPK.G	
													520.7356	1039.4567	2	1039.5702	-0.1135	0	48	43	K.YSEILFLR.-	
													561.7514	1121.4882	2	1121.6193	-0.1311	0	58	45	R.AVDIHADLLR.A	
													648.7744	1295.5343	2	1295.6761	-0.1418	0	47	44	R.QEILFEIYNK.S	
													688.7599	1375.5053	2	1375.6367	-0.1314	0	47	43	K.GEPDASSFPSGGIR.S	
													550.2231	1647.6474	3	1647.8045	-0.1571	1	44	43	R.TSPFAFTGNKFEFR.A	
													863.9113	1725.8080	2	1725.9664	-0.1585	0	24	44	R.LGANEAPPAISIYLGK.E	
													669.3195	2004.9365	3	2005.0884	-0.1518	1	23	43	R.ISPTLGIEQEFLIDRK.F	

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		gi	accession number	DDB	protein ID	gene name							observed	Mr(expt)	charge	Mr(calc)	delta	miss	score	ion score (identity)	sequence	modifications
Ni EC25	4106	28828367	AAO51015	DDB0231647	peroxiredoxin	prdx4	Q555L5	23234/6.09	25460/6.56	7 (4)	5 (3)	31%	433.9084	1298.7033	3	1298.7558	-0.0525	1	57	53	R.GSILIDKEGLVR.V	
													650.3643	1298.7141	2	1298.7558	-0.0416	1	62	57	R.GSILIDKEGLVR.V	
													556.2546	1665.7419	3	1665.7635	-0.0216	0	64	55	K.DYGVYIEEDGHTIR.G	
													597.2857	1788.8353	3	1788.9410	-0.1057	1	21	53	R.KPAPAFKQAVVNGEFK.E	2 Deamidated (NQ)
													721.3781	2161.1126	3	2161.1743	-0.0617	0	56	53	K.EGGLGGINIPLLSDLTHQISK.D	
													764.0539	2289.1398	3	2289.2692	-0.1294	1	21	54	R.KEGGLGGINIPLLSDLTHQISK.D	
													573.2971	2289.1592	4	2289.2692	-0.1101	1	34	55	R.KEGGLGGINIPLLSDLTHQISK.D	
Ni EC25	5108	66823097	XP_644903	DDB0237752	dihydropteridine reductase	qdpr	Q86A17	24625/6.43	25230/6.79	9 (5)	8 (4)	55%	798.9336	1595.8526	2	1595.9247	-0.0720	0	76	57	K.NILVLGGSGALGAEVVK.F	
													957.9704	1913.9263	2	1914.0687	-0.1424	0	60	57	K.LLNQGGLFVLTGASAALNR.T	
													639.3400	1914.9982	3	1915.0527	-0.0545	0	66	57	K.LLNQGGLFVLTGASAALNR.T	Deamidated (NQ)
													673.7113	2018.1121	3	2018.1564	-0.0443	1	22	55	K.NILVLGGSGALGAEVVKFFK.S	
													676.9654	2027.8744	3	2027.9445	-0.0700	0	60	55	K.GMIDMNLYSAFASAHIGAK.L	Oxidation (M)
													713.6565	2137.9477	3	2138.0280	-0.0803	0	14	53	K.LFEWSTNSDSRPTNGSLVK.F	Deamidated (NQ)
													781.6601	2341.9586	3	2342.1399	-0.1813	1	15	53	K.SVKGMIDMNLYSAFASAHIGAK.L	2 Oxidation (M)
													787.9897	2360.9474	3	2361.0471	-0.0997	1	28	55	R.KYMSDANFDDWTPLEVAEK.L	Oxidation (M)
													956.0974	2865.2704	3	2865.4720	-0.2016	0	56	55	K.DLASENGGLPAGSTSLGILPV TLDTPTNR.K	
		66815899	XP_641966	DDB0206195	regulator of microtubule dynamics protein 1	DDB_G0278793	Q54XR4	25954/7.06	25230/6.79	4 (2)	4 (2)	19%	636.3246	1270.6346	2	1270.7132	-0.0787	0	57	55	K.LIEQALELTNK.A	
													692.8123	1383.6101	2	1383.7034	-0.0934	0	18	55	R.NALFTGDTYAALK.D	
													604.9563	1811.8471	3	1811.9053	-0.0583	1	48	53	R.NALFTGDTYAALKDNAK.A	
													621.6396	1861.8971	3	1862.0010	-0.1039	0	69	56	K.ANELKPNDATTLHLLGR.W	
		66821043	XP_644052	DDB0231647	peroxiredoxin	prdx4	Q555L5	22949/6.09	25230/6.79	3 (2)	3 (2)	22%	650.3380	1298.6615	2	1298.7558	-0.0943	1	55	53	R.GSILIDKEGLVR.V	
													556.2302	1665.6688	3	1665.7635	-0.0946	0	61	57	K.DYGVYIEEDGHTIR.G	
													721.3706	2161.0899	3	2161.1743	-0.0844	0	28	55	K.EGGLGGINIPLLSDLTHQISK.D	

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		gi	accession number	DDB	protein ID	gene name							observed	Mr(expt)	charge	Mr(calc)	delta	miss	score	ion score (identity)	sequence	modifications
Ni EC25	5412	66803080	XP_635383	DDB0230070	S-adenosylmethionine synthetase	metK	Q54F07	41737/6.14	45050/6.59	12 (6)	9 (4)	26%	486.7301	971.4456	2	971.5400	-0.0944	0	42	53	K.SLVAAGLADR.C	
													514.7674	1027.5203	2	1027.6277	-0.1074	1	47	52	R.ADLKELVIK.A	
													676.2447	1350.4749	2	1350.6092	-0.1343	0	49	51	R.NDPDFTWETVK.E	
													679.8276	1357.6406	2	1357.7718	-0.1312	0	63	52	R.DLQLTRPIFQK.T	
													697.3024	1392.5902	2	1392.7357	-0.1455	0	67	53	K.TGMVMILGEITTK.A	
													705.2993	1408.5841	2	1408.7306	-0.1465	0	49	51	K.TGMVMILGEITTK.A	Oxidation (M)
													713.3043	1424.5941	2	1424.7255	-0.1314	0	62	51	K.TGMVMILGEITTK.A	2 Oxidation (M)
													732.2961	1462.5776	2	1462.7239	-0.1463	0	74	53	R.FVIGGPMGDSGLTGR.K	
													740.2970	1478.5794	2	1478.7188	-0.1394	0	68	53	R.FVIGGPMGDSGLTGR.K	Oxidation (M)
													747.7598	1493.5050	2	1493.6674	-0.1624	1	30	53	K.IGYDDSSKGFYK.T	
													804.3302	1606.6459	2	1606.8138	-0.1679	1	37	51	R.FVIGGPMGDSGLTGRK.I	Oxidation (M)
													650.6102	1948.8089	3	1948.9432	-0.1343	0	55	52	K.IIDSYGGWGAHGGGAFSGK.D	
Ni EC25	5718	66813780	XP_641069	DDB0214886	succinate dehydrogenase	sdhA	Q9U3X4	68472/6.46	62360/6.63	10 (5)	8 (5)	21%	636.8148	1271.6150	2	1271.6721	-0.0571	0	19	55	R.AVANEIENTLAK.D	
													699.3181	1396.6216	2	1396.6908	-0.0692	0	17	55	R.ETAMIFAGVDVTK.E	Oxidation (M)
													737.3869	1472.7593	2	1472.8351	-0.0758	0	67	57	R.LGANSLLDIVVFGR.A	
													498.5848	1492.7324	3	1492.7998	-0.0673	0	67	54	R.GVVAINLEDGTIHR.F	
													747.5000	1492.9854	2	1492.7998	0.1857	0	17	53	R.GVVAINLEDGTIHR.F	
													569.2766	1704.8079	3	1704.8795	-0.0716	1	59	53	R.YAPSVADLASRDVVS.R.S	
													1017.4664	2032.9182	2	2033.0470	-0.1288	0	58	57	K.EAVPTVLELEQYGVPF.S.R.M	
													740.3390	2217.9952	3	2218.1019	-0.1066	0	75	57	R.DYAVVDHTYDAIVVGAGGAGLR.A	
													819.0317	2454.0732	3	2454.2503	-0.1770	0	17	53	K.DTPHKPLPPNAGEESIANIDAIR.F	
													614.7966	2455.1574	4	2455.2343	-0.0769	0	16	55	K.DTPHKPLPPNAGEESIANIDAIR.F	Deamidated (NQ)
Ni EC25	6106	66821505	XP_644221	DDB0167610	similar to ribosomal protein	DDB_G0274407	Q86KA1	19511/9.13	20950/7.32	2 (2)	2 (2)	29%	688.0028	2060.9866	3	2061.0590	-0.0724	1	54	53	K.LTTIENGKSSTEVADLVER.I	
													996.1797	2985.5172	3	2985.6134	-0.0963	1	57	52	K.KLSIPDIDLSSLGSGAPAGGAA PAAAAAPAAVAK.T	
Ni EC25	6414	60463691	EAL61873	DDB0230070	S-adenosyl-methionine synthetase	metK	Q54F07	42079/6.14	42420/7.18	6 (5)	4 (3)	15%	514.8598	1027.7050	2	1027.6277	0.0773	1	27	41	R.ADLKELVIK.A	
													697.4315	1392.8484	2	1392.7357	0.1128	0	51	47	K.TGMVMILGEITTK.A	
													713.4197	1424.8248	2	1424.7255	0.0993	0	62	47	K.TGMVMILGEITTK.A	2 Oxidation (M)
													732.4202	1462.8259	2	1462.7239	0.1021	0	57	47	R.FVIGGPMGDSGLTGR.K	
													740.4217	1478.8288	2	1478.7188	0.1100	0	67	45	R.FVIGGPMGDSGLTGR.K	Oxidation (M)
													781.7931	2342.3574	3	2342.1655	0.1919	0	65	47	K.AVVPAQYLDDNTIYHLNPSGR.F	

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		gi	accession number	DDB	protein ID	gene name							observed	Mr(expt)	charge	Mr(calc)	delta	miss	score	ion score (identity)	sequence	modifications
Ni EC25	7112	60475381	EAL73316	DDB0233902	hypothetical protein DDB_0233902	DDB_G0267726	Q55GC5	19517/6.90	21000/8.20	5 (4)	4 (3)	41%	687.3722	1372.7252	2	1372.6987	0.0265	0	38	41	R.VILVNESNGWNK.A	Deamidated (NQ)
													699.3801	1396.7546	2	1396.7027	0.0519	0	65	47	K.YSIQTIDFPWK.S	
													739.3951	1476.7711	2	1476.7612	0.0099	0	59	47	K.ALGIWYDLEEIR.I	
													858.9899	1715.9746	2	1715.9359	0.0387	0	54	45	K.SGGQQYIALQLWKPK.A	
													573.0015	1715.9751	3	1715.9359	0.0392	0	63	45	K.SGGQQYIALQLWKPK.A	
Ni EC25	7414	10801150	AAG23402	DDB0191174	elongation factor 1 beta	efa1B	Q9GRF8	24220/4.54	39090/8.30	4 (3)	4 (3)	29%	722.3772	1442.7358	2	1442.7102	0.0256	1	56	45	K.TAPCATKYPHAAR.W	
													693.0136	2076.0405	3	2075.9643	0.0762	0	54	45	R.WFNTIASYSAAEQGFQEK.V	
													684.9389	1367.8632	2	1367.7721	0.0911	0	37	43	K.VTETVTIAAPAAPK.A	
													696.8784	1391.7558	2	1391.6789	0.0769	0	62	47	R.SIEMDGLVWGASK.L	
Ni EC25	7609	66805581	XP_636512	DDB0191139	cyclase associated protein	cap	P54654	49611/6.97	54250/7.83	7 (5)	7 (5)	22%	389.2746	776.5347	2	776.4796	0.0551	1	17	32	R.ILKEFK.G	
													562.8352	1123.6559	2	1123.5873	0.0686	1	49	31	K.NFTDKSSVVK.A	
													564.8236	1127.6326	2	1127.5822	0.0503	0	46	31	K.EIVIAEPDSR.Q	
													762.4610	1522.9074	2	1522.8355	0.0719	0	71	30	K.LAPEVGNQVEQLVK.A	
													962.0340	1922.0534	2	1921.9972	0.0562	0	16	31	R.QTVYIFQCVNSLVQIK.G	Carbamidomethyl (C); Gln->pyro-Glu (N-term Q)
													816.8008	2447.3807	3	2447.2544	0.1263	0	38	31	K.SATPAPASSAAPVAPAVSSTPVESK.K	
													847.1907	2538.5501	3	2538.4057	0.1445	0	40	32	K.KPSQETLLELIKPLNNFAAEV GK.I	
Ni EC50	0124	66812950	XP_640654	DDB0233328	putative polypeptide-associated complex alpha subunit	nacA	Q54U07	17357/5.08	21390/4.81	3 (2)	3 (2)	13%	487.2490	972.4835	2	972.5855	-0.1020	0	51	43	K.VVETLIATK.N	
													594.2901	1186.5657	2	1186.6710	-0.1052	0	44	41	K.LGLAPVSDIFR.V	
													615.8158	1229.6170	2	1229.7231	-0.1060	1	33	41	R.EKVVETLIATK.N	
Ni EC50	0125	66826197	XP_646453	DDB0191107	cytosolic glycoprotein FP21	fpaA	P52285	18706/4.74	21370/4.55	8 (5)	7 (5)	41%	381.7043	761.3941	2	761.4799	-0.0859	1	47	43	R.KIFNIK.N	
													382.6678	763.3211	2	763.4116	-0.0904	0	51	43	K.VFEIEK.E	
													584.2381	1166.4616	2	1166.5675	-0.1059	0	44	41	K.EIACMSVTIK.N	Carbamidomethyl (C); Oxidation (M)
													630.2619	1258.5092	2	1258.6306	-0.1214	1	36	41	K.RLDDIPPYDR.D	
													638.7750	1275.5355	2	1275.6558	-0.1203	1	52	43	M.SLVKLESSDEK.V	N-Acetyl (Protein)
													776.8170	1551.6195	2	1551.7668	-0.1473	1	43	41	K.LESSDEKVFEIEK.E	
													904.7178	2711.1316	3	2711.3575	-0.2259	0	28	41	K.NMIEDIGESDSPIPLPNVTSTILE K.V	
													910.0512	2727.1318	3	2727.3524	-0.2206	0	27	41	K.NMIEDIGESDSPIPLPNVTSTILE K.V	Oxidation (M)

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Ni EC50	0526	4336714	AAD17913	DDB0191177	repC-binding protein A	rcbA	Q54LV1	37621/4.89	56020/4.37	6 (3)	5 (3)	19%	383.1675	1146.4807	3	1146.6046	-0.1239	0	31	41	R.NHPHFNLLR.E	
													574.2492	1146.4839	2	1146.6046	-0.1207	0	17	40	R.NHPHFNLLR.E	
													694.2874	1386.5602	2	1386.6891	-0.1289	0	41	40	R.QIQENPNEFIR.L	
													748.3710	2242.0913	3	2242.2797	-0.1884	0	48	41	K.NPSIIPGILQQLAQTNPALVR.Q	
													803.3544	2407.0413	3	2407.2634	-0.2221	1	13	40	K.NINKEIYVFEVNGDLTVaelK.N	
													924.4549	2770.3429	3	2770.5704	-0.2275	1	49	43	R.EAISKNPsiipgilqqlaqtnpalvr.q	
		66810606	XP_639010	DDB0191384	calreticulin	crtA	Q23858	48506/4.63	56020/4.37	3 (2)	3 (2)	8%	493.2375	984.4604	2	984.5756	-0.1152	0	36	41	R.VHVILNYK.G	
													539.7627	1077.5108	2	1077.6070	-0.0962	0	49	41	K.DLVLYQYTVK.N	
													650.7846	1299.5546	2	1299.6823	-0.1277	0	47	43	K.QSKPVDWVDVK.E	
													699.7779	1397.5413	2	1397.6827	-0.1414	0	52	42	K.EGQDQIYFITGK.S	
Ni EC50	0721	66814268	XP_641313	DDB0215015	glucose-regulated protein 94	grp94	Q9NkX1	87227/4.88	87220/4.88	3 (2)	3 (2)	5%	772.8446	1543.6746	2	1543.8205	-0.1459	1	37	43	R.ELISNASDALDKIR.F	
													929.9177	1857.8209	2	1857.9836	-0.1628	0	55	43	R.FLVGVIDSDDLPLNVSr.e	
													594.2902	1186.5658	2	1186.6710	-0.1052	0	66	45	K.LGLAPVSDIFR.V	
Ni EC50	1125	66812950	XP_640654	DDB0233328	putative nascent polypeptide-associated complex alpha subunit	nacA	Q54U07	17357/5.08	21100/5.08	2 (2)	2 (2)	6%	615.8176	1229.6287	2	1229.7231	-0.0944	1	59	43	R.EKVVETLIATK.N	
													413.1854	824.3563	2	824.4432	-0.0869	0	19	43	K.FASYIPK.N	
Ni EC50	2334	66825457	XP_646083	DDB0201767	N-acyl-L-amino-acid amidohydrolase	acy1	Q55DP8	46824/5.69	42460/6.00	9 (4)	8 (4)	24%	497.6821	993.3497	2	993.4515	-0.1018	0	51	43	K.DESGNIFGR.G	
													506.7285	1011.4424	2	1011.5600	-0.1176	0	38	41	K.IEGLEPNLK.T	
													545.2379	1088.4612	2	1088.5654	-0.1043	1	44	41	K.FVYTEKFR.Q	
													750.8797	1499.7448	2	1499.8922	-0.1474	1	53	41	K.KLGDVTSLNLTVLK.A	
													515.5408	1543.6004	3	1543.7670	-0.1666	1	25	43	K.AKEYNIPYEVYR.E	
													772.8215	1543.6284	2	1543.7670	-0.1386	1	46	41	K.AKEYNIPYEVYR.E	
													582.8955	1745.6647	3	1745.8220	-0.1573	1	29	43	K.IRTDHPTPDYESSTK.F	
													982.7356	2945.1849	3	2945.4307	-0.2458	0	25	41	K.AGIPIDHSNfSYNVIPTQAEAGFDIR.I	
		66826503	XP_646606	DDB0232985	26S proteasome non-ATPase regulatory subunit 6	psmD6	Q55C75	44309/5.71	42460/6.00	6 (4)	6 (4)	15%	421.7247	841.4349	2	841.5273	-0.0924	0	42	41	K.ILVEQLK.W	
													545.2664	1088.5182	2	1088.6593	-0.1412	0	39	43	K.LDIVFTLIR.M	
													557.7712	1113.5278	2	1113.6070	-0.0792	1	52	41	R.LKTYEAVYK.M	
													581.7379	1161.4612	2	1161.5666	-0.1053	0	27	41	K.WTEDQGLVSK.L	
													659.3046	1316.5946	2	1316.7299	-0.1353	1	52	43	K.IDKVSGVIETTR.S	
													798.3067	1594.5989	2	1594.7474	-0.1486	0	47	41	K.ITDSVENfGESEIR.E	

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		gi	accession number	DDB	protein ID	gene name							observed	Mr(expt)	charge	Mr(calc)	delta	miss	score	ion score (identity)	sequence	modifications
Ni EC50	2831	66799895	XP_628873	DDB0192196	hypothetical protein DDBDRAFT_0192196	DDB_G0293920	Q54B43	97775/5.44	96880/6.02	14 (4)	14 (4)	18%	360.6945	719.3745	2	719.4581	-0.0836	0	18	41	R.LFVLTK.Y	
													492.2393	982.4641	2	982.5712	-0.1071	0	34	41	K.LLINAFHR.I	
													501.2699	1000.5252	2	1000.6280	-0.1028	1	46	41	R.KLVLAGSVSK.G	
													518.2471	1034.4797	2	1034.5760	-0.0963	0	24	40	K.GALSFAQTIK.S	
													560.7906	1119.5666	2	1119.6036	-0.0370	0	31	42	K.AEPIVDHIAR.T	
													686.7952	1371.5759	2	1371.7146	-0.1387	0	53	42	R.ESHLYNLVEIR.T	
													691.2827	1380.5508	2	1380.6673	-0.1165	0	63	42	R.VFNLDDEFAGIDR.N	
													747.3339	1492.6532	2	1492.7885	-0.1354	0	43	41	K.TTVAISSISTPNFR.A	
													748.8642	1495.7139	2	1495.8497	-0.1359	0	23	41	R.TLIDIPVPTADITK.I	
													503.8880	1508.6422	3	1508.7947	-0.1525	1	22	41	K.SSSKAEPIVDHIAR.T	
													812.8763	1623.7381	2	1623.8943	-0.1562	0	29	40	R.NSEGAVNLTPVLAALR.H	
													558.5874	1672.7403	3	1672.9049	-0.1646	0	46	41	K.EIPLLLADVFHHR.T	
													582.2316	1743.6730	3	1743.8652	-0.1922	0	29	40	K.SSSNIAHLNLANNSFR.K	
													660.3101	1977.9086	3	1978.0735	-0.1649	0	19	41	R.KPLVHINLEETQLDTTK.V	
Ni EC50	3423	22711882	AAG34561	DDB0191349	phosphoglycerate kinase	pgkA	Q9GPM4	45966/6.01	49510/6.79	12 (8)	10 (8)	36%	669.9107	1337.8154	2	1337.8030	0.0123	1	51	47	K.VLEDQLKRPIK.F	
													691.3743	1380.7266	2	1380.7183	0.0080	0	47	43	R.AHSSSMVGINLPQK.A	
													699.3605	1396.7521	2	1396.7132	0.0380	0	28	41	R.AHSSSMVGINLPQK.A	Oxidation (M)
													739.3381	1476.7626	2	1476.7435	0.0190	0	46	43	K.TIVWNGPMGVFEK.S	
													747.3883	1492.7574	2	1492.7384	0.0190	0	25	41	K.TIVWNGPMGVFEK.S	Oxidation (M)
													761.8976	1521.7874	2	1521.7748	0.0126	0	56	47	R.IDASIPTLEYCLK.N	
													802.3815	1602.7561	2	1602.7161	0.0399	0	63	47	R.FHIEEESGVDAEGK.K	
													813.9051	1625.8421	2	1625.8300	0.0121	1	54	45	K.FIDNKEIGSSLFEK.T	
													817.9105	1633.8016	2	1633.7848	0.0168	0	37	41	K.LGDVYVNDAFGTAHR.A	
													849.9802	1697.9444	2	1697.9715	-0.0271	0	49	45	K.ALESPSKPFLAILGGAK.V	
													866.4100	1730.8194	2	1730.8110	0.0084	1	41	45	R.FHIEEESGVDAEGKK.V	
													778.7167	2333.1371	3	2333.1691	-0.0320	1	62	47	K.LHFPVDYVIADKFDNDANIK.T	

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		gi	accession number	DDB	protein ID	gene name							observed	Mr(expt)	charge	Mr(calc)	delta	miss	score	ion score (identity)	sequence	modifications
Ni EC50	3721	66815105	XP_641648	DDB0231551	glutamate-ammonia ligase	glnA3	Q54WR9	83077/5.80	82320/6.67	8 (5)	8 (5)	13%	462.7489	923.4801	2	923.5804	-0.1003	0	52	41	R.TLIGAKPPK.G	
													520.7542	1039.4748	2	1039.5702	-0.0954	0	33	43	K.YSEILFLR.-	
													561.7635	1121.5270	2	1121.6193	-0.0923	0	53	44	R.AVDIHADLLR.A	
													648.7934	1295.5840	2	1295.6761	-0.0921	0	51	44	R.QEILFEIYNK.S	
													688.7782	1375.5456	2	1375.6367	-0.0911	0	53	41	K.GEPDASSFPSSGGIR.S	
													550.2343	1647.7167	3	1647.8045	-0.0878	1	47	42	R.TSPFAFTGNKFEFR.A	
													863.9265	1725.8511	2	1725.9664	-0.1153	0	34	41	R.LGANEAPPAHSIYLGK.E	
													669.3301	2004.9872	3	2005.0884	-0.1012	1	33	41	R.ISPTLGIEQEFFLIDRK.F	
		4584573	CAB40787	DDB0185041	prolyl oligopeptidase	dpoA	Q86AS5	87987/5.76	82320/6.67	8 (3)	8 (3)	12%	516.2167	1030.4188	2	1030.5447	-0.1259	0	23	41	K.YSPLNNVPK.D	
													517.7108	1033.4071	2	1033.5192	-0.1121	0	28	41	R.NFQEAIANK.S	
													527.7774	1053.5402	2	1053.6546	-0.1144	1	51	43	K.KVDTPLLIR.V	
													602.7397	1203.4648	2	1203.5771	-0.1123	0	57	45	K.AGSDWEEIAVK.K	
													621.2465	1240.4784	2	1240.6088	-0.1303	1	42	41	R.RDDSVFDIFK.S	
													592.9246	1775.7521	3	1775.9305	-0.1784	1	31	45	K.EHPEKDYVLESVSR.S	
													922.3581	1842.7017	2	1842.8788	-0.1770	0	23	45	K.GFENAIEFLNPNTYSK.D	
													643.6102	1927.8088	3	1928.0043	-0.1955	1	36	41	K.NDELLLFKEPHIEGFK.S	
Ni EC50	3826	66825911	XP_646310	DDB0191259	major vault protein	mvpA	P34118	94072/6.05	94290/6.89	12 (6)	11 (6)	15%	569.7939	1137.5732	2	1137.7121	-0.1390	0	66	45	K.VTALQVVAPLK.A	
													601.7918	1201.5690	2	1201.6918	-0.1228	0	42	41	K.SVQLAIEITTK.S	
													651.3224	1300.6302	2	1300.7350	-0.1048	1	17	41	K.AIVESIGRDTLK.S	
													711.7592	1421.5038	2	1421.6787	-0.1749	0	49	41	R.QSVFGLDESGEVR.K	
													739.9020	1477.7895	2	1477.9344	-0.1450	1	22	40	K.VTALQVVAPLKALR.L	
													756.2849	1510.5553	2	1510.7126	-0.1574	0	32	40	K.IFQVPDFVGDSCK.A	Carbamidomethyl (C)
													756.7744	1511.5342	2	1511.6967	-0.1624	0	31	41	K.IFQVPDFVGDSCK.A	Carbamidomethyl (C); Deamidated (NQ)
													769.7984	1537.5823	2	1537.7453	-0.1630	0	44	41	R.FSQEPFPLYPGEK.I	
													530.9199	1589.7378	3	1589.9028	-0.1651	1	46	41	K.VVEIVNAYVLTDDK.A	
													800.3346	1598.6547	2	1598.8160	-0.1613	0	21	40	K.LVSGPEPMIMIPQR.N	2 Oxidation (M)
													817.3163	1632.6180	2	1632.7995	-0.1814	0	62	45	R.ESIPLDENEGIYVR.D	
													833.3078	1664.6010	2	1664.7893	-0.1883	0	31	41	R.NENGSLVLDEYGVVK.L	Deamidated (NQ)

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		gi	accession number	DDB	protein ID	gene name							observed	Mr(expt)	charge	Mr(calc)	delta	miss	score	ion score (identity)	sequence	modifications
Ni EC50	4529	66827977	XP_647343	DDB0191115	actin binding protein	corA	P27133	49697/6.81	56150/7.21	9 (4)	9 (4)	25%	425.7074	849.4003	2	849.4960	-0.0956	0	30	45	K.VITVGFSK.T	
													495.7342	989.4539	2	989.5480	-0.0941	1	33	45	R.GLCFLPKR.C	
													547.2630	1092.5115	2	1092.6179	-0.1063	1	53	47	K.DKVITVGFSK.T	
													639.8123	1277.6101	2	1277.7230	-0.1130	1	52	47	R.VAYLESEIVKK.D	
													696.8153	1391.6160	2	1391.7449	-0.1289	0	51	45	K.VTPFTVEPISFR.V	
													727.7614	1453.5083	2	1453.6586	-0.1502	0	59	48	K.SAWDSNYVAANTR.Y	
													604.9451	1811.8134	3	1811.9781	-0.1647	0	33	43	K.ASAVEFKPVVQVQEGPK.N	
													760.3012	2277.8818	3	2278.0833	-0.2015	0	14	43	R.YYELVDESPYIHFLSEFK.S	
													855.7163	2564.1271	3	2564.3485	-0.2215	1	23	45	R.KVGTISFNPVADNVAVTSSGDFLVK.T	
Ni EC50	4732	66805423	XP_636444	DDB0231600	AAA ATPase domain-containing protein	DDB_G0289047	Q54I27	88859/8.51	84480/7.24	2 (2)	2 (2)	3%	685.8560	1369.6974	2	1369.8181	-0.1207	0	60	43	R.VLTLDLASIVAGAK.F	
Ni EC50	6132	66808689	XP_638067	DDB0238212	peroxiredoxin	prdx5	Q54N76	18350/6.74	21630/8.22	2 (2)	2 (2)	14%	606.2692	1210.5238	2	1210.6268	-0.1029	0	54	45	R.YAMILDSGVVK.H	Oxidation (M)
Ni EC50	6218	66820416	XP_643826	DDB0167407	putative epimerase	DDB_G0275053	Q86I47	33977/6.97	28190/8.02	8 (4)	8 (4)	33%	721.2967	1440.5788	2	1440.7105	-0.1317	0	69	45	K.ALPPVDGVCAMAPK.V	Carbamidomethyl (C); Oxidation (M)
													553.8499	1105.6852	2	1105.6019	0.0833	0	48	41	K.LTNLEEFLK.K	
													412.2803	1233.8190	3	1233.6969	0.1221	1	36	41	K.LTNLEEFLKK.T	
													535.0136	1602.0190	3	1601.8314	0.1876	1	31	41	K.ISGGRYNVPHFDLK.H	
													614.0527	1839.1364	3	1838.9890	0.1474	0	61	45	K.ELEYGLNIAHAALAAGVK.H	
													740.7721	2219.2944	3	2219.1144	0.1800	0	64	45	R.TVNEATQEVTYVLGMPLNPK.M	Oxidation (M)
													566.0851	2260.3112	4	2260.1232	0.1880	1	25	40	K.IIPFSGDCLHGEKIAEIMSK.V	Carbamidomethyl (C); Oxidation (M)
													792.8106	2375.4099	3	2375.2155	0.1944	1	45	41	K.RTVNEATQEVTYVLGMPLNP K.M	Oxidation (M)
													1217.1378	2432.2611	2	2432.1035	0.1576	0	12	4	K.ENPSFVTSFVYAPFYMQNFK.T	Deamidated (NQ); Oxidation (M)
Ni EC50	6223	66809487	XP_638466	DDB0237882	phosphoribosyl pyrophosphate synthetase	prsA	Q54PA9	34443/7.68	30880/8.29	3 (3)	3 (3)	13%	692.8592	1383.7039	2	1383.7722	-0.0682	0	62	45	K.LVANLIETAGIDR.V	
Ni EC50													724.3359	1446.6573	2	1446.7388	-0.0815	0	54	45	K.ANEVSGMILVGDVK.D	Oxidation (M)
													836.8576	1671.7007	2	1671.7774	-0.0767	0	46	41	K.FSNGETSVMISESIR.D	Oxidation (M)

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		gi	accession number	DDB	protein ID	gene name							observed	Mr(expt)	charge	Mr(calc)	delta	miss	score	ion score (identity)	sequence	modifications
Chp EC25	0605	66825227	XP_645968	DDB0304584	ZPR1-type zinc finger-containing protein	zpr1	Q55E13	53516/4.53	58980/4.51	27 (12)	17 (10)	51%	511.2930	1020.5714	2	1020.5491	0.0223	0	32	41	K.EELLGFVSK.L	
													613.8344	1225.6542	2	1225.6417	0.0125	0	75	45	K.MVLTDIPYFK.S	
													621.8355	1241.6564	2	1241.6366	0.0198	0	59	45	K.MVLTDIPYFK.S	Oxidation (M)
													436.8979	1307.6719	3	1307.6510	0.0209	1	17	41	K.EELEKNPFFR.G	
													654.8448	1307.6750	2	1307.6510	0.0240	1	37	41	K.EELEKNPFFR.G	
													667.9154	1333.8162	2	1333.7857	0.0305	0	46	45	K.FTTVEGLITIHK.E	
													703.3826	1404.7507	2	1404.7323	0.0184	0	25	40	K.LSNLLMVDEPFK.I	
													711.3855	1420.7565	2	1420.7272	0.0293	0	54	45	K.LSNLLMVDEPFK.I	Oxidation (M)
													809.9264	1617.8382	2	1617.8210	0.0172	0	49	45	R.VTTTSVSIPSGDLADR.E	
													850.4362	1698.8579	2	1698.8465	0.0114	0	22	45	R.YQEITSQLDSFIAGK.K	
													851.4261	1700.8376	2	1700.8145	0.0231	0	35	43	R.YQEITSQLDSFIAGK.K	2 Deamidated (NQ)
													897.4076	1792.8006	2	1792.7834	0.0172	0	70	45	K.SILLMAFSCDECGYK.T	2 Carbamidomethyl (C)
													905.4115	1808.8085	2	1808.7783	0.0302	0	82	45	K.SILLMAFSCDECGYK.T	2 Carbamidomethyl (C); Oxidation (M)
													619.9925	1856.9558	3	1856.9115	0.0443	0	24	41	K.EAITNLTNASEIHTESK.E	
													620.3193	1857.9362	3	1857.8956	0.0406	0	20	41	K.EAITNLTNASEIHTESK.E	Deamidated (NQ)
													929.9768	1857.9390	2	1857.8956	0.0434	0	82	45	K.EAITNLTNASEIHTESK.E	Deamidated (NQ)
													633.9649	1898.8729	3	1898.8266	0.0463	0	23	45	K.EIMVFAFHCPECGFR.S	2 Carbamidomethyl (C)
													639.2912	1914.8518	3	1914.8215	0.0303	0	40	41	K.EIMVFAFHCPECGFR.S	2 Carbamidomethyl (C); Oxidation (M)
													965.4988	1928.9831	2	1928.9439	0.0392	0	29	41	R.TAEQNASLGLGINEEQQK.Q	
													966.4865	1930.9584	2	1930.9119	0.0465	0	22	43	R.TAEQNASLGLGINEEQQK.Q	2 Deamidated (NQ)
													655.0463	1962.1170	3	1962.0925	0.0245	1	19	41	K.FTTVEGLITIHKKELEK.N	
													1014.0097	2026.0048	2	2026.0007	0.0041	0	60	43	K.IVDDPSGNSFIENPNAPK.A	
													793.7615	2378.2627	3	2378.2329	0.0298	0	76	43	K.SDTANVIIPELEIEVTHGSLGG K.F	
													715.8854	2859.5124	4	2859.4501	0.0623	1	37	40	K.EAITNLTNASEIHTESKSELLGF VSK.L	
													954.1786	2859.5141	3	2859.4501	0.0640	1	23	40	K.EAITNLTNASEIHTESKSELLGF VSK.L	
													1023.4550	3067.3433	3	3067.3135	0.0298	0	91	45	K.NISHENEVTEIESYCVNCEAE NGITR.I	2 Carbamidomethyl (C); Deamidated (NQ)
													1112.2306	3333.6698	3	3333.6292	0.0406	0	77	45	K.KPFTIELDDPISNSYIQNLFAP DDDPQLK.I	Deamidated (NQ)
Chp EC25	3711	60469746	EAL67734	DDB0231551	glutamate-ammonia ligase	glnA3	Q54WR9	83077/5.80	76430/6.23	6 (5)	6 (5)	9%	561.8511	1121.6929	2	1121.6193	0.0736	0	56	43	R.AVDIHADLLR.A	
													648.8497	1295.6861	2	1295.6761	0.0100	0	65	47	R.QEILFEIYNK.S	
													688.8712	1375.7374	2	1375.6367	0.1007	0	59	47	K.GEPDASSFPSGGIR.S	
													550.2943	1647.8517	3	1647.8045	0.0472	1	42	45	R.TSPFAFTGNKFEFR.A	
													864.0201	1726.0411	2	1725.9664	0.0747	0	54	41	R.LGANEAPPAHSIYLGK.E	

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													669.3694	2005.0985	3	2005.0884	0.0101	1	46	45	R.ISPTLGIEQEFFLIDRK.F												
Treatment	Spot n°	ID by www.ncbi.nlm.nih.gov		ID by www.dictybase.org			UniPROT ID	MW(Da)/pI expected	MW(Da)/pI observed	n° matches	n° sequences	% coverage	mass					peptide															
		gi	accession number	DDB	protein ID	gene name							observed	Mr(expt)	charge	Mr(calc)	delta	miss	score	ion score (identity)	sequence	modifications											
Chp EC25	4610	66818493	XP_642906	DDB0231504	aldehyde dehydrogenase	DDB_G0276821	P83401	55155/5.78	53860/6.41	2 (2)	2 (2)	5%	653.7964	1305.5783	2	1305.7041	-0.1258	0	57	45	R.AVLFASVGTTGQR.C												
													674.8157	1347.6169	2	1347.7609	-0.1440	0	78	49	K.GASTTSLITLAVSK.I												
Chp EC25	4613	66826743	XP_646726	DDB0232964	26S proteasome ATPase 1 subunit	psmC1	Q55BV5	49161/5.90	59820/6.39	13 (8)	13 (8)	31%	428.2099	854.4052	2	854.4208	-0.0155	0	52	41	R.IMSFVDK.S	Oxidation (M)											
													479.7765	957.5384	2	957.5283	0.0100	0	55	43	K.IFEIHTAK.M												
													486.7975	971.5804	2	971.5651	0.0154	0	63	45	R.VVGSELIQK.Y												
													536.3026	1070.5907	2	1070.6012	-0.0105	0	40	45	K.IEFPLPDIK.T												
													577.2927	1152.5708	2	1152.5485	0.0224	1	20	41	R.KTAGAPEGLYM.-	Oxidation (M)											
													595.8338	1189.6530	2	1189.6342	0.0188	0	55	41	K.GVILYGEPTGK.T												
													600.3659	1198.7172	2	1198.6961	0.0211	1	45	40	R.KIEFPLPDIK.T												
													639.8528	1277.6911	2	1277.6728	0.0183	0	58	41	K.AVANQTSATFLR.V												
													652.3639	1302.7133	2	1302.6965	0.0167	0	25	41	K.AICTESGLLALR.E	Carbamidomethyl (C)											
													659.8882	1317.7618	2	1317.7656	-0.0038	0	62	42	K.LYLGATVLLNNK.T												
													678.8497	1355.6849	2	1355.6874	-0.0025	0	21	42	K.YQPPPPPTQFGK.K												
													484.2924	1449.8554	3	1449.8303	0.0250	0	16	40	R.IETLDPALIRPGR.I												
													839.4763	2515.4072	3	2515.3573	0.0499	0	48	43	K.EAIELPLTHPELYEEIGIKPPK.G												
													Chp EC25	6310	66799989	XP_628920	DDB0231294	isocitrate dehydrogenase (NAD+)	idhB	Q54B68	38663/8.48	37240/7.61	16 (8)	14 (7)	44%	428.2565	854.4985	2	854.4974	0.0011	0	23	41
446.2133	890.4120	2	890.4174	-0.0054	0	26	41	R.YAFEYAK.A																									
539.2787	1076.5428	2	1076.5349	0.0079	0	50	41	K.EGTLTSDIGGK.S																									
560.2995	1118.5844	2	1118.5832	0.0012	0	65	45	K.HLGLNEHATK.V																									
683.8610	1365.7074	2	1365.6816	0.0258	0	28	45	K.QFTGAVIDYIEK.N	Gln->pyro-Glu (N-term Q)																								
692.3619	1382.7092	2	1382.7081	0.0011	0	48	42	K.QFTGAVIDYIEK.N																									
693.3800	1384.7454	2	1384.7173	0.0282	0	20	41	K.ALDLYAHVVPCK.Q	Carbamidomethyl (C)																								
476.2625	1425.7658	3	1425.7616	0.0042	0	54	45	R.HDDVLVDFVVIRE																									
713.9141	1425.8137	2	1425.7616	0.0522	0	59	45	R.HDDVLVDFVVIRE																									
744.9210	1487.8274	2	1487.8195	0.0080	1	22	41	K.AVIKEGTLTSDIGGK.S																									
754.4057	1506.7969	2	1506.7678	0.0291	0	56	40	K.GPLYTEILSGSQSR.N																									
795.9400	1589.8654	2	1589.8520	0.0133	0	47	40	K.ANPTGLLLASVMMLK.H	2 Oxidation (M)																								
612.0151	1833.0236	3	1832.9739	0.0496	1	35	42	K.DKANPTGLLLASVMMLK.H	2 Oxidation (M)																								
640.3706	1918.0900	3	1918.0523	0.0377	1	23	42	K.VALKGPLYTEILSGSQSR.N																									
826.1040	2475.2902	3	2475.2492	0.0410	0	17	43	R.ENTQGEYSGLEQVLTGQVQSLK.I																									
864.1405	2589.3996	3	2589.3359	0.0637	0	51	45	K.TVTVIPGDGIGPEITSSVMGVFQAAK.V	Oxidation (M)																								

Supplemental table 1 - Details about identified proteins

Treatment	Spot n°	ID by www.ncbi.nlm.nih.gov		ID by www.dictybase.org			UniPROT ID	MW(Da)/pI expected	MW(Da)/pI observed	n° matches	n° sequences	% coverage	mass					peptide				
		gi	accession number	DDB	protein ID	gene name							observed	Mr(expt)	charge	Mr(calc)	delta	miss	score	ion score (identity)	sequence	modifications
Chp EC25	7609	66805581	XP_636512	DDB0191139	cyclase associated protein	cap	P54654	49611/6.97	54250/7.83	15 (9)	14 (9)	41%	562.8330	1123.6515	2	1123.5873	0.0642	1	48	45	K.NFTDKSSVVK.A	
													604.3354	1206.6562	2	1206.5979	0.0582	0	64	45	K.DSLETEIVSSK.S	
													616.3750	1230.7354	2	1230.6608	0.0745	0	19	41	K.GPGLGAVFGELSK.G	
													680.4244	1358.8342	2	1358.7558	0.0784	1	25	41	K.KGPGLGAVFGELSK.G	
													762.4584	1522.9022	2	1522.8355	0.0667	0	76	43	K.LAPEVGNQVEQLVK.A	
													551.3375	1650.9906	3	1650.9305	0.0601	1	47	45	K.KLAPEVGNQVEQLVK.A	
													830.4641	1658.9137	2	1658.8839	0.0298	1	63	45	K.AIDAEKALINTASQSK.K	
													970.5619	1939.1093	2	1939.0237	0.0856	0	22	43	R.QTVYIFQCVNSLVQIK.G	Carbamidomethyl (C)
													660.7228	1979.1467	3	1979.0397	0.1070	1	13	43	R.VPSIAIDKTSGCQIYLSK.D	Carbamidomethyl (C)
													696.0742	2085.2007	3	2085.0895	0.1112	0	49	45	K.EFQNLVDQHITPFVALSK.K	
													782.4296	2344.2670	3	2344.1468	0.1202	1	37	45	K.TSGCQIYLSKDSLETEIVSSK.S	Carbamidomethyl (C)
													1199.1096	2396.2046	2	2396.1303	0.0743	0	53	45	K.SIASGVASSSSSSPSSGAAGPS SASVK.E	
													816.8008	2447.3807	3	2447.2544	0.1263	0	57	41	K.SATPAPASSAPAAPVAPAVSST PVESK.K	
													847.1798	2538.5174	3	2538.4057	0.1117	0	63	41	K.KPSQETLLELIKPLNNFAAEV GK.I	
													870.8012	2609.3818	3	2609.2762	0.1056	1	22	45	K.GVNQDQVDWVSNYVNFLKDL EK.Y	
Chp EC50	1617	66809891	XP_638669	DDB0233767	Protein phosphatase 2C-like domain-containing protein	DDB_G0284243	Q54PX6	44393/4.98	65360/5.00	6 (3)	6 (3)	13%	464.6662	927.3179	2	927.4338	-0.1159	0	51	45	R.DFGVSFEK.N	
													471.7271	941.4396	2	941.5658	-0.1262	0	53	45	R.VNGILAVTR.S	
													606.7266	1211.4387	2	1211.5935	-0.1548	0	23	41	K.YLYVANAGDAR.A	
													618.7220	1235.4294	2	1235.5717	-0.1423	0	15	40	R.IDAAGGFVCNGR.V	Carbamidomethyl(C)
													635.2375	1268.4605	2	1268.6149	-0.1545	1	63	45	R.DFGVSFEKNAR.Y	
													638.2555	1274.4965	2	1274.6507	-0.1542	0	41	43	K.SPEGDILELFR.N	
Chp EC50	3326	60475385	EAL73320	DDB0233903	Putative SAM dependent methyltransferase	DDB_G0267734	Q55GC0	33419/5.76	32460/5.97	2 (2)	2 (2)	9%	592.3420	1182.6695	2	1182.6608	0.0087	1	71	45	K.AGNKDVLPEIK.E	
													772.4224	1542.8302	2	1542.8001	0.0301	0	65	45	R.DLAIDIGAGSGQATVRL	

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		gi	accession number	DDB	protein ID	gene name							observed	Mr(expt)	charge	Mr(calc)	delta	miss	score	ion score (identity)	sequence	modifications
Chp EC50	3424	66803080	XP_635383	DDB0230070	S-adenosylmethionine synthetase	metK	Q54F07	41737/6.14	49340/6.11	12 (9)	9 (6)	26%	486.7301	971.4456	2	971.5400	-0.0944	0	42	45	K.SLVAAGLADR.C	
													514.7674	1027.5203	2	1027.6277	-0.1074	1	47	45	R.ADLKELVIK.A	
													676.2447	1350.4749	2	1350.6092	-0.1343	0	49	45	R.NDPDFTWETVK.E	
													679.8276	1357.6406	2	1357.7718	-0.1312	0	43	41	R.DLQLTRPIFQK.T	
													697.3024	1392.5902	2	1392.7357	-0.1455	0	67	47	K.TGMVMILGEITTK.A	
													705.2993	1408.5841	2	1408.7306	-0.1465	0	49	45	K.TGMVMILGEITTK.A	Oxidation (M)
													713.3043	1424.5941	2	1424.7255	-0.1314	0	62	45	K.TGMVMILGEITTK.A	2 Oxidation (M)
													732.2961	1462.5776	2	1462.7239	-0.1463	0	74	47	R.FVIGGPMGDSGLTGR.K	
													740.2970	1478.5794	2	1478.7188	-0.1394	0	68	45	R.FVIGGPMGDSGLTGR.K	Oxidation (M)
													747.7598	1493.5050	2	1493.6674	-0.1624	1	30	41	K.IGYDDSSKGF DYK.T	
													804.3302	1606.6459	2	1606.8138	-0.1679	1	37	41	R.FVIGGPMGDSGLTGRK.I	Oxidation (M)
													650.6102	1948.8089	3	1948.9432	-0.1343	0	55	47	K.IIDSYGGWGAHGGGAFSGK.D	
Chp EC50	3536	66818493	XP_642906	DDB0231504	Aldehyde dehydrogenase	DDB_G0276821	P83401	55155/5.78	60980/5.96	2 (2)	2 (2)	5%	653.7964	1305.5783	2	1305.7041	-0.1258	0	67	45	R.AVLFASVGTTGQR.C	
													674.8157	1347.6169	2	1347.7609	-0.1440	0	78	45	K.GASTTSLITLAVSK.I	
Chp EC50	3725	66801325	XP_629588	DDB0237783	Tetratricopeptide-like helical domain-containing protein (TPR) stress-induced-phosphoprotein 1	sti1	Q54DA8	63170/6.16	80380/6.08	3 (3)	3 (3)	6%	692.9541	1383.8937	2	1383.7795	0.1142	0	47	41	K.ILSDPIMNQILK.D	
													742.4518	1482.8891	2	1482.7678	0.1213	0	95	41	R.IEANNPELLDLSR.K	
													856.4687	1710.9229	2	1710.8213	0.1016	0	58	45	R.EYQQALEVYDQGLR.I	
													393.6579	785.3012	2	785.3959	-0.0947	0	26	41	R.YELYAK.F	
													540.2296	1078.4447	2	1078.5593	-0.1146	0	46	41	K.IAINICYGR.H	Carbamidomethyl (C)
													631.7666	1261.5186	2	1261.6190	-0.1004	0	44	43	K.QFESVQATLEK.Y	Gln->pyro-Glu (N-termQ)
													639.2759	1276.5373	2	1276.6550	-0.1178	0	37	41	K.YIPAEELSEVK.R	
													640.2685	1278.5224	2	1278.6455	-0.1232	0	71	45	K.QFESVQATLEK.Y	
													438.1689	1311.4847	3	1311.6030	-0.1183	1	17	41	K.DKWNFQMTAR.Y	Oxidation (M)
													672.8045	1343.5945	2	1343.5533	0.0412	0	18	41	K.QFESVQATLEK.Y	2 Deamidated (NQ); Phospho (ST); Gln->pyro-Glu (N-termQ)
Chp EC50	4432	66821393	XP_644181	DDB0185221	Beta-alanine synthase	pyd3	Q964D8	44088/6.32	44280/6.78	15 (7)	12 (5)	36%	717.3246	1432.6346	2	1432.7561	-0.1215	1	50	45	K.YIPAEELSEVKR.I	
													768.8312	1535.6479	2	1535.7831	-0.1352	1	18	42	M.SKQFESVQATLEK.Y	Acetyl (K)
													542.5669	1624.6789	3	1624.8316	-0.1528	1	22	41	R.KYNMVIISPLER.D	2 Oxidation (M)
													836.3322	1670.6499	2	1670.7834	-0.1335	0	52	42	R.NAAMTNNYFVGSINR.V	
													844.3277	1686.6408	2	1686.7783	-0.1375	0	105	45	R.NAAMTNNYFVGSINR.V	Oxidation (M)
													1065.9681	2129.9216	2	2130.0626	-0.1410	0	43	41	R.VSDGLNISEVDLNL CQQVK.D	Carbamidomethyl (C)
													719.6220	2155.8442	3	2156.0425	-0.1983	1	18	41	R.EKYPWVEFAESASTGQSIK.F	
													920.0959	2757.2659	3	2757.4436	-0.1776	0	23	41	R.LGHIQNSIGAETTAPIQDQYLAIEAK.I	Deamidated (NQ)

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		gi	accession number	DDB	protein ID	gene name							observed	Mr(expt)	charge	Mr(calc)	delta	miss	score	ion score (identity)	sequence	modifications
Chp EC50	4642	66822027	XP_644368	DDB0266926	Transketolase	tkt-2	Q556J0	71912/6.39	74280/6.92	21 (10)	14 (8)	31%	572.2671	1142.5197	2	1142.6295	-0.1098	0	60	45	R.ADGPTLLSLTR.Q	
													648.7862	1295.5579	2	1295.6874	-0.1295	0	21	41	R.QNLPFLPGTAQK.K	Gln->pyro-Glu (N-termQ)
													681.3010	1360.5875	2	1360.7351	-0.1476	0	54	41	R.GGYIVVSETAPLR.M	
													702.8239	1403.6333	2	1403.7773	-0.1440	1	29	41	K.YVGLDGKVIGIDR.F	
													727.2683	1452.5221	2	1452.6741	-0.1520	0	49	41	R.VVSMPCTELFDR.Q	Carbamidomethyl (C)
													735.2723	1468.5300	2	1468.6691	-0.1391	0	61	45	R.VVSMPCTELFDR.Q	Carbamidomethyl (C); Oxidation (M)
													751.8019	1501.5891	2	1501.7275	-0.1384	0	29	42	R.IAMEAGVTSFWYK.Y	
													759.7895	1517.5645	2	1517.7224	-0.1579	0	62	45	R.IAMEAGVTSFWYK.Y	Oxidation (M)
													783.8354	1565.6563	2	1565.8454	-0.1891	0	43	41	K.QIPEFPTTPIIATR.K	Gln->pyro-Glu (N-termQ)
													792.3628	1582.7110	2	1582.8719	-0.1609	0	40	41	K.QIPEFPTTPIIATR.K	
													831.3459	1660.6773	2	1660.7978	-0.1205	1	19	40	K.QLGMTSENLVNISKQ.-	Deamidated (NQ); Oxidation (M); Gln->pyro-Glu (N-termQ)
													839.3320	1676.6494	2	1676.8403	-0.1909	1	20	40	K.QLGMTSENLVNISKQ.-	Oxidation(M)
													839.8313	1677.6481	2	1677.8243	-0.1762	1	17	41	K.QLGMTSENLVNISKQ.-	Deamidated (NQ); Oxidation (M)
													632.2686	1893.7841	3	1893.9441	-0.1600	1	15	41	K.VIGIDRFGMSAPGNAVMK.Q	2 Oxidation (M)
													639.9581	1916.8524	3	1917.0320	-0.1796	1	48	45	R.EGTLRGGYIVVSETAPLR.M	
													652.9417	1955.8033	3	1955.9808	-0.1775	0	58	45	R.MILIATGSEVQHCVEAAK.L	Carbamidomethyl (C)
													986.9082	1971.8018	2	1971.9758	-0.1740	0	15	40	R.MILIATGSEVQHCVEAAK.L	Carbamidomethyl (C); Oxidation (M)
													658.2803	1971.8191	3	1971.9758	-0.1567	0	48	45	R.MILIATGSEVQHCVEAAK.L	Carbamidomethyl (C); Oxidation (M)
													671.3141	2010.9204	3	2011.0891	-0.1687	0	41	41	K.VSGATFLVFS DYLRPAIR.L	
													731.3256	2190.9550	3	2191.1306	-0.1756	1	31	40	K.LAQLLESAHEKHEAIDIMK.Q	Oxidation (M)
													803.4000	3209.5709	4	3209.6833	-0.1124	1	35	41	K.AASGHLGLPLGSAEIGAALFGNS LIYNPKDTR.W	

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		gi	accession number	DDB	protein ID	gene name							observed	Mr(expt)	charge	Mr(calc)	delta	miss	score	ion score (identity)	sequence	modifications
Chp EC50	4655	66813780	XP_641069	DDB0214886	Succinate dehydrogenase (ubiquinone)	sdhA	Q9U3X4	68472/6.46	67690/6.73	11 (6)	9 (5)	20%	451.7293	901.4440	2	901.4756	-0.0316	0	39	41	K.EGVELIDK.C	
													575.2937	1148.5728	2	1148.5826	-0.0097	0	24	41	R.YAPSVADLASR.D	
													575.2959	1148.5773	2	1148.5826	-0.0052	0	55	45	R.YAPSVADLASR.D	
													636.8571	1271.6997	2	1271.6721	0.0276	0	63	45	R.AVANEIENTLAK.D	
													674.3688	1346.7230	2	1346.6830	0.0400	0	14	41	K.HTLSYLDVNTGK.V	
													737.4274	1472.8402	2	1472.8350	0.0052	0	91	45	R.LGANSLLDIVVFGR.A	
													747.4162	1492.8178	2	1492.7997	0.0180	0	61	45	R.GVVAINLEDGTIHR.F	
													498.6147	1492.8222	3	1492.7997	0.0224	0	52	43	R.GVVAINLEDGTIHR.F	
													804.9705	1607.9264	2	1607.8783	0.0481	0	29	41	R.TGHALLHTLYGQAVK.H	
													606.9696	1817.8869	3	1817.8478	0.0391	0	37	41	K.GLYAAGESACVSVHGANR.L	Carbamidomethyl (C)
													819.1061	2454.2965	3	2454.2502	0.0462	0	48	45	K.DTPHKPLPPNAGEESIANIDAI R.F	
		66807283	XP_637364	DDB0218901	Hypothetical protein DDBDRAFT_0218901	DDB_ G0287201	Q54KR6	70872/5.93	67690/6.73	9 (4)	7 (4)	13%	493.8028	985.5910	2	985.5807	0.0103	0	53	45	K.NLGLLEVTK.S	
													698.8961	1395.7777	2	1395.7609	0.0168	0	56	41	K.VLSTHEVIEIEK.V	
													477.9194	1430.7363	3	1430.8020	-0.0658	0	13	41	R.IDKPIEITVFEK.E	
													728.8612	1455.7078	2	1455.6816	0.0261	0	43	45	K.SLPFFSLCENS.R	Carbamidomethyl (C)
													728.8662	1455.7179	2	1455.6816	0.0363	0	46	41	K.SLPFFSLCENS.R	Carbamidomethyl (C)
													744.3000	1486.5854	2	1486.7820	-0.1965	0	37	41	K.FTGLPFTKETIPK.K	
													496.6105	1486.8098	3	1486.7820	0.0278	0	27	42	K.FTGLPFTKETIPK.K	
													563.6600	1687.9581	3	1687.9396	0.0185	1	16	41	R.IDKPIEITVFEKEK.I	
													794.1188	2379.3346	3	2379.2797	0.0549	0	46	41	K.YTELGGSVVHPLNENIIGLIN K.L	

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		gi	accession number	DDB	protein ID	gene name							observed	Mr(expt)	charge	Mr(calc)	delta	miss	score	ion score (identity)	sequence	modifications
Chp EC50	4730	66815641	XP_641837	DDB0229908	Putative iron regulatory protein	aco1	Q54X73	97929/6.03	87050/6.79	28 (12)	21 (11)	40%	433.2646	864.5147	2	864.4705	0.0442	0	47	45	K.SFETILR.F	
													547.8084	1093.6023	2	1093.5590	0.0432	0	46	45	K.CVIAISFER.I	Carbamidomethyl (C)
													373.5760	1117.7062	3	1117.6495	0.0567	1	54	45	R.IEKLPSYIR.I	
													655.8769	1309.7393	2	1309.6990	0.0403	0	38	43	K.EDLVVAGVLSG NR.N	Glu->pyro-Glu (N-termE)
													664.8815	1327.7485	2	1327.7096	0.0389	0	58	47	K.EDLVVAGVLSG NR.N	
													667.3550	1332.6955	2	1332.6561	0.0394	0	25	41	K.EQFNIELPTDK.S	
													450.9219	1349.7439	3	1349.6768	0.0671	0	15	40	K.STYIHNPFFK.T	
													709.3970	1416.7795	2	1416.7289	0.0506	0	52	45	K.VPTGLLYPWDEK.S	
													770.4361	1538.8577	2	1538.8093	0.0484	0	64	45	K.NAVEHGLEVAPYIK.T	
													513.9652	1538.8738	3	1538.8093	0.0645	0	35	41	K.NAVEHGLEVAPYIK.T	
													793.3997	1584.7848	2	1584.7243	0.0605	0	15	40	K.QDFNSCLSSPVGFK.G	Carbamidomethyl (C)
													610.0047	1826.9923	3	1826.9275	0.0648	1	19	40	R.TVDALEQNQKIEFHR.N	
													966.9986	1931.9826	2	1931.9265	0.0561	0	44	43	K.FVEFYGEGVSTLSVQDR.A	
													1008.0749	2014.1352	2	2014.0921	0.0430	0	40	41	R.VLLQDFTGVP AVVDLAAMR.D	
													672.3986	2014.1738	3	2014.0921	0.0817	0	56	46	R.VLLQDFTGVP AVVDLAAMR.D	
													1016.0778	2030.1411	2	2030.0871	0.0541	0	35	40	R.VLLQDFTGVP AVVDLAAMR.D	Oxidation (M)
													677.7299	2030.1677	3	2030.0871	0.0807	0	61	45	R.VLLQDFTGVP AVVDLAAMR.D	Oxidation (M)
													725.7382	2174.1927	3	2174.1048	0.0879	1	21	40	K.SWNE LKVPTGLLYPWDEK.S	
													771.0616	2310.1628	3	2310.0876	0.0752	0	48	45	K.YQSEGHQLIVLAGSDYGS GS R.D	
													772.1280	2313.3621	3	2313.2693	0.0928	0	54	45	K.INPLVPVDLVIDHSVQVDVSR.T	
													675.1347	2696.5099	4	2696.3922	0.1177	1	43	45	K.DVENILNWENTANKVEIPFKPA R.V	
													908.1455	2721.4148	3	2721.3571	0.0577	0	25	41	K.LAPAVGPQTTYVPTGELMFISD AAEK.Y	Oxidation (M)
													914.5128	2740.5165	3	2740.4582	0.0583	0	22	40	R.SNLVGMGHIPLQFQPGQNASTLG LTGK.E	
													919.8458	2756.5155	3	2756.4531	0.0624	0	29	40	R.SNLVGMGHIPLQFQPGQNASTLG LTGK.E	Oxidation (M)
													924.8403	2771.4990	3	2771.4052	0.0938	0	64	45	K.SQSHPIFTTTMELDLSTV VPS LSGPK.R	
													930.1718	2787.4934	3	2787.4001	0.0933	0	29	40	K.SQSHPIFTTTMELDLSTV VPSLS GPK.R	Oxidation (M)
													1042.9032	3125.6876	3	3125.6087	0.0789	0	32	41	K.WGAQAFDGLFIAPPGSGIVHQV NLEYIAR.E	
													817.6986	3266.7653	4	3266.6466	0.1187	0	15	41	K.RPAITNAYCLLN LGDSITTDHISF AGNINR.K	Carbamidomethyl (C)
Chp EC50	6523	66825303	XP_646006	DDB0191502	Annexin VII	nxaA	P24639	49395/7.75	55270/8.04	4 (3)	3 (3)	11%	749.8410	1497.6675	2	1497.8191	-0.1516	0	53	45	R.SLPHIAAVASEYIK.H	
													912.3581	1822.7017	2	1822.8949	-0.1931	1	21	41	K.DLIQDIKSETSGNFEK.C	
													608.5823	1822.7250	3	1822.8949	-0.1698	1	54	43	K.DLIQDIKSETSGNFEK.C	
													635.8985	1904.6737	3	1904.8687	-0.1950	1	48	43	K.NSLAHDIQADCSGDFKK.L	Carbamidomethyl (C)

Supplemental table 1 - Details about identified proteins

Treatment	Spot n°	ID by www.ncbi.nlm.nih.gov		ID by www.dictybase.org			UniPROT ID	MW(Da)/pI expected	MW(Da)/pI observed	n° matches	n° sequences	% coverage	mass					peptide				
		gi	accession number	DDB	protein ID	gene name							observed	Mr(expt)	charge	Mr(calc)	delta	miss	score	ion score (identity)	sequence	modifications
Chp EC50	7323	66811048	XP_639231	DDB0231355	Phosphopyruvate hydratase	enoA	Q54RK5	46961/5.67	41590/8.59	36 (14)	28 (15)	70%	368.7250	735.4354	2	735.3915	0.0439	0	43	41	K.LGDLYR.E	
													374.2473	746.4801	2	746.4326	0.0475	0	16	41	R.NLPLYK.Y	
													396.7436	791.4726	2	791.4290	0.0436	0	38	41	K.YNQLVR.I	
													397.2336	792.4527	2	792.4130	0.0397	0	46	45	K.YNQLVR.I	Deamidated (NQ)
													401.2629	800.5113	2	800.4643	0.0469	0	59	45	K.EGLELLK.L	
													404.7533	807.4920	2	807.4491	0.0429	0	41	41	K.AGYTGLVK.I	
													451.7827	901.5508	2	901.5055	0.0453	0	41	41	K.ACNALLLK.V	Carbamidomethyl (C)
													457.7265	913.4385	2	913.3930	0.0455	0	39	41	K.DFNEAYR.M	
													480.2905	958.5665	2	958.5195	0.0469	1	32	40	K.AREILNSR.G	Deamidated (NQ)
													491.2859	980.5572	2	980.5178	0.0394	0	52	47	K.YISEIAGTK.M	
													515.8311	1029.6476	2	1029.6004	0.0471	1	20	40	K.KACNALLLK.V	Carbamidomethyl (C)
													552.8542	1103.6938	2	1103.6451	0.0487	1	20	40	R.LAKYNQLVR.I	
													597.3026	1192.5907	2	1192.5546	0.0360	0	18	40	R.MGSEVYHNLK.N	Oxidation (M)
													597.8396	1193.6647	2	1193.5387	0.1261	0	17	41	R.MGSEVYHNLK.N	Deamidated (NQ); Oxidation (M)
													622.3275	1242.6404	2	1242.5928	0.0476	0	57	41	K.NASWGVMSHR.S	
													622.7889	1243.5633	2	1243.5213	0.0420	0	29	42	K.IGMDCAASEFK.V	Carbamidomethyl (C); Oxidation (M)
													630.7966	1259.5786	2	1259.5717	0.0069	0	65	47	K.NASWGVMSHR.S	Deamidated (NQ); Oxidation (M)
													644.8752	1287.7359	2	1287.6935	0.0424	1	45	43	R.AGAADRNLPLYK.Y	
													651.8769	1301.7393	2	1301.6939	0.0454	0	66	45	K.VNQIGSVTESIR.A	
													697.4453	1392.8760	2	1392.8340	0.0420	0	22	41	K.NILEVIQPAVIGK.S	
													697.9412	1393.8679	2	1393.8180	0.0498	0	14	40	K.NILEVIQPAVIGK.S	Deamidated (NQ)
													732.8922	1463.7698	2	1463.7144	0.0554	0	16	40	R.GNPTVEVDLYTEK.D	
													774.4366	1546.8586	2	1546.8251	0.0335	0	47	43	K.LAMQEFMILPVGAK.D	
													782.9533	1563.8921	2	1563.8040	0.0880	0	18	40	K.LAMQEFMILPVGAK.D	Deamidated (NQ); Oxidation (M)
													790.4393	1578.8641	2	1578.8150	0.0492	0	18	40	K.LAMQEFMILPVGAK.D	2 Oxidation (M)
													569.3834	1705.1284	3	1705.0502	0.0783	1	22	40	K.AIKNILEVIQPAVIGK.S	
													895.9913	1789.9681	2	1789.9210	0.0471	0	49	45	R.AAVPSGASTGIYEAVELR.D	
													598.3424	1792.0055	3	1791.9268	0.0787	0	32	41	R.LPVPFAFNVINGGSHAGNK.L	Deamidated (NQ)
													636.6837	1907.0292	3	1906.9384	0.0908	1	63	45	K.NNDGSAVISGEKLGDLYR.E	
													659.6878	1976.0417	3	1975.9388	0.1029	0	51	43	R.INEELGENHNYAGLTFR.K	
													694.0651	2079.1736	3	2079.0684	0.1052	1	17	41	K.MRLPVPFAFNVINGGSHAGNK.L	Deamidated (NQ)
													699.3929	2095.1568	3	2095.0633	0.0935	1	26	40	K.MRLPVPFAFNVINGGSHAGNK.L	Deamidated (NQ); Oxidation (M)

Supplemental table 1 - Details about identified proteins

													1134.6304	2267.2463	2	2267.2009	0.0454	0	13	40	K.LTASVDIQIVGDDLLVTNPER.I	
													759.7305	2276.1696	3	2276.0709	0.0986	0	17	41	R.YGQDAINVGDEGGFAPPIQSNK.E	
													771.4168	2311.2286	3	2311.1332	0.0954	1	42	42	R.GNPTVEVDLYTEKDGVVSSFR.A	
													1036.5187	3106.5344	3	3106.4335	0.1009	1	7	40	R.EFIKEYPIISIEDPFDQDDWESYT K.L	
Chp EC50	8432	66817212	XP_642484	DDB0231241	60S ribosomal protein L4	rpl4	Q54Z69	40221/11.58	40190/9.16	7 (6)	7 (6)	35%	627.8361	1253.6576	2	1253.6728	-0.0152	0	54	42	R.NIPGVEVANVSR.L	
													657.8615	1313.7084	2	1313.6939	0.0145	0	67	42	R.LVNSDEIQAAVR.A	
													824.9019	1647.7893	2	1647.7781	0.0112	0	75	41	K.SAFEQLDSTFGTFAK.S	
													930.5027	1858.9909	2	1859.0339	-0.0430	0	73	44	R.YAVVSALAASAVPALVMARG	
													1129.5262	2257.0378	2	2257.0036	0.0342	0	62	41	R.QAYGAAPYAGEQTSAESWGT GR.A	
													654.6408	2614.5339	4	2614.4595	0.0744	0	49	43	K.LPNVLTTPIRPDLVNFVHTNL NK.N	
													711.4062	2841.5955	4	2841.6229	-0.0274	1	41	44	K.VKLPNVLTTPIRPDLVNFVHTNL NK.N	
													556.2793	1110.5257	2	1110.5413	-0.0156	1	45	41	K.KMLCSSQGLK.Y	Deamidated (NQ); Oxidation (M)
Mix EC25	0510	66806459	XP_636952	DDB0187751	Hypothetical protein DDBDRAFT_0187751	DDB_G0288041	Q54JH9	336221/5.39	65810/4.81	5 (4)	5 (4)	3%	623.7254	1245.4859	2	1245.5601	-0.0742	0	66	47	R.NGYTFSCWIR.T	
													979.0832	1956.1502	2	1956.1660	-0.0158	1	58	45	K.SINGIDKLFQLLLILEK.K	
													769.0325	2304.0759	3	2304.1110	-0.0351	1	29	41	K.FAFSECGSWNHVVLTHSKQK.I	
													792.7501	2375.2302	3	2375.2525	-0.0223	1	61	45	K.ITLYVNGKFIQNYSTLNYPK.S	
Mix EC25	1114	66818919	XP_643119	DDB0229442	Pyruvate dehydrogenase E1 beta subunit	pdhB	Q86HX0	39043/5.69	31550/5.42	3 (3)	3 (3)	16%	782.9008	1563.7870	2	1563.7636	0.0234	0	60	45	R.IVSNCEAAEILAK.E	Carbamidomethyl (C); Oxidation (M)
													596.9767	1787.9082	3	1787.8537	0.0545	1	52	47	R.DAINSALDEELARDEK.V	
													952.1539	2853.4399	3	2853.3657	0.0742	0	59	45	R.GPNGPPTAVGAQHSQCFAAW YGSVPGLK.V	Carbamidomethyl (C)
Mix EC25	1119	60464861	EAL62977	DDB0237965	Putative delta-24-sterol methyltransferase	smt1	Q54I98	39819/6.16	38150/5.20	12 (8)	9 (7)	37%	545.7840	1089.5535	2	1089.6434	-0.0899	0	61	45	K.FTQLLEIVK.L	
													546.2775	1090.5405	2	1090.6274	-0.0869	0	38	41	K.FTQLLEIVK.L	Deamidated (NQ)
													700.7983	1399.5820	2	1399.6983	-0.1163	0	60	45	K.FNPEDPVEVNIK.K	
													479.8728	1436.5965	3	1436.7048	-0.1083	1	57	45	R.HKYESFEASIAR.H	
													646.5804	1936.7195	3	1936.8634	-0.1439	0	41	43	R.HEMYMAHQLGLFPGMK.V	3 Oxidation (M)
													1011.9108	2021.8071	2	2021.9919	-0.1848	0	67	45	R.FSGANVVGLNNNEYQIQR.G	
													675.9742	2024.9008	3	2025.0394	-0.1386	0	47	45	R.IVKPGGLEGGYEWIMTNK.F	Oxidation (M)
													1144.0534	2286.0922	2	2286.2471	-0.1548	0	28	40	K.QIELGNGLPDLVKPAEIINAAK.A	Deamidated (NQ); Gln->pyro-Glu (N-termQ)
													768.3878	2302.1417	3	2302.2896	-0.1479	0	58	47	K.QIELGNGLPDLVKPAEIINAA K.A	
													768.7235	2303.1488	3	2303.2736	-0.1248	0	50	45	K.QIELGNGLPDLVKPAEIINAA K.A	Deamidated (NQ)
													811.4068	2431.1986	3	2431.3686	-0.1699	1	48	45	K.KQIELGNGLPDLVKPAEIINA AK.A	Deamidated (NQ)
													917.0855	2748.2346	3	2748.3871	-0.1525	0	39	42	K.LAPAGSYNTNVWLQNAATFLV QGGEK.Q	
Mix EC25	2722	66818048	XP_642717	DDB0185029	Clathrin heavy chain	chcA	P25870	193477/5.45	96480/5.70	2 (2)	2 (2)	1%	555.8417	1109.6688	2	1109.6597	0.0091	0	74	47	K.LLLPWLEAR.V	
													657.3579	1312.7012	2	1312.6775	0.0237	0	60	45	K.VLYTNISNFSR.L	

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		gi	accession number	DDB	protein ID	gene name							observed	Mr(expt)	charge	Mr(calc)	delta	miss	score	ion score (identity)	sequence	modifications
Mix EC25	2803	134047850	P08799	DDB0191444	Myosin II heavy chain	mhcA	P08799	244124/5.47	99350/5.70	6 (5)	6 (5)	5%	542.2899	1623.8660	3	1623.8508	0.0152	1	27	43	R.IIQQNLRAYIDFK.S	3 Deamidated (NQ)
													576.9783	1727.9339	3	1727.9305	0.0034	2	59	45	K.LELEAEQKAKQALEK.K	Deamidated (NQ)
													674.8245	1347.6480	2	1347.6379	0.0101	1	61	47	K.RVNDGQSDTISR.L	Deamidated (NQ)
													697.3540	2089.0601	3	2089.0174	0.0427	1	46	45	K.TAESALESLKDEIDAANNAK.A	
													848.7500	2543.2448	3	2543.1445	0.1003	2	53	45	K.YEEEELEEMKRVNDGQSDTISR.L	Oxidation (M)
													959.5402	1917.0783	2	1917.0207	0.0576	0	57	45	K.TALNAASTVFGVNPSVLEK.A	
Mix EC25	3110	38637654	DAA01127	DDB0215363	Aldehyde reductase	alrA	Q6IMN8	33855/5.95	29940/6.39	15 (9)	14 (9)	55%	863.9285	1725.9057	2	1725.9565	-0.0508	1	51	45	K.LSSGHKIPLVGFGTWK.A	
													559.2486	1116.5296	2	1116.6331	-0.1035	0	56	45	K.IPLVGFGTWK.A	
													959.0392	1916.0586	2	1916.0770	-0.0184	1	63	47	K.IPLVGFGTWKAETTLVGK.A	
													716.8569	1431.7316	2	1431.6816	0.0500	0	27	41	R.HIDCAAVYLNEK.E	
													765.3931	2293.1704	3	2293.1048	0.0656	1	39	43	R.HIDCAAVYLNEKEVGAEFTK.K	
													986.5225	1971.0705	2	1971.0312	0.0393	2	41	43	K.FTTEATVKREDVFITSK.L	
													674.3374	2019.9823	3	2020.0530	-0.0707	2	58	47	K.REDFVITSKLWNTFHK.K	
													997.0221	1992.0442	2	1992.0468	-0.0026	2	64	47	R.EDVFITSKLWNTFHKK.E	
													938.9679	1875.9358	2	1875.9287	0.0071	1	45	45	R.ETWEEMEKLVDAGLVK.S	
													733.3836	2197.1507	3	2197.1200	0.0307	0	42	45	K.SIGLSNFNVQGLMEVLSYAR.I	
													738.7093	2213.1279	3	2213.1149	0.0130	0	25	40	K.SIGLSNFNVQGLMEVLSYAR.I	Oxidation (M)
													753.7359	2258.2792	3	2258.2422	0.0370	0	57	45	R.IKPAANQVELHPFLSQPELK.K	
													796.4263	2386.2998	3	2386.3372	-0.0374	1	41	47	R.IKPAANQVELHPFLSQPELKK.F	
													715.8422	1429.7568	2	1429.8081	-0.0513	1	64	47	K.WAIQKNFSVIPK.S	
													826.3505	1650.7381	2	1650.7864	-0.0483	1	66	46	R.TCDPAKFWGVPLFN.-	

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Treatment	Spot n°	ID by www.ncbi.nlm.nih.gov		ID by www.dictybase.org			UniPROT ID	MW(Da)/pI expected	MW(Da)/pI observed	n° matches	n° sequences	% coverage	mass					peptide				
		gi	accession number	DDB	protein ID	gene name							observed	Mr(expt)	charge	Mr(calc)	delta	miss	score	ion score (identity)	sequence	modifications
Mix EC25	3414	66818493	XP_642906	DDB0231504	Aldehyde dehydrogenase	DDB_G0276821	P83401	55155/5.78	60720/6.34	15 (9)	15 (9)	38%	453.7508	905.4870	2	905.4892	-0.0022	0	51	45	K.LISLEMGK.I	Oxidation (M)
													456.2619	910.5093	2	910.5025	0.0069	0	46	45	K.WALTPAPR.R	
													465.7537	929.4928	2	929.4970	-0.0043	0	31	43	K.WGGAGEIHK.C	
													472.2840	942.5534	2	942.5386	0.0149	1	27	40	R.EKIEPLSK.L	
													597.8039	1193.5932	2	1193.5815	0.0116	0	24	40	K.EFTEGLEEIK.K	
													653.8682	1305.7218	2	1305.7040	0.0178	0	47	45	R.AVLFASVGTGQR.C	
													661.8575	1321.7005	2	1321.6765	0.0240	1	58	45	K.EFTEGLEEIKK.Q	
													674.8000	1347.5854	2	1347.7609	-0.1755	0	83	47	K.GASTTSLITLAVSK.I	
													735.9037	1469.7928	2	1469.7514	0.0414	0	55	47	R.FGLISFTGSTEVGR.R	
													741.9390	1481.8634	2	1481.8203	0.0430	0	15	40	K.TELFVPILYIMK.F	Oxidation (M)
													578.9789	1733.9148	3	1733.8988	0.0160	0	38	40	R.LFVHESLYDTILER.L	
													1030.0197	2058.0249	2	2057.9364	0.0886	0	69	47	K.GEVQEFIDVCDYATGLSR.S	Carbamidomethyl (C)
													720.0905	2157.2497	3	2157.1793	0.0704	0	41	43	K.IGNPLEEGVLVGPLHTQSAVK.E	
													840.8042	2519.3909	3	2519.3271	0.0638	0	47	43	K.LDISGGNFVEPTVVAIEHDAPIVK.T	
													846.4895	2536.4468	3	2536.3747	0.0720	0	45	43	K.TILELGGNNAIVVAEDADIELVLR.A	
Mix EC25	3416	22711882	AAG34561	DDB0191349	Phosphoglycerate kinase	pgkA	Q9GPM4	45681/6.01	56650/6.53	9 (6)	9 (6)	31%	669.9366	1337.8592	2	1337.8030	0.0562	1	38	43	K.VLEDQLKRPIK.F	
													691.3804	1380.7404	2	1380.7183	0.0221	0	52	45	R.AHSSMVGINLPQK.A	
													739.4193	1476.8438	2	1476.7435	0.1003	0	57	45	K.TIVWNGPMGVFEK.S	
													761.9612	1521.8524	2	1521.7748	0.0776	0	63	47	R.IDASIPTLEYCLK.N	
													802.4385	1602.8174	2	1602.7161	0.1013	0	66	45	R.FHIEEESGVD AEGK.K	
													813.9641	1625.9242	2	1625.8300	0.0942	1	26	41	K.FIDNKEIGSSLFEK.T	
													817.9525	1633.8705	2	1633.7848	0.0857	0	54	47	K.LGDVYVND AFGTAHR.A	
													850.0125	1698.0041	2	1697.9715	0.0326	0	45	47	K.ALESPSKPFLAILGGAK.V	
													778.7567	2333.2247	3	2333.1691	0.0556	1	62	47	K.LHFPVDYVIADKFDNDANIK.T	

Supplemental table 1 - Details about identified proteins

Treatment	Spot n°	ID by www.ncbi.nlm.nih.gov		ID by www.dictybase.org			UniPROT ID	MW(Da)/pI expected	MW(Da)/pI observed	n° matches	n° sequences	% coverage	mass					peptide				
		gi	accession number	DDB	protein ID	gene name							observed	Mr(expt)	charge	Mr(calc)	delta	miss	score	ion score (identity)	sequence	modifications
Mix EC25	4613	66808101	XP_637773	DDB0234127	Glucosamine-6-phosphate isomerase	nagB1	Q54M58	82645/6.14	85390/6.67	20 (9)	18 (7)	28%	421.7713	841.5280	2	841.4810	0.0470	0	38	42	K.WSPLLAR.K	
													429.7782	857.5419	2	857.4970	0.0448	0	64	47	K.AILSAIDRL	
													550.3665	1098.7184	2	1098.6761	0.0423	1	44	45	K.AILSAIDRLK.T	
													554.8281	1107.6417	2	1107.5998	0.0419	0	49	45	R.IILMAFSEGK.A	
													562.8297	1123.6448	2	1123.5947	0.0501	0	47	45	R.IILMAFSEGK.A	Oxidation (M)
													574.2959	1146.5772	2	1146.5346	0.0426	0	41	41	R.FANFASEFSK.L	
													625.8431	1249.6717	2	1249.6302	0.0415	0	59	47	K.LFSLGNESVER.S	
													669.3668	1336.7190	2	1336.6623	0.0567	0	38	40	R.IGFNESGSLANTK.T	
													448.9309	1343.7708	3	1343.7157	0.0551	1	32	40	K.TRLVDLEQNTR.I	
													498.6129	1492.8169	3	1492.7634	0.0535	1	35	40	K.RIGFNESGSLANTK.T	
													512.6297	1534.8671	3	1534.7991	0.0681	1	31	41	R.SNTIEKNVNEFIK.T	
													584.0025	1748.9856	3	1748.9138	0.0719	0	66	45	R.IHFLDLPFYETGAVK.K	
													600.6746	1799.0018	3	1798.9175	0.0844	1	26	41	R.YMQENLFELIDIKK.E	Oxidation (M)
													931.0079	1860.0012	2	1859.9629	0.0383	0	49	43	K.TTEGEITPAIPSTIFQR.H	
													623.3822	1867.1249	3	1867.0601	0.0648	1	49	45	K.IEQVGGIDLMLPIGKR.I	Oxidation (M)
													936.4863	1870.9581	2	1870.9101	0.0480	0	20	41	K.NVITFNVDEYYPIER.N	
													678.0036	2030.9889	3	2030.9255	0.0634	1	16	41	K.INSETGLFECNEEFKSK.E	Carbamidomethyl (C)
													768.0826	2301.2260	3	2301.1464	0.0796	0	37	41	R.VIVFSPHPDDDVISMGGTFIR.L	
													773.4118	2317.2135	3	2317.1413	0.0722	0	54	47	R.VIVFSPHPDDDVISMGGTFIR.L	Oxidation (M)
													645.6165	2578.4370	4	2578.3220	0.1150	1	17	40	R.YAGVAPDRIHFLDLPFYETGAVK.K	
Mix EC25	4615	166240434	XP_640392	DDB0235163	Putative transport protein	sec23	Q54T59	84646/6.07	83890/6.63	4 (3)	4 (3)	10%	723.8612	1445.7199	2	1445.7297	-0.0098	1	63	47	K.VGSPETMNLQSKR.F	
													912.9215	1823.8025	2	1823.8360	-0.0335	0	54	47	K.TSCVGENEIGIGGTSSWK.V	
													753.3508	2257.0246	3	2257.0831	-0.0585	0	37	43	R.ATGMAFSVANALLSTVASNMGGR.I	2 Oxidation (M)
													655.7254	2619.1397	4	2619.2138	-0.0741	0	58	45	K.LTGGYMLVLA DSFDHPMFTQS FQK.I	

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Treatment	Spot n°	ID by www.ncbi.nlm.nih.gov		ID by www.dictybase.org			UniPROT ID	MW(Da)/pI expected	MW(Da)/pI observed	n° matches	n° sequences	% coverage	mass					peptide				
		gi	accession number	DDB	protein ID	gene name							observed	Mr(expt)	charge	Mr(calc)	delta	miss	score	ion score (identity)	sequence	modifications
Mix EC25	5208	60462281	EAL60507	DDB0231294	Isocitrate dehydrogenase (NAD ⁺)	idhB	Q54B68	38891/8.48	38830/7.67	16 (8)	14 (7)	44%	428.2565	854.4985	2	854.4974	0.0011	0	33	41	K.QIPGITAR.H	
													446.2133	890.4120	2	890.4174	-0.0054	0	46	43	R.YAFEYAK.A	
													539.2787	1076.5428	2	1076.5349	0.0079	0	50	45	K.EGTLTSDIGGK.S	
													560.2995	1118.5844	2	1118.5832	0.0012	0	25	41	K.HLGLNEHATK.V	
													683.8610	1365.7074	2	1365.6816	0.0258	0	28	41	K.QFTGAVIDYIEK.N	Gln->pyro-Glu (N-termQ)
													692.3767	1382.7389	2	1382.7081	0.0308	0	51	45	K.QFTGAVIDYIEK.N	
													693.3800	1384.7454	2	1384.7173	0.0282	0	30	41	K.ALDLYAHVVPCK.Q	Carbamidomethyl (C)
													476.2625	1425.7658	3	1425.7616	0.0042	0	54	47	R.HDDVLVDFVVIR.E	
													713.8991	1425.7836	2	1425.7616	0.0221	0	59	47	R.HDDVLVDFVVIR.E	
													744.9210	1487.8274	2	1487.8195	0.0080	1	52	47	K.AVIKEGTLTSDIGGK.S	
													754.4057	1506.7969	2	1506.7678	0.0291	0	36	40	K.GPLYTEILSGSQSR.N	
													795.9400	1589.8654	2	1589.8520	0.0133	0	27	40	K.ANPTGLLLASVMMLK.H	2 Oxidation (M)
													612.0151	1833.0236	3	1832.9739	0.0496	1	25	40	K.DKANPTGLLLASVMMLK.H	2 Oxidation (M)
													640.3706	1918.0900	3	1918.0523	0.0377	1	53	45	K.VALKGPLYTEILSGSQSR.N	
													826.1040	2475.2902	3	2475.2492	0.0410	0	47	45	R.ENTQGEYSGLEQVLTPGVVQSLK.I	
Mix EC25	5307	60463691	EAL61873	DDB0230070	S-adenosyl-methionine synthetase	metK	Q54F07	42079/6.14	46310/7.10	8 (5)	6 (4)	19%	864.1626	2589.4659	3	2589.3359	0.1300	0	39	41	K.TVTVIPGDGIGPEITSSVMGVFQAAK.V	Oxidation (M)
													486.7229	971.4313	2	971.5399	-0.1086	0	57	45	K.SLVAAGLADR.C	
													676.2448	1350.4751	2	1350.6092	-0.1341	0	46	45	R.NDPDFTWETVK.E	
													679.8260	1357.6375	2	1357.7718	-0.1343	0	39	41	R.DLQLTRPIFQK.T	
													697.3111	1392.6077	2	1392.7356	-0.1279	0	55	47	K.TGMVMILGEITTK.A	
													713.2997	1424.5849	2	1424.7254	-0.1405	0	58	47	K.TGMVMILGEITTK.A	2 Oxidation (M)
													740.2956	1478.5767	2	1478.7187	-0.1420	0	49	47	R.FVIGGPMGDSGLTGR.K	Oxidation (M)
Mix EC25	5415	66813238	XP_640798	DDB0230052	3-phosphoglycerate dehydrogenase	serA	Q54UH8	44720/6.61	54160/7.30	2 (2)	2 (2)	8%	498.8474	1493.5203	3	1493.6674	-0.1471	1	29	40	K.IGYDDSSKGFQDYK.T	
													747.7755	1493.5365	2	1493.6674	-0.1309	1	22	40	K.IGYDDSSKGFQDYK.T	
Mix EC25	6016	60468343	EAL66350	DDB0215335	Actin binding protein	hatA	P13231	13505/6.89	15860/8.06	5 (3)	3 (2)	25%	858.9617	1715.9089	2	1715.9491	-0.0402	0	67	45	R.SVAELIICEIITLSR.K	Carbamidomethyl (C)
													1060.5388	2119.0631	2	2119.0909	-0.0278	0	61	47	R.DINNILSEFNVSAQVLSTR.K	
													772.3401	1542.6657	2	1542.7361	-0.0704	0	52	45	R.NSAIWASGTMGHGVR.G	
													520.5611	1558.6614	3	1558.7311	-0.0697	0	63	45	R.NSAIWASGTMGHGVR.G	Oxidation (M)
													780.3459	1558.6772	2	1558.7311	-0.0538	0	21	41	R.NSAIWASGTMGHGVR.G	Oxidation (M)
Mix EC25	6016	60468343	EAL66350	DDB0215335	Actin binding protein	hatA	P13231	13505/6.89	15860/8.06	5 (3)	3 (2)	25%	878.3686	1754.7226	2	1754.8145	-0.0919	0	44	41	R.LSMQEDGNLVIYDSR.N	Oxidation (M)
													953.9711	1905.9276	2	1906.0234	-0.0957	0	13	40	K.LIMQNDGNLVLYIGSLK.S	Oxidation (M)

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Treatment	Spot n°	ID by www.ncbi.nlm.nih.gov		ID by www.dictybase.org			UniPROT ID	MW(Da)/pI expected	MW(Da)/pI observed	n° matches	n° sequences	% coverage	mass					peptide				
		gi	accession number	DDB	protein ID	gene name							observed	Mr(expt)	charge	Mr(calc)	delta	miss	score	ion score (identity)	sequence	modifications
Mix EC25	6210	66820452	XP_643839	DDB0185122	G beta like protein	gpbB	P46800	36208/7.64	32900/7.91	4 (3)	4 (3)	15%	557.8021	1113.5896	2	1113.6798	-0.0902	0	58	45	K.IIIWDL LTK.Q	
													612.7880	1223.5615	2	1223.7125	-0.1510	0	56	47	K.QVLA EIVPEVK.E	
													817.8252	1633.6358	2	1633.8134	-0.1776	1	27	41	R.DATIKVWNTLGECK.F	Carbamidomethyl (C)
													659.6268	1975.8585	3	1976.0004	-0.1419	1	63	45	R.FSPNTPTIVSGSWDNKVK.I	
Mix EC25	6607	66805581	XP_636512	DDB0191139	Cyclase associated protein	cap	P54654	49611/6.97	73600/7.70	9 (7)	9 (7)	42%	562.8284	1123.6460	2	1123.5873	0.0587	1	54	47	K.NFTDKSSVVK.A	
													604.3306	1206.6612	2	1206.5979	0.0633	0	57	47	K.DSLETEIVSSK.S	
													680.4076	1358.8121	2	1358.7558	0.0563	1	49	45	K.KGPGLGAVFGELSK.G	
													830.4659	1658.9318	2	1658.8839	0.0479	1	62	45	K.AIDAEKALINTASQSK.K	
													660.7084	1979.1252	3	1979.0397	0.0855	1	37	41	R.VPSIAIDKTSGCQIYLSK.D	Carbamidomethyl (C)
													696.0456	2085.1320	3	2085.0895	0.0425	0	42	45	K.EFQNLVDQHITPFVALSK.K	
													782.3905	2344.1600	3	2344.1468	0.0132	1	49	43	K.TSGCQIYLSKDSLETEIVSSK.S	Carbamidomethyl (C)
													816.7704	2447.3084	3	2447.2544	0.0540	0	63	43	K.SATPAPASSAPAAPVAPAVSSTPVESK.K	
													870.7896	2609.3542	3	2609.2762	0.0780	1	61	47	K.GVNQDQVDWVSNYVNFLK DLEK.Y	
													844.4332	1686.8519	2	1686.9127	-0.0609	0	57	47	K.VIIGPATVGGIQAGCFK.I	Carbamidomethyl(C)
Mix EC25	6608	66816585	XP_642302	DDB0235360	ATP citrate synthase	acly	Q54YA0	67278/6.94	75850/7.69	4 (3)	4 (3)	14%	628.3510	1882.0312	3	1882.0888	-0.0575	1	79	47	R.AGKDLVSSLVSGLLTIGPR.F	
													1194.0733	2386.1321	2	2386.1692	-0.0372	0	48	45	R.EAGAVVPTSFEDFSNVIAATYAK.L	
													1114.2280	3339.6622	3	3339.7674	-0.1052	1	33	43	R.SAYQSSLLALREPSIQTVVIIAEGVPENEAR.S	

Treatment	Spot n°	ID by www.ncbi.nlm.nih.gov		ID by www.dictybase.org			UniPROT ID	MW(Da)/pI expected	MW(Da)/pI observed	n° matches	n° sequences	% coverage	mass					peptide				
		gi	accession number	DDB	protein ID	gene name							observed	Mr(expt)	charge	Mr(calc)	delta	miss	score	ion score (identity)	sequence	modifications
Mix EC25	6612	60470010	EAL67991	DDB0230168	Aconitase, mitochondrial	aco2	Q54XS2	83889/8.19	83600/7.93	37 (18)	32 (16)	42%	372.2567	742.4988	2	742.4953	0.0035	0	54	47	R.ISIIGLK.D	
													407.7711	813.5277	2	813.5324	-0.0047	0	33	43	K.QLTLIVK.S	
													429.7750	857.5354	2	857.5222	0.0132	0	58	45	R.VADILTVK.G	
													468.7641	935.5137	2	935.5076	0.0061	0	23	41	K.AGSALNYIK.S	
													511.7642	1021.5139	2	1021.5080	0.0059	0	16	41	K.LNYEGIDAK.L	
													536.7778	1071.5411	2	1071.5349	0.0063	0	51	45	K.TNNWPAELK.V	
													568.7884	1135.5623	2	1135.5621	0.0002	0	59	45	R.SNIANAANSFK.H	
													624.8337	1247.6528	2	1247.6510	0.0018	0	30	40	K.FTITPGSEQIR.A	
													630.3150	1258.6155	2	1258.6081	0.0073	0	18	40	K.EVYDFLSTSAK.K	
													427.5653	1279.6740	3	1279.6772	-0.0032	1	54	45	K.AGSALNYIKSEK.A	
													641.8465	1281.6784	2	1281.6565	0.0219	0	68	47	K.LTPPTGDELP SR.G	
													438.2541	1311.7405	3	1311.7299	0.0106	1	36	45	R.GITYLKLHPDR.V	
													442.2779	1323.8119	3	1323.8126	-0.0006	1	45	47	R.ISIIGLKDLAPGK.Q	
													458.2476	1371.7210	3	1371.7034	0.0176	0	59	47	K.IYGHLEDPSTK.V	
													462.9414	1385.8025	3	1385.7878	0.0147	1	19	40	K.ISGDDRISIIGLK.D	
													465.9617	1394.8633	3	1394.8497	0.0136	1	22	40	K.DLAPGKQLTLIVK.S	
													483.2695	1446.7868	3	1446.7831	0.0037	1	58	47	K.AKFTITPGSEQIR.A	
													528.6384	1582.8933	3	1582.8871	0.0061	1	56	45	R.LQLLQPFAPWDKK.D	
													529.9665	1586.8777	3	1586.8628	0.0149	1	61	45	R.SASVAQQALDKGITAK.A	
													534.6444	1600.9112	3	1600.8858	0.0254	1	23	40	K.DLVDMQVLIKVGQK.C	Oxidation (M)
													539.5891	1615.7456	3	1615.7487	-0.0031	0	28	40	K.CTTDHISMAGPWLK.Y	Carbamidomethyl (C)
													544.9247	1631.7524	3	1631.7436	0.0088	0	33	40	K.CTTDHISMAGPWLK.Y	Carbamidomethyl (C); Oxidation (M)
													549.6020	1645.7841	3	1645.7671	0.0171	0	61	47	K.ANHTMNAGQIEWFK.A	
													554.9293	1661.7659	3	1661.7620	0.0039	0	35	40	K.ANHTMNAGQIEWFK.A	Oxidation (M)
													578.6338	1732.8796	3	1732.8784	0.0012	1	21	40	K.FAESVKTNNWP AELK.V	
													586.3204	1755.9395	3	1755.9155	0.0239	1	60	47	K.IYGHLEDPSTKVER.G	
													439.9969	1755.9584	4	1755.9155	0.0429	1	62	47	K.IYGHLEDPSTKVER.G	
													889.9461	1777.8776	2	1777.8887	-0.0110	0	25	39	K.QGILPLTFANPSDYDK.I	
													943.4673	1884.9200	2	1884.9339	-0.0139	0	28	39	K.VGGVVLANACGPCIGQWK.R	2 Carbamidomethyl (C)
													946.4134	1890.8121	2	1890.8088	0.0034	0	26	39	K.VGLIGSCTNSSYEDMSR.S	Carbamidomethyl (C); Oxidation (M)
969.4456	1936.8767	2	1936.8915	-0.0148	0	49	45	R.GVNWIVVGDENYEGSSR.E														
681.3589	2041.0548	3	2041.0350	0.0198	1	58	45	K.VGGVVLANACGPCIGQWKR.E	2 Carbamidomethyl (C)													

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																		1027.5486	2053.0826	2	2053.0956	-0.0130	0	35	41	K.ANAVLNQFTGEIGPVPTVAR.D	
																		685.7026	2054.0861	3	2054.0797	0.0064	0	23	40	K.ANAVLNQFTGEIGPVPTVAR.D	Deamidated (NQ)
																		738.0320	2211.0741	3	2211.0589	0.0151	0	46	41	R.GHLDNISNNMLIGAINSENGK.A	Deamidated (NQ)
																		743.3635	2227.0688	3	2227.0539	0.0150	0	20	40	R.GHLDNISNNMLIGAINSENGK.A	Deamidated (NQ); Oxidation (M)
																		808.0706	2421.1901	3	2421.1812	0.0089	1	62	47	K.QGILPLTFANPSDYDKISGDD R.I	