Supplementary Table 2: MIAPE-MS Data for Identified Proteins

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Neurofilament medium polypeptide	spt|P12839	11	98	100	31	95.97	18	19.54	21.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
858.4791	858.4767	-0.0024	-3	16	22	RVPTETR			
909.4312	909.4222	-0.009	-10	314	320	EEIAEYR			
980.4795	980.474	-0.0055	-6	28	37	VSGSPSSGFR			
1072.5382	1072.5387	0.0005	0	102	110	EQLQGLNDR			
1072.5382	1072.5387	0.0005	0	102	110	EQLQGLNDR			
1159.6066	1159.6035	-0.0031	-3	194	203	LRDDTEAAIR	16	0	
1159.6066	1159.6035	-0.0031	-3	194	203	LRDDTEAAIR			
1180.6321	1180.6343	0.0022	2	127	136	EIEAEIHALR			
1180.6321	1180.6343	0.0022	2	127	136	EIEAEIHALR			
1281.6508	1281.6483	-0.0025	-2	391	401	MALDIEIAAYR			Oxidation (M)[1]
1281.6508	1281.6483	-0.0025	-2	391	401	MALDIEIAAYR			Oxidation (M)[1]
1404.7482	1404.7605	0.0123	9	223	234	VQSLQDEVAFLR	17	0	
1404.7482	1404.7605	0.0123	9	223	234	VQSLQDEVAFLR			
1530.7506	1530.7688	0.0182	12	98	110	SNEKEQLQGLNDR			
1585.8003	1585.7633	-0.037	-23	155	167	ELRATLEMVNHEK			Oxidation (M)[8]
1585.8003	1585.7633	-0.037	-23	155	167	ELRATLEMVNHEK			Oxidation (M)[8]
1770.881	1770.8979	0.0169	10	411	426	FSTFSGSITGPLYTHR			
1770.881	1770.8979	0.0169	10	411	426	FSTFSGSITGPLYTHR	13	0	
1801.8463	1801.861	0.0147	8	139	154	QASHAQLGDAYDQEIR			
1801.8463	1801.861	0.0147	8	139	154	QASHAQLGDAYDQEIR	35	92.524	
1904.9097	1904.922	0.0123	6	168	183	AQVQLDSDHLEEDIHR	35	92.35	
1904.9097	1904.922	0.0123	6	168	183	AQVQLDSDHLEEDIHR			
2440.1487	2440.1406	-0.0081	-3	351	370	HNHDLSSYQDTIQQLENELR			
2589.2903	2589.2759	-0.0144	-6	235	257	SNHEEEVADLLAQIQASHITVER			
2589.2903	2589.2759	-0.0144	-6	235	257	SNHEEEVADLLAQIQASHITVER			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Neurofilament triplet L protein	spt|P19527	15	174	100	73	100	25	46.848	22.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
801.4213	801.4008	-0.0205	-26	157	163	QALQGER			
801.4213	801.4008	-0.0205	-26	157	163	QALQGER			
869.4515	869.4414	-0.0101	-12	100	106	FASFIER	6	0	
869.4515	869.4414	-0.0101	-12	100	106	FASFIER			
920.4948	920.4838	-0.011	-12	16	22	RYVETPR			
1021.5312	1021.5305	-0.0007	-1	136	143	ALYEQEIR	24	28.465	
1021.5312	1021.5305	-0.0007	-1	136	143	ALYEQEIR			
1024.4945	1024.4996	0.0051	5	177	184	YEEEVLSR			
1024.4945	1024.4996	0.0051	5	177	184	YEEEVLSR	8	0	
1072.5382	1072.5426	0.0044	4	91	99	AQLQDLNDR			
1072.5382	1072.5426	0.0044	4	91	99	AQLQDLNDR	13	0	
1154.7144	1154.7183	0.0039	3	116	125	VLEAELLVLR			
1154.7144	1154.7183	0.0039	3	116	125	VLEAELLVLR	25	46.848	
1281.6508	1281.6486	-0.0022	-2	380	390	MALDIEIAAYR			Oxidation (M)[1]
1281.6508	1281.6486	-0.0022	-2	380	390	MALDIEIAAYR			Oxidation (M)[1]
1405.7434	1405.7041	-0.0393	-28	136	146	ALYEQEIRDLR			
1410.7185	1410.7251	0.0066	5	212	223	IDSLMDEIAFLK			Oxidation (M)[5]
1723.7955	1723.8022	0.0067	4	422	437	SAYSGLQSSSYLMSAR			Oxidation (M)[13]
1723.7955	1723.8022	0.0067	4	422	437	SAYSGLQSSSYLMSAR	8	0	Oxidation (M)[13]
1747.8497	1747.8656	0.0159	9	37	53	SAYSSYSAPVSSSLSVR			

1747.8497	1747.8656	0.0159	9	37	53	SAYSSYSAPVSSSLSVR	5	0	
1922.9719	1922.932	-0.0399	-21	91	106	AQLQDLNDRFASFIER			
2021.8304	2021.8333	0.0029	1	482	499	EKEEGEEEEGAEEEEAAK			
2295.1252	2295.126	0.0008	0	400	421	LSFTSVGSITSGYSQSSQVFGR			
2295.1252	2295.126	0.0008	0	400	421	LSFTSVGSITSGYSQSSQVFGR			

Protein Name	**Accession No.**	**Peptide Count**	**Protein Score**	**Protein Score C.I.%**	**Total Ion Score**	**Total Ion C.I. %**	**Best Ion Score**	**Best Ion C.I.%**	**% Coverage**
Dihydropyrimidase related protein-2 (DRP-2)	XP_341343.1	17	321	100	184	100	41	97.86	43.4

Peptide Information

Calc. Mass	**Obsrv. Mass**	**± da**	**± ppm**	**Start Seq.**	**End Seq.**	**Sequence**	**Ion Score**	**C. I. %**	**Modification**
813.4213	813.444	0.0227	28	57	63	TIEAHSR			
813.4213	813.444	0.0227	28	57	63	TIEAHSR			
844.4999	844.535	0.0351	42	486	492	SRLAELR			
844.4999	844.535	0.0351	42	486	492	SRLAELR			
908.4988	908.5211	0.0223	25	391	397	VFNLYPR	41	97.859	
908.4988	908.5211	0.0223	25	391	397	VFNLYPR			
1015.553	1015.5809	0.0279	27	259	268	SAAEVIAQAR			
1015.553	1015.5809	0.0279	27	259	268	SAAEVIAQAR	24	0	
1140.6088	1140.6323	0.0235	21	472	480	KPFPDFVYK			
1140.6088	1140.6323	0.0235	21	472	480	KPFPDFVYK	10	0	
1262.6296	1262.6587	0.0291	23	147	157	GIQEEMEALVK			Oxidation (M)[6]
1310.6885	1310.7094	0.0209	16	64	75	MVIPGGIDVHTR			Oxidation (M)[1]
1310.6885	1310.7094	0.0209	16	64	75	MVIPGGIDVHTR	14	0	Oxidation (M)[1]
1323.7631	1323.7733	0.0102	8	44	56	QIGENLIVPGGVK			
1682.8707	1682.8927	0.022	13	452	467	IVLEDGTLHVTEGSGR			
1682.8707	1682.8927	0.022	13	452	467	IVLEDGTLHVTEGSGR	27	36.518	
1741.8062	1741.8192	0.013	7	375	390	MDENQFVAVTSTNAAK			Oxidation (M)[1]
1792.8348	1792.8547	0.0199	11	346	361	DNFTLIPEGTNGTEER			
1792.8348	1792.8547	0.0199	11	346	361	DNFTLIPEGTNGTEER	27	44.837	
1822.9368	1822.9402	0.0034	2	239	254	SITIANQTNCPLYVTK			Carbamidomethyl (C)[10]
2169.0684	2169.0784	0.01	5	533	552	NLHQSGFSLSGAQIDDNIPR			
2169.0684	2169.0784	0.01	5	533	552	NLHQSGFSLSGAQIDDNI	25	16.891	
2182.9055	2182.9775	0.072	33	76	94	FQMPDQGMTSADDFFQGTK			Oxidation (M)[3,8]
2365.0903	2365.0908	0.0005	0	24	43	IVNDDQSFYADIYMEDGLIK			Oxidation (M)[14]
2377.1741	2377.1721	-0.002	-1	190	211	DIGAIAQVHAENGDIIAEEQQR	16	0	
2377.1741	2377.1721	-0.002	-1	190	211	DIGAIAQVHAENGDIIAEEQQR			
2900.5112	2900.4856	-0.0256	-9	212	238	ILDLGITGPEGHVLSRPEEVEAEAVNR			

Protein Name	**Accession No.**	**Peptide Count**	**Protein Score**	**Protein Score C.I.%**	**Total Ion Score**	**Total Ion C.I. %**	**Best Ion Score**	**Best Ion C.I.%**	**% Coverage**
Chaperonin 60	gb|AAC53362.1	13	145	100	61	99.982	45	99.356	

Peptide Information

Calc. Mass	**Obsrv. Mass**	**± da**	**± ppm**	**Start Seq.**	**End Seq.**	**Sequence**	**Ion Score**	**C. I. %**	**Modification**
833.39	833.3374	-0.0526	-63	302	309	APGFGDNR			
833.39	833.3374	-0.0526	-63	302	309	APGFGDNR			
855.4682	855.4188	-0.0494	-58	134	141	GANPVEIR			
855.4682	855.4188	-0.0494	-58	134	141	GANPVEIR			
960.5109	960.476	-0.0349	-36	421	429	VTDALNATR			
960.5109	960.476	-0.0349	-36	421	429	VTDALNATR	0	0	
961.4849	961.4625	-0.0224	-23	302	310	APGFGDNRK			
1520.7512	1520.7368	-0.0144	-9	206	218	TLNDELEIIEGMK			Oxidation (M)[12]
1520.7512	1520.7368	-0.0144	-9	206	218	TLNDELEIIEGMK			Oxidation (M)[12]
1601.7516	1601.7375	-0.0141	-9	237	249	CEFQDAYVLLSEK			Carbamidomethyl (C)[1]
1684.905	1684.9156	0.0106	6	430	446	AAVEEGIVLGGGCALLR	15	0	Carbamidomethyl (C)[13]
1684.905	1684.9156	0.0106	6	430	446	AAVEEGIVLGGGCALLR			Carbamidomethyl (C)[13]
1798.9004	1798.8853	-0.0151	-8	447	462	CIPALDSLKPANEDQK			Carbamidomethyl (C)[1]
1798.9004	1798.8853	-0.0151	-8	447	462	CIPALDSLKPANEDQK			Carbamidomethyl (C)[1]

1905.0552	1905.0682	0.013	7	251	268	ISSVQSIVPALEIANAHR	45	99.356	
1905.0552	1905.0682	0.013	7	251	268	ISSVQSIVPALEIANAHR			
1922.9528	1922.9332	-0.0196	-10	206	221	TLNDELEIIEGMKFDR			
1922.9528	1922.9332	-0.0196	-10	206	221	TLNDELEIIEGMKFDR			
2040.002	2039.9945	-0.0075	-4	371	387	IQEITEQLDITTSEYEK			
2040.002	2039.9945	-0.0075	-4	371	387	IQEITEQLDITTSEYEK			
2365.3337	2365.3264	-0.0073	-3	269	290	KPLVIIAEDVDGEALSTLVLNR			
2365.3337	2365.3264	-0.0073	-3	269	290	KPLVIIAEDVDGEALSTLVLNR			
2565.3955	2565.1934	-0.2021	-79	447	469	CIPALDSLKPANEDQKIGIEIIK			Carbamidomethyl (C)[1]
2565.3955	2565.1934	-0.2021	-79	447	469	CIPALDSLKPANEDQKIGIEIIK			Carbamidomethyl (C)[1]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
ATPase, H transporting, lysosomal V1 subu	gi|16758754	10	123	100	44	99.17	21	0	27.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
877.4526	877.4891	0.0365	42	38	44	NYLSQPR	9	0	
877.4526	877.4891	0.0365	42	38	44	NYLSQPR			
1189.6323	1189.6149	-0.0174	-15	131	141	VFNGSGKPIDR			
1338.6437	1338.6146	-0.0291	-22	461	471	NFITQGPYENR			
1338.6437	1338.6146	-0.0291	-22	461	471	NFITQGPYENR	21	0	
1437.7373	1437.698	-0.0393	-27	495	506	IPQSTLSEFYPR			
1437.7373	1437.698	-0.0393	-27	495	506	IPQSTLSEFYPR	14	0	
1520.7954	1520.7367	-0.0587	-39	94	108	AVVQVFEGTSGIDAK			
1593.8384	1593.7827	-0.0557	-35	494	506	RIPQSTLSEFYPR			
1596.9108	1596.8643	-0.0465	-29	387	400	QIYPPINVLPSLSR			
1596.9108	1596.8643	-0.0465	-29	387	400	QIYPPINVLPSLSR			
2048.0593	2048.0225	-0.0368	-18	8	29	GIVNGAAPELPVPTGGPMAGAR			Oxidation (M)[18]
2384.1221	2383.9829	-0.1392	-58	110	130	TSCEFTGDILRTPVSEDMLGR			Carbamidomethyl (C)[3]
2722.3538	2722.405	0.0512	19	164	188	IYPEEMIQTGISAIDGMNSIARGQK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Alpha enolase	spt|P04764	15	244	100	111	100	48	99.486	41.0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
800.3824	800.3577	-0.0247	-31	256	261	YDLDFK			
800.3824	800.3577	-0.0247	-31	256	261	YDLDFK			
806.4518	806.4189	-0.0329	-41	406	411	YNQILR	36	91.793	
806.4518	806.4189	-0.0329	-41	406	411	YNQILR			
810.4468	810.4134	-0.0334	-41	64	70	AVEHINK			
840.4474	840.4634	0.016	19	422	428	FAGRSFR			
1086.6154	1086.6071	-0.0083	-8	80	88	KLNVVEQEK			
1086.6154	1086.6071	-0.0083	-8	80	88	KLNVVEQEK			
1143.6156	1143.6096	-0.006	-5	183	192	IGAEVYHNLK	48	99.486	
1143.6156	1143.6096	-0.006	-5	183	192	IGAEVYHNLK			
1406.7162	1406.719	0.0028	2	15	27	GNPTVEVDLYTAK			
1406.7162	1406.719	0.0028	2	15	27	GNPTVEVDLYTAK			
1439.7417	1439.7416	-0.0001	0	269	280	YITPDQLADLYK			
1439.7417	1439.7416	-0.0001	0	269	280	YITPDQLADLYK			
1633.8214	1633.8226	0.0012	1	343	357	VNQIGSVTESLQACK			Carbamidomethyl (C)[14]
1633.8214	1633.8226	0.0012	1	343	357	VNQIGSVTESLQACK			Carbamidomethyl (C)[14]
1668.7455	1668.7473	0.0018	1	89	102	IDQLMIEMDGTENK			Oxidation (M)[5,8]
1668.7455	1668.7473	0.0018	1	89	102	IDQLMIEMDGTENK			Oxidation (M)[5,8]
1804.9438	1804.9647	0.0209	12	32	49	AAVPSGASTGIYEALELR			
1804.9438	1804.9647	0.0209	12	32	49	AAVPSGASTGIYEALELR	28	48.454	
1928.9608	1928.9664	0.0056	3	162	178	LAMQEFMILPVGASSFR			Oxidation (M)[3,7]
1928.9608	1928.9664	0.0056	3	162	178	LAMQEFMILPVGASSFR			Oxidation (M)[3,7]

2047.0706	2047.0695	-0.0011	-1	306	325	FTATAGIQVVGDDLTVTNPK			
2208.0278	2208.0249	-0.0029	-1	233	252	AGYTDQVVIGMDVAASEFYR			Oxidation (M)[11]
2208.0278	2208.0249	-0.0029	-1	233	252	AGYTDQVVIGMDVAASEFYR			Oxidation (M)[11]
2384.1924	2383.9441	-0.2483	-104	162	182	LAMQEFMILPVGASSFREAMR			
2384.1924	2383.9441	-0.2483	-104	162	182	LAMQEFMILPVGASSFREAMR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
ATP synthase beta subunit	gb|AAB02288.1	12	348	100	265	100	62	99.98	30.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
899.5196	899.4961	-0.0235	-26	71	79	VLDSGAPIK	24	0	
899.5196	899.4961	-0.0235	-26	71	79	VLDSGAPIK			
975.5621	975.5485	-0.0136	-14	148	158	IGLFGGAGVGK			
975.5621	975.5485	-0.0136	-14	148	158	IGLFGGAGVGK	16	0	
1038.5942	1038.5953	0.0011	1	80	89	IPVGPETLGR	62	99.978	
1038.5942	1038.5953	0.0011	1	80	89	IPVGPETLGR			
1088.635	1088.6204	-0.0146	-13	135	144	VVDLLAPYAK			
1088.635	1088.6204	-0.0146	-13	135	144	VVDLLAPYAK			
1278.6359	1278.6464	0.0105	8	56	67	TIAMDGTEGLVR	23	0	Oxidation (M)[4]
1278.6359	1278.6464	0.0105	8	56	67	TIAMDGTEGLVR			Oxidation (M)[4]
1401.7042	1401.7222	0.018	13	90	101	IMNVIGEPIDER	22	0	Oxidation (M)[2]
1401.7042	1401.7222	0.018	13	90	101	IMNVIGEPIDER			Oxidation (M)[2]
1435.7539	1435.7854	0.0315	22	257	270	FTQAGSEVSALLGR	14	0	
1435.7539	1435.7854	0.0315	22	257	270	FTQAGSEVSALLGR			
1601.8104	1601.8553	0.0449	28	211	225	VALVYGQMNEPPGAR	25	0	
1601.8104	1601.8553	0.0449	28	211	225	VALVYGQMNEPPGAR			
1617.8053	1617.845	0.0397	25	211	225	VALVYGQMNEPPGAR			Oxidation (M)[8]
1617.8053	1617.845	0.0397	25	211	225	VALVYGQMNEPPGAR	49	99.454	Oxidation (M)[8]
1650.9174	1650.9677	0.0503	30	41	55	LVLEVAQHLGESTVR	0	0	
1650.9174	1650.9677	0.0503	30	41	55	LVLEVAQHLGESTVR			
1815.8694	1815.928	0.0586	32	353	368	IMDPNIVGSEHYDVAR			
1831.8643	1831.921	0.0567	31	353	368	IMDPNIVGSEHYDVAR			Oxidation (M)[2]
1831.8643	1831.921	0.0567	31	353	368	IMDPNIVGSEHYDVAR	39	94.841	Oxidation (M)[2]
2076.9905	2077.0637	0.0732	35	188	205	EGNDLYHEMIESGVINLK			Oxidation (M)[9]
2076.9905	2077.0637	0.0732	35	188	205	EGNDLYHEMIESGVINLK			Oxidation (M)[9]
2282.0791	2282.1812	0.1021	45	271	291	IPSAVGYQPTLATDMGTMQER	5	0	Oxidation (M)[15]
2282.0791	2282.1812	0.1021	45	271	291	IPSAVGYQPTLATDMGTMQER			Oxidation (M)[15]
2298.074	2298.1733	0.0993	43	271	291	IPSAVGYQPTLATDMGTMQER	16	0	Oxidation (M)[15,18]
2298.074	2298.1733	0.0993	43	271	291	IPSAVGYQPTLATDMGTMQER			Oxidation (M)[15,18]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
ATP synthase beta subunit	gb|AAB02288.1	14	508	100	408	100	77	100	36.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
899.5196	899.5611	0.0415	46	71	79	VLDSGAPIK			
899.5196	899.5611	0.0415	46	71	79	VLDSGAPIK	31	83.097	
975.5621	975.6062	0.0441	45	148	158	IGLFGGAGVGK	53	99.893	
975.5621	975.6062	0.0441	45	148	158	IGLFGGAGVGK			
1038.5942	1038.6564	0.0622	60	80	89	IPVGPETLGR	77	100	
1038.5942	1038.6564	0.0622	60	80	89	IPVGPETLGR			
1088.635	1088.676	0.041	38	135	144	VVDLLAPYAK			
1088.635	1088.676	0.041	38	135	144	VVDLLAPYAK	41	98.023	
1262.6409	1262.7006	0.0597	47	56	67	TIAMDGTEGLVR	21	0	
1262.6409	1262.7006	0.0597	47	56	67	TIAMDGTEGLVR			
1278.6359	1278.6913	0.0554	43	56	67	TIAMDGTEGLVR			Oxidation (M)[4]
1278.6359	1278.6913	0.0554	43	56	67	TIAMDGTEGLVR	34	91.928	Oxidation (M)[4]

1385.7094	1385.7738	0.0644	46	90	101	IMNVIGEPIDER			
1401.7042	1401.7615	0.0573	41	90	101	IMNVIGEPIDER	19	0	Oxidation (M)[2]
1401.7042	1401.7615	0.0573	41	90	101	IMNVIGEPIDER			Oxidation (M)[2]
1435.7539	1435.8254	0.0715	50	257	270	FTQAGSEVSALLGR			
1435.7539	1435.8254	0.0715	50	257	270	FTQAGSEVSALLGR	28	60.193	
1439.7893	1439.8452	0.0559	39	228	240	VALTGLTVAEYFR			
1439.7893	1439.8452	0.0559	39	228	240	VALTGLTVAEYFR			
1601.8104	1601.8856	0.0752	47	211	225	VALVYGQMNEPPGAR			
1601.8104	1601.8856	0.0752	47	211	225	VALVYGQMNEPPGAR	35	92.536	
1617.8053	1617.8741	0.0688	43	211	225	VALVYGQMNEPPGAR			Oxidation (M)[8]
1617.8053	1617.8741	0.0688	43	211	225	VALVYGQMNEPPGAR	40	97.667	Oxidation (M)[8]
1650.9174	1650.9932	0.0758	46	41	55	LVLEVAQHLGESTVR	13	0	
1650.9174	1650.9932	0.0758	46	41	55	LVLEVAQHLGESTVR			
1815.8694	1815.9465	0.0771	42	353	368	IMDPNIVGSEHYDVAR			
1831.8643	1831.9375	0.0732	40	353	368	IMDPNIVGSEHYDVAR			Oxidation (M)[2]
1831.8643	1831.9375	0.0732	40	353	368	IMDPNIVGSEHYDVAR	41	98.386	Oxidation (M)[2]
1988.0334	1988.1144	0.081	41	334	352	AIAELGIYPAVDPLDSTSR			
1988.0334	1988.1144	0.081	41	334	352	AIAELGIYPAVDPLDSTSR	18	0	
2076.9905	2077.0706	0.0801	39	188	205	EGNDLYHEMIESGVINLK			Oxidation (M)[9]
2076.9905	2077.0706	0.0801	39	188	205	EGNDLYHEMIESGVINLK			Oxidation (M)[9]
2282.0791	2282.178	0.0989	43	271	291	IPSAVGYQPTLATDMGTMQER			Oxidation (M)[15]
2282.0791	2282.178	0.0989	43	271	291	IPSAVGYQPTLATDMGTMQER	7	0	Oxidation (M)[15]
2298.074	2298.1699	0.0959	42	271	291	IPSAVGYQPTLATDMGTMQER			Oxidation (M)[15,18]
2298.074	2298.1699	0.0959	42	271	291	IPSAVGYQPTLATDMGT	13	0	Oxidation (M)[15,18]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Similar to ubiquinol-cytochrome c reductase	rf|XP_217267.2	12	207	100	110	100	30	71.047	27.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
809.4151	809.3976	-0.0175	-22	270	276	FTGSEIR			
809.4515	809.3976	-0.0539	-67	416	422	SLLTYGR	19	0	
900.5261	900.4976	-0.0285	-32	164	170	ERDVILR			
998.5377	998.5308	-0.0069	-7	103	111	NRPGNALEK			
998.5377	998.5308	-0.0069	-7	103	111	NRPGNALEK	16	0	
1083.5317	1083.5312	-0.0005	0	214	222	TDLTDYLSR			
1083.5317	1083.5312	-0.0005	0	214	222	TDLTDYLSR	30	71.047	
1205.583	1205.5842	0.0012	1	433	442	IEEVDAQMVR			Oxidation (M)[8]
1205.583	1205.5842	0.0012	1	433	442	IEEVDAQMVR	27	41.832	Oxidation (M)[8]
1256.6746	1256.6409	-0.0337	-27	423	432	RIPLAEWESR			
1256.7144	1256.6409	-0.0735	-58	226	238	APRMVLAAAGGVK			Oxidation (M)[4]
1353.6315	1353.6486	0.0171	13	379	390	LCTSATESEVTR			Carbamidomethyl (C)[2]
1580.7855	1580.7921	0.0066	4	86	99	NNGAGYFLEHLAFK			
1646.8132	1646.8392	0.026	16	112	126	EVESIGAHLNAYSTR	19	0	
1646.8132	1646.8392	0.026	16	112	126	EVESIGAHLNAYSTR			
2068.0127	2068.0288	0.0161	8	397	415	NALISHLDGTTPVCEDIGR			Carbamidomethyl (C)[14]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Creatine kinase	gb|AAA40932.1	7	98	100	40	98.707	24	51.968	30.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1232.6157	1232.5919	-0.0238	-19	87	96	DLFDPIIEDR			
1232.6157	1232.5919	-0.0238	-19	87	96	DLFDPIIEDR	11	0	
1290.5896	1290.6183	0.0287	22	1	11	MPFSNSHNTQK			
1303.7256	1303.7172	-0.0084	-6	33	43	VLTPELYAELR	9	0	
1303.7256	1303.7172	-0.0084	-6	33	43	VLTPELYAELR			
1602.8334	1602.839	0.0056	3	157	172	LAVEALSSLDGDLSGR	24	51.968	

1602.8334	1602.839	0.0056	3	157	172	LAVEALSSLDGDLSGR			
1964.9308	1964.9399	0.0091	5	321	341	GTGGVDTAAVGGVFDVSNADR			
1964.9308	1964.9399	0.0091	5	321	341	GTGGVDTAAVGGVFDVSNADR	7	0	
2518.1692	2518.1384	-0.0308	-12	108	130	TDLNPDNLQGGDDLDPNYVLSSR			
2953.4124	2953.2546	-0.1578	-53	268	292	NYEFMWNPHLGYILTCPSNLGTGLR			Carbamidomethyl (C)[16]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Guanine nucleotide binding protein, alpha o	cra|rCP51914	7	96	100	47	99.547	35	92.279	22.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
891.4682	891.4868	0.0186	21	155	162	LFDVGGQR	12	0	
891.4682	891.4868	0.0186	21	155	162	LFDVGGQR			
1298.5933	1298.6516	0.0583	45	43	54	AMDTLGVEYGDK			
1298.5933	1298.6516	0.0583	45	43	54	AMDTLGVEYGDK			
1380.7158	1380.7291	0.0133	10	138	149	TTGIVETHFTFK			
1380.7158	1380.7291	0.0133	10	138	149	TTGIVETHFTFK			
1445.6907	1445.7073	0.0166	11	11	23	IIHEDGFSGEDVK			
1445.6907	1445.7073	0.0166	11	11	23	IIHEDGFSGEDVK			
1599.7319	1599.7345	0.0026	2	43	56	AMDTLGVEYGDKER			Oxidation (M)[2]
1689.8442	1689.8634	0.0192	11	119	133	IGAADYQPTEQDILR			
1689.8442	1689.8634	0.0192	11	119	133	IGAADYQPTEQDILR	35	92.279	
2150.1968	2150.1899	-0.0069	-3	24	42	QYKPVVYSNTIQSLAAIVR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Simlar to capping protein beta subunit	rf|XP_21656.2	10	172	100	76	100	28	47.31	41.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1057.6	1057.5259	-0.0741	-70	260	268	NDLVEALKR			
1057.6	1057.5259	-0.0741	-70	260	268	NDLVEALKR			
1108.6473	1108.589	-0.0583	-53	15	23	RLPPQQIEK			
1108.6473	1108.589	-0.0583	-53	15	23	RLPPQQIEK	14	0	
1171.5994	1171.536	-0.0634	-54	226	235	STLNEIYFGK			
1231.5413	1231.5054	-0.0359	-29	58	66	DYLLCDYNR			Carbamidomethyl (C)[5]
1231.5413	1231.5054	-0.0359	-29	58	66	DYLLCDYNR	28	47.309	Carbamidomethyl (C)[5]
1353.6427	1353.6108	-0.0319	-24	182	195	SGSGTMNLGGSLTR			Oxidation (M)[6]
1353.6427	1353.6108	-0.0319	-24	182	195	SGSGTMNLGGSLTR			Oxidation (M)[6]
1534.6842	1534.6639	-0.0203	-13	79	92	YDPPLEDGAMPSAR			Oxidation (M)[10]
1550.8247	1550.6805	-0.1442	-93	169	181	LTSTVMLWLQTNK			Oxidation (M)[6]
1568.7339	1568.7338	-0.0001	0	96	108	LEVEANNAFDQYR			
1568.7339	1568.7338	-0.0001	0	96	108	LEVEANNAFDQYR	12	0	
1696.8289	1696.8372	0.0083	5	95	108	KLEVEANNAFDQYR	22	0	
1696.8289	1696.8372	0.0083	5	95	108	KLEVEANNAFDQYR			
2303.0391	2303.0471	0.008	3	196	215	QMEKDETVSDCSPHIANI			Carbamidomethyl (C)[11]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Similar to HT014	rf|XP_216543.2	8	89	99.996	24	26.006	24	26.006	22.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
881.5243	881.5007	-0.0236	-27	210	216	IFYIGLR			
881.5243	881.5007	-0.0236	-27	210	216	IFYIGLR			
884.4108	884.3918	-0.019	-21	62	68	EEPPEQR			
884.4108	884.3918	-0.019	-21	62	68	EEPPEQR	24	26.006	
1025.5779	1025.574	-0.0039	-4	69	77	GLAYGLYLR			
1025.5779	1025.574	-0.0039	-4	69	77	GLAYGLYLR	4	0	
1206.575	1206.6005	0.0255	21	165	174	EPDQTFSLNR			

1468.6373	1468.6478	0.0105	7	153	164	NIPQMSFDDTER			Oxidation (M)[5]
1468.6373	1468.6478	0.0105	7	153	164	NIPQMSFDDTER			Oxidation (M)[5]
1544.822	1544.8287	0.0067	4	189	201	FSNVYHLSIHISK			
1933.8267	1933.8235	-0.0032	-2	133	149	GIIIMGEDDDSHPSEMR			Oxidation (M)[5,16]
1933.8267	1933.8235	-0.0032	-2	133	149	GIIIMGEDDDSHPSEMR			Oxidation (M)[5,16]
2656.1943	2656.147	-0.0473	-18	153	174	NIPQMSFDDTEREPDQTFSLNR			Oxidation (M)[5]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Phosphatidylethanolamine-binding protein (F	rf|NP_058932.1	5	211	100	169	100	84	100	29.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
912.4937	912.4659	-0.0278	-30	149	155	FKVESFR			
912.4937	912.4659	-0.0278	-30	149	155	FKVESFR	30	85.471	
1351.674	1351.6658	-0.0082	-6	27	39	VDYGGVTVDELGK			
1560.8268	1560.8411	0.0143	9	63	76	LYTLVLTDPDAPSR			
1560.8268	1560.8411	0.0143	9	63	76	LYTLVLTDPDAPSR	56	99.964	
1688.9218	1688.9341	0.0123	7	63	77	LYTLVLTDPDAPSRK			
1963.9607	1963.9636	0.0029	1	94	113	GNDISSGTVLSEYVGSGPPK	84	100	
1963.9607	1963.9636	0.0029	1	94	113	GNDISSGTVLSEYVGSGPPK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Similar to NADH dehydrogenase:ubiquinone	rf|XP_215197.1	6	90	99.997	29	60.737	15	0	12.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
837.3737	837.3371	-0.0366	-44	106	112	YPSGEER			
837.3737	837.3371	-0.0366	-44	106	112	YPSGEER			
858.5043	858.4598	-0.0445	-52	4	11	LSSSVLPR			
858.5043	858.4598	-0.0445	-52	4	11	LSSSVLPR	15	0	
993.4748	993.4468	-0.028	-28	105	112	RYPSGEER	4	0	
993.4748	993.4468	-0.028	-28	105	112	RYPSGEER			
1273.6609	1273.6387	-0.0222	-17	69	79	GLGMTLSYLFR			Oxidation (M)[4]
1308.647	1308.627	-0.02	-15	80	90	EPATINYPFEK			
1308.7092	1308.627	-0.0822	-63	1	11	MYRLSSSVLPR	15	0	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Dynamin-1	spt|P21575	16	136	100	61	99.99	35	94.41	19.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
804.4362	804.3316	-0.1046	-130	446	451	LQQYPR	18	0	
804.4362	804.3316	-0.1046	-130	446	451	LQQYPR			
839.5097	839.4064	-0.1033	-123	459	465	IVTTHIR			
839.5097	839.4064	-0.1033	-123	459	465	IVTTHIR			
877.489	877.396	-0.093	-106	230	237	GYIGVVNR			
1065.6415	1065.5826	-0.0589	-55	114	123	GISPVPINLR			
1065.6415	1065.5826	-0.0589	-55	114	123	GISPVPINLR			
1087.528	1087.4742	-0.0538	-49	316	324	NFRPDDPAR			
1107.5792	1107.5286	-0.0506	-46	45	54	SSVLENFVGR			
1153.5789	1153.542	-0.0369	-32	258	266	FFLSHPSYR			
1213.6284	1213.5955	-0.0329	-27	774	784	SPTSSPTPQRR			
1272.6616	1272.6207	-0.0409	-32	5	15	GMEDLIPLVNR			Oxidation (M)[2]
1281.6738	1281.6516	-0.0222	-17	257	266	KFFLSHPSYR			
1335.7491	1335.7313	-0.0178	-13	280	290	VLNQQLTNHIR	9	0	
1335.7491	1335.7313	-0.0178	-13	280	290	VLNQQLTNHIR			
1344.7118	1344.6942	-0.0176	-13	511	522	TSGNQDEILVIR			
1375.7117	1375.6948	-0.0169	-12	584	594	HIFALFNTEQR			

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1709.8857	1709.8916	0.0059	3	143	157	VPVGDQPPDIEFQIR			
1709.8857	1709.8916	0.0059	3	143	157	VPVGDQPPDIEFQIR	35	94.406	
1867.8668	1867.8815	0.0147	8	344	361	IEGSGDQIDTYELSGGAR			
1923.0156	1922.9351	-0.0805	-42	328	343	ALLQMVQQFAVDFEKR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Similar to Beta-soluble NSF attachment prot	rf|XP_345448.1	12	184	100	62	99.989	28	69.815	45.0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
817.4315	817.3925	-0.039	-48	23	29	ASHSFLR			
817.4315	817.3925	-0.039	-48	23	29	ASHSFLR	12	0	
821.4263	821.3889	-0.0374	-46	30	37	GLFGGNTR	6	0	
821.4263	821.3889	-0.0374	-46	30	37	GLFGGNTR			
853.405	853.3757	-0.0293	-34	314	320	EFDSISR			
853.405	853.3757	-0.0293	-34	314	320	EFDSISR			
1290.5808	1290.5914	0.0106	8	335	347	SIQGDGEGDGDLK			
1317.5449	1317.5488	0.0039	3	38	47	IEEACEMYTR			Oxidation (M)[7]
1390.6995	1390.7059	0.0064	5	9	20	EAVQLMAEAEKR			Oxidation (M)[6]
1482.7587	1482.7645	0.0058	4	217	229	VAAYAAQLEQYQK	23	10.917	
1482.7587	1482.7645	0.0058	4	217	229	VAAYAAQLEQYQK			
1508.6362	1508.6476	0.0114	8	277	288	YEEMFPAFTDSR			Oxidation (M)[4]
1508.6362	1508.6476	0.0114	8	277	288	YEEMFPAFTDSR	28	69.815	Oxidation (M)[4]
1582.7133	1582.7227	0.0094	6	79	93	HDSATSFVDAGNAYK			
2060.9771	2060.9822	0.0051	2	296	313	LLEAHEEQNSEAYTEAVK			
2135.0688	2135.0667	-0.0021	-1	230	248	AIEIYEQVGANTMDNPLLK			Oxidation (M)[13]
2301.1372	2301.1565	0.0193	8	253	271	DYFFKAALCHFIVDELNAK			Carbamidomethyl (C)[9]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Similar to Endoplasmin precursor	rf|XP_343193.1	15	97	100	23	0.315	13	0	21.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
876.4573	876.4227	-0.0346	-39	684	690	TFEINPR	10	0	
876.4573	876.4227	-0.0346	-39	684	690	TFEINPR			
982.4839	982.4222	-0.0617	-63	169	177	SGTSEFLNK			
993.5251	993.482	-0.0431	-43	725	733	SGYLLPDTK			
1015.473	1015.4648	-0.0082	-8	396	404	GLFDEYGSK			
1081.5425	1081.5229	-0.0196	-18	76	84	FAFQAEVNR			
1081.5425	1081.5229	-0.0196	-18	76	84	FAFQAEVNR	13	0	
1139.5803	1139.5702	-0.0101	-9	494	503	LGVIEDHSNR	12	0	
1139.5803	1139.5702	-0.0101	-9	494	503	LGVIEDHSNR			
1150.5375	1150.5322	-0.0053	-5	548	557	EAESSPFVER	2	0	
1150.5375	1150.5322	-0.0053	-5	548	557	EAESSPFVER			
1187.6782	1187.6688	-0.0094	-8	385	395	SILFVPTSAPR	7	0	
1187.6782	1187.6688	-0.0094	-8	385	395	SILFVPTSAPR			
1278.6324	1278.6666	0.0342	27	547	557	KEAESSPFVER			
1314.7627	1314.7678	0.0051	4	157	168	EELVKNLGTIAK			
1485.7544	1485.7611	0.0067	5	435	448	GVVDSDDLPLNVSR			
1529.774	1529.7706	-0.0034	-2	143	156	NLLHVTDTGVGMTR			Oxidation (M)[12]
1785.8977	1785.9075	0.0098	5	52	67	EEEAIQLDGLNASQIR			
2250.0422	2250.0491	0.0069	3	512	530	FQSSHHSTDITSLDQYVER			
2510.2332	2510.1072	-0.126	-50	703	724	EDEDDKTVMDLAVVLFETATLR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Ischemia responsive 94 kDa protein	trm|O88600	12	135	100	68	99.996	31	81.481	19.0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1149.5535	1149.525	-0.0285	-25	689	697	FQESEERPK			
1149.5535	1149.525	-0.0285	-25	689	697	FQESEERPK	2	0	
1239.5891	1239.5656	-0.0235	-19	74	84	AFSDPFVEAEK			
1295.6954	1295.6725	-0.0229	-18	186	196	QDLPALEEKPR			
1295.6954	1295.6725	-0.0229	-18	186	196	QDLPALEEKPR	31	81.481	
1321.7111	1321.6946	-0.0165	-12	222	234	VLATAFDTTLGGR	10	0	
1321.7111	1321.6946	-0.0165	-12	222	234	VLATAFDTTLGGR			
1418.6256	1418.6123	-0.0133	-9	619	629	NAVEEYVYEMR			Oxidation (M)[10]
1492.7642	1492.7632	-0.001	-1	333	346	EDIYAVEIVGGATR			
1492.7642	1492.7632	-0.001	-1	333	346	EDIYAVEIVGGATR			
1495.7023	1495.7091	0.0068	5	20	33	AGGIETIANEYSDR			
1495.7023	1495.7091	0.0068	5	20	33	AGGIETIANEYSDR	28	60.315	
1519.7599	1519.7595	-0.0004	0	361	374	ELSTTLNADEAVTR			
1584.7653	1584.7662	0.0009	1	639	651	FVSEDDRNNFTLK			
1584.7653	1584.7662	0.0009	1	639	651	FVSEDDRNNFTLK	9	0	
1664.8094	1664.8004	-0.009	-5	155	169	SVMDATQIAGLNCLR			Carbamidomethyl (C)[13]
1923.8389	1923.8826	0.0437	23	718	733	NKEDQYEHLDAADMTK			Oxidation (M)[14]
2168.0691	2168.073	0.0039	2	135	153	KPVVDCVVSVPSFYTDAER			Carbamidomethyl (C)[6]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Ischemia responsive 94 kDa protein	trm|O88600	13	112	100	18	0	18	0	20.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1149.5535	1149.5164	-0.0371	-32	689	697	FQESEERPK			
1149.5535	1149.5164	-0.0371	-32	689	697	FQESEERPK			
1239.5891	1239.5692	-0.0199	-16	74	84	AFSDPFVEAEK			
1295.6954	1295.6669	-0.0285	-22	186	196	QDLPALEEKPR	18	0	
1295.6954	1295.6669	-0.0285	-22	186	196	QDLPALEEKPR			
1321.7111	1321.6921	-0.019	-14	222	234	VLATAFDTTLGGR			
1321.7111	1321.6921	-0.019	-14	222	234	VLATAFDTTLGGR	10	0	
1406.7023	1406.7363	0.034	24	687	697	TRFQESEERPK			
1418.6256	1418.6183	-0.0073	-5	619	629	NAVEEYVYEMR			Oxidation (M)[10]
1418.6256	1418.6183	-0.0073	-5	619	629	NAVEEYVYEMR			Oxidation (M)[10]
1492.7642	1492.767	0.0028	2	333	346	EDIYAVEIVGGATR			
1495.7023	1495.7106	0.0083	6	20	33	AGGIETIANEYSDR			
1495.7023	1495.7106	0.0083	6	20	33	AGGIETIANEYSDR	5	0	
1519.7599	1519.7598	-0.0001	0	361	374	ELSTTLNADEAVTR			
1584.7653	1584.7729	0.0076	5	639	651	FVSEDDRNNFTLK			
1584.7653	1584.7729	0.0076	5	639	651	FVSEDDRNNFTLK			
1923.8389	1923.9281	0.0892	46	718	733	NKEDQYEHLDAADMTK			Oxidation (M)[14]
2168.0691	2168.0793	0.0102	5	135	153	KPVVDCVVSVPSFYTDAER			Carbamidomethyl (C)[6]
2609.1421	2609.1243	-0.0178	-7	522	543	MQVDQEEPHTEEQQPQTPAENK			Oxidation (M)[1]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Similar to inner membrane protein, mitochor	rf|XP_232055.2	21	286	100	95	100	37	95.792	17.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
847.3845	847.4361	0.0516	61	67	72	WDSHFR			
914.5166	914.5511	0.0345	38	395	401	RIDQLNR			
967.5934	967.6302	0.0368	38	102	110	KPIQSGPLK			
1053.5211	1053.5651	0.044	42	608	616	GVYSEETLR			
1053.5211	1053.5651	0.044	42	608	616	GVYSEETLR			
1075.5015	1075.5474	0.0459	43	442	450	SEIQAEQDR			
1075.5015	1075.5474	0.0459	43	442	450	SEIQAEQDR			
1119.5654	1119.6067	0.0413	37	470	479	QAAAHTDHLR			

1119.5654	1119.6067	0.0413	37	470	479	QAAAHTDHLR	20	0	
1153.5959	1153.6321	0.0362	31	180	189	ERPPEEVAAR			
1153.5959	1153.6321	0.0362	31	180	189	ERPPEEVAAR	10	0	
1271.579	1271.619	0.04	31	491	500	FEFEQDLSEK			
1271.579	1271.619	0.04	31	491	500	FEFEQDLSEK			
1287.6328	1287.6731	0.0403	31	501	510	LSEQELEFHR			
1287.6328	1287.6731	0.0403	31	501	510	LSEQELEFHR	37	95.792	
1314.7263	1314.8013	0.075	57	271	283	AVDEAADALLKAK			
1442.7961	1442.8079	0.0118	8	221	234	QTITAQNAAVQAVK			
1443.7339	1443.7886	0.0547	38	501	511	LSEQELEFHRR			
1518.7759	1518.8079	0.032	21	207	220	SLEDALNQTATVTR			
1527.8278	1527.8624	0.0346	23	338	350	VVSQYHELVVQAR	28	65.241	
1527.8278	1527.8624	0.0346	23	338	350	VVSQYHELVVQAR			
1563.79	1563.8019	0.0119	8	300	314	EIAGATPYITAAEEK			
1823.8882	1823.9142	0.026	14	532	548	GIEQAVQSHAVAEEEAR			
1945.9899	1945.9927	0.0028	1	566	584	TSSAEMPTIPLGSAVEAIR			Oxidation (M)[6]
1951.9832	1951.9971	0.0139	7	532	549	GIEQAVQSHAVAEEEARK			
2003.0485	2003.048	-0.0005	0	657	673	QLKPPAELYPEDINTFK			
2132.9553	2132.9539	-0.0014	-1	512	529	SQEQMDNFTLDINTAYAR			Oxidation (M)[5]
2507.2083	2507.2253	0.017	7	585	607	VSCSDNEFTQALTAAIPPESLTR			Carbamidomethyl (C)[3]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Similar to inner membrane protein, mitochor	rf|XP_232055.2	18	222	100	59	99.979	30	82.805	16.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
914.5166	914.4207	-0.0959	-105	395	401	RIDQLNR			
967.5934	967.5105	-0.0829	-86	102	110	KPIQSGPLK			
1053.5211	1053.4613	-0.0598	-57	608	616	GVYSEETLR			
1053.5211	1053.4613	-0.0598	-57	608	616	GVYSEETLR			
1075.5015	1075.4496	-0.0519	-48	442	450	SEIQAEQDR			
1119.5654	1119.5154	-0.05	-45	470	479	QAAAHTDHLR	9	0	
1119.5654	1119.5154	-0.05	-45	470	479	QAAAHTDHLR			
1153.5959	1153.5476	-0.0483	-42	180	189	ERPPEEVAAR	3	0	
1153.5959	1153.5476	-0.0483	-42	180	189	ERPPEEVAAR			
1271.579	1271.5503	-0.0287	-23	491	500	FEFEQDLSEK			
1287.6328	1287.6105	-0.0223	-17	501	510	LSEQELEFHR			
1287.6328	1287.6105	-0.0223	-17	501	510	LSEQELEFHR	30	82.805	
1314.7263	1314.7397	0.0134	10	271	283	AVDEAADALLKAK			
1442.7961	1442.7732	-0.0229	-16	221	234	QTITAQNAAVQAVK			
1443.7339	1443.7538	0.0199	14	501	511	LSEQELEFHRR			
1518.7759	1518.7734	-0.0025	-2	207	220	SLEDALNQTATVTR			
1527.8278	1527.8322	0.0044	3	338	350	VVSQYHELVVQAR			
1527.8278	1527.8322	0.0044	3	338	350	VVSQYHELVVQAR	20	0	
1563.79	1563.7688	-0.0212	-14	300	314	EIAGATPYITAAEEK			
1823.8882	1823.9055	0.0173	9	532	548	GIEQAVQSHAVAEEEAR			
1945.9899	1945.9873	-0.0026	-1	566	584	TSSAEMPTIPLGSAVEAIR			Oxidation (M)[6]
2003.0485	2003.0488	0.0003	0	657	673	QLKPPAELYPEDINTFK			
2132.9553	2132.9534	-0.0019	-1	512	529	SQEQMDNFTLDINTAYAR			Oxidation (M)[5]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
TOAD-64	emb|CAA86981.1	10	89	99.996	37	96.134	24	20.71	23.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
844.4999	844.4651	-0.0348	-41	486	492	SRLAELR			
844.4999	844.4651	-0.0348	-41	486	492	SRLAELR			
908.4988	908.4571	-0.0417	-46	391	397	VFNLYPR			

1140.6088	1140.5663	-0.0425	-37	472	480	KPFPDFVYK			
1262.6296	1262.6003	-0.0293	-23	147	157	GIQEEMEALVK			Oxidation (M)[6]
1310.6885	1310.6648	-0.0237	-18	64	75	MVIPGGIDVHTR			Oxidation (M)[1]
1310.6885	1310.6648	-0.0237	-18	64	75	MVIPGGIDVHTR			Oxidation (M)[1]
1323.7631	1323.6582	-0.1049	-79	44	56	QIGENLIVPGGVK			
1323.7631	1323.6582	-0.1049	-79	44	56	QIGENLIVPGGVK			
1682.8707	1682.8744	0.0037	2	452	467	IVLEDGTLHVTEGSGR	13	0	
1682.8707	1682.8744	0.0037	2	452	467	IVLEDGTLHVTEGSGR			
1741.8062	1741.7601	-0.0461	-26	375	390	MDENQFVAVTSTNAAK			Oxidation (M)[1]
1741.8062	1741.7601	-0.0461	-26	375	390	MDENQFVAVTSTNAAK			Oxidation (M)[1]
2169.0684	2169.0725	0.0041	2	533	552	NLHQSGFSLSGAQIDDNIPR			
2169.0684	2169.0725	0.0041	2	533	552	NLHQSGFSLSGAQIDDNIPR	24	20.71	
2377.1741	2377.1707	-0.0034	-1	190	211	DIGAIAQVHAENGDIIAEEQQR			
2377.1741	2377.1707	-0.0034	-1	190	211	DIGAIAQVHAENGDIIAEEQQR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Unnamed protein product	emb|CAA37654.1	9	67	99.377	10	0	10	0	20.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
833.39	833.3402	-0.0498	-60	276	283	APGFGDNR			
833.39	833.3402	-0.0498	-60	276	283	APGFGDNR			
855.4682	855.4205	-0.0477	-56	108	115	GANPVEIR			
855.4682	855.4205	-0.0477	-56	108	115	GANPVEIR			
961.4849	961.4583	-0.0266	-28	276	284	APGFGDNRK			
1320.6827	1320.7155	0.0328	25	155	166	DIGNIISDAMKK			Oxidation (M)[10]
1320.6827	1320.7155	0.0328	25	155	166	DIGNIISDAMKK			Oxidation (M)[10]
1389.7048	1389.6965	-0.0083	-6	196	207	GYISPYFINTSK			
1684.905	1684.9152	0.0102	6	404	420	AAVEEGIVLGGGCALLR			Carbamidomethyl (C)[13]
1684.905	1684.9152	0.0102	6	404	420	AAVEEGIVLGGGCALLR			Carbamidomethyl (C)[13]
1905.0552	1905.0712	0.016	8	225	242	ISSVQSIVPALEIANAHR			
1905.0552	1905.0712	0.016	8	225	242	ISSVQSIVPALEIANAHR			
2040.002	2040.0024	0.0004	0	345	361	IQEITEQLDITTSEYEK			
2040.002	2040.0024	0.0004	0	345	361	IQEITEQLDITTSEYEK			
2560.2485	2560.2329	-0.0156	-6	71	95	LVQDVANNTNEEAGDGTTTATVLAR			
2560.2485	2560.2329	-0.0156	-6	71	95	LVQDVANNTNEEAGDGTTTATVLAR	10	0	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
GRP75	gb|AAB34982.1	21	434	100	238	100	54	99.836	36.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
863.4039	863.3914	-0.0125	-14	301	307	DNMALQR			Oxidation (M)[3]
863.4039	863.3914	-0.0125	-14	301	307	DNMALQR			Oxidation (M)[3]
938.4326	938.4202	-0.0124	-13	568	574	YAEEDRR			
938.4326	938.4202	-0.0124	-13	568	574	YAEEDRR	13	0	
958.4952	958.4924	-0.0028	-3	77	85	VLENAEGAR	32	73.467	
958.4952	958.4924	-0.0028	-3	77	85	VLENAEGAR			
1148.5542	1148.5575	0.0033	3	625	634	KDSETGENIR	7	0	
1148.5542	1148.5575	0.0033	3	625	634	KDSETGENIR			
1149.5535	1149.556	0.0025	2	127	135	RYDDPEVQK			
1149.5535	1149.556	0.0025	2	127	135	RYDDPEVQK	5	0	
1231.6641	1231.6561	-0.008	-6	635	646	QAASSLQQASLK			
1242.6801	1242.688	0.0079	6	207	218	DAGQISGLNVLR			
1242.6801	1242.688	0.0079	6	207	218	DAGQISGLNVLR	28	31.169	
1290.6801	1290.6891	0.009	7	395	405	VQQTVQDLFGR			
1290.6801	1290.6891	0.009	7	395	405	VQQTVQDLFGR	54	99.836	
1333.6383	1333.6694	0.0311	23	176	187	ETAENYLGHTAK			

1333.6383	1333.6694	0.0311	23	176	187	ETAENYLGHTAK			
1462.757	1462.751	-0.006	-4	378	391	SDIGEVILVGGMTR	15	0	Oxidation (M)[12]
1462.757	1462.751	-0.006	-4	378	391	SDIGEVILVGGMTR			Oxidation (M)[12]
1473.7908	1473.7863	-0.0045	-3	542	555	EQQIVIQSSGGLSK			
1473.7908	1473.7863	-0.0045	-3	542	555	EQQIVIQSSGGLSK			
1476.7329	1476.743	0.0101	7	86	99	TTPSVVAFTPDGER	19	0	
1476.7329	1476.743	0.0101	7	86	99	TTPSVVAFTPDGER			
1568.7704	1568.7688	-0.0016	-1	108	121	QAVTNPNNTFYATK			
1568.7704	1568.7688	-0.0016	-1	108	121	QAVTNPNNTFYATK			
1592.9523	1592.9652	0.0129	8	499	513	LLGQFTLIGIPPAPR	16	0	
1592.9523	1592.9652	0.0129	8	499	513	LLGQFTLIGIPPAPR			
1608.7687	1608.7673	-0.0014	-1	174	187	MKETAENYLGHTAK			Oxidation (M)[1]
1608.7687	1608.7673	-0.0014	-1	174	187	MKETAENYLGHTAK			Oxidation (M)[1]
1645.8795	1645.8699	-0.0096	-6	219	234	VINEPTAAALAYGLDK			
1694.8496	1694.8625	0.0129	8	188	202	NAVITVPAYFNDSQR			
1694.8496	1694.8625	0.0129	8	188	202	NAVITVPAYFNDSQR	31	68.538	
1808.9025	1808.8992	-0.0033	-2	469	485	SQVFSTAADGQTQVEIK			
1808.9025	1808.8992	-0.0033	-2	469	485	SQVFSTAADGQTQVEIK			
1872.9008	1872.8928	-0.008	-4	579	595	VEAVNMAEGIIHDTETK			Oxidation (M)[6]
2055.9617	2055.9753	0.0136	7	266	284	STNGDTFLGGEDFDQALLR	25	0	
2055.9617	2055.9753	0.0136	7	266	284	STNGDTFLGGEDFDQALLR			
2158.0444	2158.0415	-0.0029	-1	577	595	ERVEAVNMAEGIIHDTETK			Oxidation (M)[8]
2158.0444	2158.0415	-0.0029	-1	577	595	ERVEAVNMAEGIIHDTETK			Oxidation (M)[8]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
GRP75	gb|AAB34982.1	23	459	100	240	100	53	99.825	39.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
863.4039	863.3858	-0.0181	-21	301	307	DNMALQR			Oxidation (M)[3]
863.4039	863.3858	-0.0181	-21	301	307	DNMALQR			Oxidation (M)[3]
917.4437	917.4251	-0.0186	-20	647	653	LFEMAYK			Oxidation (M)[4]
938.4326	938.418	-0.0146	-16	568	574	YAEEDRR			
938.4326	938.418	-0.0146	-16	568	574	YAEEDRR	16	0	
958.4952	958.4919	-0.0033	-3	77	85	VLENAEGAR	31	68.216	
958.4952	958.4919	-0.0033	-3	77	85	VLENAEGAR			
1020.4592	1020.4608	0.0016	2	626	634	DSETGENIR	8	0	
1020.4592	1020.4608	0.0016	2	626	634	DSETGENIR			
1148.5542	1148.5631	0.0089	8	625	634	KDSETGENIR			
1148.5542	1148.5631	0.0089	8	625	634	KDSETGENIR			
1149.5535	1149.5597	0.0062	5	127	135	RYDDPEVQK	8	0	
1149.5535	1149.5597	0.0062	5	127	135	RYDDPEVQK			
1231.6641	1231.6611	-0.003	-2	635	646	QAASSLQQASLK			
1242.6801	1242.6963	0.0162	13	207	218	DAGQISGLNVLR	41	96.999	
1242.6801	1242.6963	0.0162	13	207	218	DAGQISGLNVLR			
1290.6801	1290.6976	0.0175	14	395	405	VQQTVQDLFGR			
1290.6801	1290.6976	0.0175	14	395	405	VQQTVQDLFGR	53	99.825	
1333.6383	1333.6544	0.0161	12	176	187	ETAENYLGHTAK			
1333.6383	1333.6544	0.0161	12	176	187	ETAENYLGHTAK	10	0	
1357.7546	1357.6287	-0.1259	-93	12	25	LVGTTASRSPAAAR			
1462.757	1462.7611	0.0041	3	378	391	SDIGEVILVGGMTR			Oxidation (M)[12]
1462.757	1462.7611	0.0041	3	378	391	SDIGEVILVGGMTR	12	0	Oxidation (M)[12]
1473.7908	1473.7924	0.0016	1	542	555	EQQIVIQSSGGLSK			
1473.7908	1473.7924	0.0016	1	542	555	EQQIVIQSSGGLSK			
1476.7329	1476.754	0.0211	14	86	99	TTPSVVAFTPDGER	19	0	
1476.7329	1476.754	0.0211	14	86	99	TTPSVVAFTPDGER			
1568.7704	1568.7734	0.003	2	108	121	QAVTNPNNTFYATK			
1568.7704	1568.7734	0.003	2	108	121	QAVTNPNNTFYATK			

1592.9523	1592.9716	0.0193	12	499	513	LLGQFTLIGIPPAPR			
1645.8795	1645.8784	-0.0011	-1	219	234	VINEPTAAALAYGLDK			
1694.8496	1694.8734	0.0238	14	188	202	NAVITVPAYFNDSQR			
1694.8496	1694.8734	0.0238	14	188	202	NAVITVPAYFNDSQR	51	99.719	
1802.9503	1802.9326	-0.0177	-10	378	394	SDIGEVILVGGMTRMPK			
1808.9025	1808.9114	0.0089	5	469	485	SQVFSTAADGQTQVEIK			
1808.9025	1808.9114	0.0089	5	469	485	SQVFSTAADGQTQVEIK			
1872.9008	1872.9015	0.0007	0	579	595	VEAVNMAEGIIHDTETK			Oxidation (M)[6]
2055.9617	2055.9641	0.0024	1	266	284	STNGDTFLGGEDFDQALLR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Serum albumin precursor [Contains: NRP}	spt|P02770	10	157	100	85	100	66	99.989	19.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
844.4998	844.4612	-0.0386	-46	453	460	NLGRVGTK			
844.4998	844.4612	-0.0386	-46	453	460	NLGRVGTK			
1017.5363	1017.509	-0.0273	-27	89	97	SIHTLFGDK			
1149.615	1149.6011	-0.0139	-12	66	75	LVQEVTDFAK			
1149.615	1149.6011	-0.0139	-12	66	75	LVQEVTDFAK	2	0	
1248.6371	1248.6411	0.004	3	35	44	FKDLGEQHFK			
1266.6365	1266.6373	0.0008	1	247	257	FPNAEFAEITK			
1266.6365	1266.6373	0.0008	1	247	257	FPNAEFAEITK			
1299.7056	1299.7208	0.0152	12	362	372	HPDYSVSLLLR			
1439.7853	1439.8132	0.0279	19	439	452	APQVSTPTLVEAAR	66	99.989	
1439.7853	1439.8132	0.0279	19	439	452	APQVSTPTLVEAAR			
1465.7798	1465.8114	0.0316	22	422	434	LGEYGFQNAVLVR	19	0	
1465.7798	1465.8114	0.0316	22	422	434	LGEYGFQNAVLVR			
1479.8569	1479.8076	-0.0493	-33	45	57	GLVLIAFSQYLQK			
1948.9181	1948.9451	0.027	14	585	602	AADKDNCFATEGPNLVAR			Carbamidomethyl (C)[7]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Serum albumin precursor [Contains: NRP}	spt|P02770	9	111	100	48	99.453	43	98.271	19.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1017.5363	1017.5228	-0.0135	-13	89	97	SIHTLFGDK			
1075.4877	1075.4866	-0.0011	-1	58	65	CPYEEHIK			Carbamidomethyl (C)[1]
1075.4877	1075.4866	-0.0011	-1	58	65	CPYEEHIK			Carbamidomethyl (C)[1]
1149.615	1149.6062	-0.0088	-8	66	75	LVQEVTDFAK			
1149.615	1149.6062	-0.0088	-8	66	75	LVQEVTDFAK			
1266.6365	1266.6385	0.002	2	247	257	FPNAEFAEITK			
1266.6365	1266.6385	0.002	2	247	257	FPNAEFAEITK			
1439.7853	1439.811	0.0257	18	439	452	APQVSTPTLVEAAR	43	98.271	
1439.7853	1439.811	0.0257	18	439	452	APQVSTPTLVEAAR			
1459.7396	1459.7402	0.0006	0	299	310	LQACCDKPVLQK			Carbamidomethyl (C)[4,5]
1465.7798	1465.8074	0.0276	19	422	434	LGEYGFQNAVLVR			
1465.7798	1465.8074	0.0276	19	422	434	LGEYGFQNAVLVR			
1746.731	1746.7449	0.0139	8	185	198	YNEVLTQCCTESDK			Carbamidomethyl (C)[8,9]
1948.9181	1948.9393	0.0212	11	585	602	AADKDNCFATEGPNLVAR	5	0	Carbamidomethyl (C)[7]
1948.9181	1948.9393	0.0212	11	585	602	AADKDNCFATEGPNLVA			Carbamidomethyl (C)[7]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
TOAD-64	emb|CAA86981.1	13	260	100	125	100	40	96.9	31.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
813.4213	813.4429	0.0216	27	57	63	TIEAHSR			

813.4213	813.4429	0.0216	27	57	63	TIEAHSR			
844.4999	844.5322	0.0323	38	486	492	SRLAELR			
844.4999	844.5322	0.0323	38	486	492	SRLAELR			
908.4988	908.5226	0.0238	26	391	397	VFNLYPR	40	96.9	
908.4988	908.5226	0.0238	26	391	397	VFNLYPR			
1015.553	1015.5812	0.0282	28	259	268	SAAEVIAQAR	24	0	
1015.553	1015.5812	0.0282	28	259	268	SAAEVIAQAR			
1310.6885	1310.7111	0.0226	17	64	75	MVIPGGIDVHTR	13	0	Oxidation (M)[1]
1310.6885	1310.7111	0.0226	17	64	75	MVIPGGIDVHTR			Oxidation (M)[1]
1323.7631	1323.7725	0.0094	7	44	56	QIGENLIVPGGVK			
1682.8707	1682.9086	0.0379	23	452	467	IVLEDGTLHVTEGSGR	26	23.388	
1682.8707	1682.9086	0.0379	23	452	467	IVLEDGTLHVTEGSGR			
1741.8062	1741.8167	0.0105	6	375	390	MDENQFVAVTSTNAAK			Oxidation (M)[1]
1741.8062	1741.8167	0.0105	6	375	390	MDENQFVAVTSTNAAK			Oxidation (M)[1]
1792.8348	1792.8622	0.0274	15	346	361	DNFTLIPEGTNGTEER	21	0	
1792.8348	1792.8622	0.0274	15	346	361	DNFTLIPEGTNGTEER			
1822.9368	1822.9539	0.0171	9	239	254	SITIANQTNCPLYVTK			Carbamidomethyl (C)[10]
2169.0684	2169.0928	0.0244	11	533	552	NLHQSGFSLSGAQIDDNIPR			
2182.9055	2182.9204	0.0149	7	76	94	FQMPDQGMTSADDFFQGTK			Oxidation (M)[3,8]
2377.1741	2377.2129	0.0388	16	190	211	DIGAIAQVHAENGDIIAEEQQR			
2377.1741	2377.2129	0.0388	16	190	211	DIGAIAQVHAENGDIIAEEQQR			

Protein Name	**Accession No.**	**Peptide Count**	**Protein Score**	**Protein Score C.I.%**	**Total Ion Score**	**Total Ion C.I. %**	**Best Ion Score**	**Best Ion C.I.%**	**% Coverage**
Similar to ATPase, H+ transporting, V1 subu	rf|XP_340988.1	28	488	100	272	100	54	99.858	42.9

Peptide Information

Calc. Mass	**Obsrv. Mass**	**± da**	**± ppm**	**Start Seq.**	**End Seq.**	**Sequence**	**Ion Score**	**C. I. %**	**Modification**
845.3934	845.3832	-0.0102	-12	394	400	CLGNPER			Carbamidomethyl (C)[1]
845.3934	845.3832	-0.0102	-12	394	400	CLGNPER			Carbamidomethyl (C)[1]
861.3963	861.3744	-0.0219	-25	531	536	FCPFYK			Carbamidomethyl (C)[2]
861.3963	861.3744	-0.0219	-25	531	536	FCPFYK			Carbamidomethyl (C)[2]
885.4464	885.4304	-0.016	-18	382	388	LASFYER	37	92.526	
885.4464	885.4304	-0.016	-18	382	388	LASFYER			
888.5302	888.4813	-0.0489	-55	565	571	ITWSIIR			
902.5053	902.4882	-0.0171	-19	121	129	GVNVSALSR			
902.5053	902.4882	-0.0171	-19	121	129	GVNVSALSR	29	51.633	
956.5523	956.5428	-0.0095	-10	213	220	QVRPVTEK			
956.5523	956.5428	-0.0095	-10	213	220	QVRPVTEK	20	0	
1016.4571	1016.4607	0.0036	4	460	467	ALDEYYDK			
1050.4884	1050.4807	-0.0077	-7	281	289	GNEMSEVLR	1	0	Oxidation (M)[4]
1050.4884	1050.4807	-0.0077	-7	281	289	GNEMSEVLR			Oxidation (M)[4]
1145.6102	1145.6176	0.0074	6	468	476	HFTEFVPLR			
1145.6102	1145.6176	0.0074	6	468	476	HFTEFVPLR	25	0	
1230.6664	1230.6661	-0.0003	0	203	212	LSMVQVWPVR			Oxidation (M)[3]
1262.678	1262.6617	-0.0163	-13	130	139	DIKWEFIPSK			
1308.7271	1308.7423	0.0152	12	45	56	VGHSELVGEIIR	29	49.702	
1308.7271	1308.7423	0.0152	12	45	56	VGHSELVGEIIR			
1316.7434	1316.7651	0.0217	16	221	232	LPANHPLLTGQR	54	99.858	
1316.7434	1316.7651	0.0217	16	221	232	LPANHPLLTGQR			
1319.655	1319.7422	0.0872	66	553	564	RAVETTAQSDNK			
1487.8038	1487.7397	-0.0641	-43	201	212	EKLSMVQVWPVR			Oxidation (M)[5]
1531.7897	1531.7991	0.0094	6	309	323	TALVANTSNMPVAAR	25	0	Oxidation (M)[10]
1531.7897	1531.7991	0.0094	6	309	323	TALVANTSNMPVAAR			Oxidation (M)[10]
1588.8792	1588.8859	0.0067	4	499	513	ASLAETDKITLEVAK			
1588.8792	1588.8859	0.0067	4	499	513	ASLAETDKITLEVAK			
1731.7609	1731.8127	0.0518	30	517	530	DDFLQQNGYTPYDR	10	0	
1731.8007	1731.8127	0.012	7	266	280	YSNSDVIIYVGCGER			Carbamidomethyl (C)[12]
1735.672	1735.7106	0.0386	22	339	353	DMGYHVSMMADSTSR			Oxidation (M)[2,8,9]

1735.672	1735.7106	0.0386	22	339	353	DMGYHVSMMADSTSR	0	0	Oxidation (M)[2,8,9]
1749.8694	1749.8475	-0.0219	-13	324	338	EASIYTGITLSEYFR			
1781.8527	1781.8738	0.0211	12	365	381	LAEMPADSGYPAYLGAR			
1797.8475	1797.8593	0.0118	7	365	381	LAEMPADSGYPAYLGAR	9	0	Oxidation (M)[4]
1797.8475	1797.8593	0.0118	7	365	381	LAEMPADSGYPAYLGAR			Oxidation (M)[4]
1800.8221	1800.8468	0.0247	14	599	613	ADYAQLLEDMQNAFR			Oxidation (M)[10]
1800.8221	1800.8468	0.0247	14	599	613	ADYAQLLEDMQNAFR			Oxidation (M)[10]
1883.8336	1883.8385	0.0049	3	537	552	TVGMLSNMISFYDMAR			Oxidation (M)[4,8,14]
2086.0239	2086.0422	0.0183	9	514	530	LIKDDFLQQNGYTPYDR	34	86.21	
2086.0239	2086.0422	0.0183	9	514	530	LIKDDFLQQNGYTPYDR			
2143.0496	2143.0613	0.0117	5	460	476	ALDEYYDKHFTEFVPLR			
2186.145	2186.1479	0.0029	1	143	163	VGSHITGGDIYGIVNENSLIK			
2681.2974	2681.2686	-0.0288	-11	57	81	LEGDMATIQVYEETSGVSVGDPVLR			Oxidation (M)[5]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
TOAD-64	emb|CAA86981.1	15	360	100	227	100	51	99.731	36.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
813.4213	813.4722	0.0509	63	57	63	TIEAHSR			
813.4213	813.4722	0.0509	63	57	63	TIEAHSR	8	0	
908.4988	908.526	0.0272	30	391	397	VFNLYPR			
908.4988	908.526	0.0272	30	391	397	VFNLYPR	43	98.423	
1015.553	1015.5582	0.0052	5	259	268	SAAEVIAQAR			
1015.553	1015.5582	0.0052	5	259	268	SAAEVIAQAR	30	64.705	
1140.6088	1140.5836	-0.0252	-22	472	480	KPFPDFVYK			
1140.6088	1140.5836	-0.0252	-22	472	480	KPFPDFVYK			
1262.6296	1262.5825	-0.0471	-37	147	157	GIQEEMEALVK			Oxidation (M)[6]
1262.6296	1262.5825	-0.0471	-37	147	157	GIQEEMEALVK			Oxidation (M)[6]
1310.6885	1310.6313	-0.0572	-44	64	75	MVIPGGIDVHTR			Oxidation (M)[1]
1310.6885	1310.6313	-0.0572	-44	64	75	MVIPGGIDVHTR	11	0	Oxidation (M)[1]
1323.7631	1323.6953	-0.0678	-51	44	56	QIGENLIVPGGVK			
1620.7938	1620.7201	-0.0737	-45	497	511	GLYDGPVCEVSVTPK			Carbamidomethyl (C)[8]
1620.7938	1620.7201	-0.0737	-45	497	511	GLYDGPVCEVSVTPK			Carbamidomethyl (C)[8]
1682.8707	1682.8064	-0.0643	-38	452	467	IVLEDGTLHVTEGSGR			
1682.8707	1682.8064	-0.0643	-38	452	467	IVLEDGTLHVTEGSGR	29	58.627	
1741.8062	1741.7249	-0.0813	-47	375	390	MDENQFVAVTSTNAAK			Oxidation (M)[1]
1792.8348	1792.7745	-0.0603	-34	346	361	DNFTLIPEGTNGTEER	51	99.731	
1792.8348	1792.7745	-0.0603	-34	346	361	DNFTLIPEGTNGTEER			
1822.9368	1822.8663	-0.0705	-39	239	254	SITIANQTNCPLYVTK			Carbamidomethyl (C)[10]
2169.0684	2169.0642	-0.0042	-2	533	552	NLHQSGFSLSGAQIDDNIPR	24	0	
2169.0684	2169.0642	-0.0042	-2	533	552	NLHQSGFSLSGAQIDDNIPR			
2182.9055	2182.9053	-0.0002	0	76	94	FQMPDQGMTSADDFFQGTK			Oxidation (M)[3,8]
2182.9055	2182.9053	-0.0002	0	76	94	FQMPDQGMTSADDFFQGTK			Oxidation (M)[3,8]
2377.1741	2377.2197	0.0456	19	190	211	DIGAIAQVHAENGDIIAEEQQR	31	76.465	
2377.1741	2377.2197	0.0456	19	190	211	DIGAIAQVHAENGDIIAEEQQR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Similar to Dihydropyrimidinase related prote	rf|XP_341343.1	17	264	100	138	100	36	89.58	36.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
813.4213	813.4432	0.0219	27	159	165	TIEAHSR			
908.4988	908.5106	0.0118	13	564	570	VFNLYPR	36	89.58	
908.4988	908.5106	0.0118	13	564	570	VFNLYPR			
1015.553	1015.5703	0.0173	17	432	441	SAAEVIAQAR	17	0	
1015.553	1015.5703	0.0173	17	432	441	SAAEVIAQAR			
1140.6088	1140.6245	0.0157	14	645	653	KPFPDFVYK			

1140.6088	1140.6245	0.0157	14	645	653	KPFPDFVYK			
1262.6296	1262.6533	0.0237	19	320	330	GIQEEMEALVK			Oxidation (M)[6]
1310.6885	1310.7009	0.0124	9	166	177	MVIPGGIDVHTR			Oxidation (M)[1]
1310.6885	1310.7009	0.0124	9	166	177	MVIPGGIDVHTR			Oxidation (M)[1]
1323.7631	1323.7594	-0.0037	-3	146	158	QIGENLIVPGGVK			
1323.7631	1323.7594	-0.0037	-3	146	158	QIGENLIVPGGVK			
1385.5977	1385.7294	0.1317	95	83	92	HLCEEFTMFR			Oxidation (M)[8]
1385.5977	1385.7294	0.1317	95	83	92	HLCEEFTMFR			Carbamidomethyl (C)[3]
1643.7886	1643.9052	0.1166	71	331	344	DHGVNSFLVYMAFK			Oxidation (M)[11]
1682.8707	1682.892	0.0213	13	625	640	IVLEDGTLHVTEGSGR	25	0	
1682.8707	1682.892	0.0213	13	625	640	IVLEDGTLHVTEGSGR			
1741.8062	1741.8083	0.0021	1	548	563	MDENQFVAVTSTNAAK			Oxidation (M)[1]
1792.8348	1792.8491	0.0143	8	519	534	DNFTLIPEGTNGTEER	30	63.115	
1792.8348	1792.8491	0.0143	8	519	534	DNFTLIPEGTNGTEER			
1822.9368	1822.9285	-0.0083	-5	412	427	SITIANQTNCPLYVTK			Carbamidomethyl (C)[10]
2169.0684	2169.0769	0.0085	4	706	725	NLHQSGFSLSGAQIDDNIPR			
2169.1484	2169.0769	-0.0715	-33	62	80	FQTMIVVAEVQSSFRASIR			
2182.9055	2182.9023	-0.0032	-1	178	196	FQMPDQGMTSADDFFQGTK			Oxidation (M)[3,8]
2377.1741	2377.1692	-0.0049	-2	363	384	DIGAIAQVHAENGDIIAEEQQR			
2377.1741	2377.1692	-0.0049	-2	363	384	DIGAIAQVHAENGDIIAEEQQR	30	57.258	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Unnamed protein product	emb|CAA37654.1	11	170	100	73	99.998	54	99.844	25.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
833.39	833.3958	0.0058	7	276	283	APGFGDNR	9	0	
833.39	833.3958	0.0058	7	276	283	APGFGDNR			
855.4682	855.4788	0.0106	12	108	115	GANPVEIR			
855.4682	855.4788	0.0106	12	108	115	GANPVEIR	4	0	
960.5109	960.5321	0.0212	22	395	403	VTDALNATR			
960.5109	960.5321	0.0212	22	395	403	VTDALNATR	19	0	
961.4849	961.5207	0.0358	37	276	284	APGFGDNRK			
961.4849	961.5207	0.0358	37	276	284	APGFGDNRK			
1215.658	1215.6681	0.0101	8	456	467	NAGVEGSLIVEK			
1520.7512	1520.7644	0.0132	9	180	192	TLNDELEIIEGMK			Oxidation (M)[12]
1520.7512	1520.7644	0.0132	9	180	192	TLNDELEIIEGMK			Oxidation (M)[12]
1684.905	1684.9344	0.0294	17	404	420	AAVEEGIVLGGGCALLR			Carbamidomethyl (C)[13]
1684.905	1684.9344	0.0294	17	404	420	AAVEEGIVLGGGCALLR			Carbamidomethyl (C)[13]
1798.9004	1798.9076	0.0072	4	421	436	CIPALDSLKPANEDQK			Carbamidomethyl (C)[1]
1798.9004	1798.9076	0.0072	4	421	436	CIPALDSLKPANEDQK			Carbamidomethyl (C)[1]
1905.0552	1905.0831	0.0279	15	225	242	ISSVQSIVPALEIANAHR			
1905.0552	1905.0831	0.0279	15	225	242	ISSVQSIVPALEIANAHR			
2040.002	2040	-0.002	-1	345	361	IQEITEQLDITTSEYEK			
2040.002	2040	-0.002	-1	345	361	IQEITEQLDITTSEYEK			
2560.2485	2560.2192	-0.0293	-11	71	95	LVQDVANNTNEEAGDGTTTATVLAR	54	99.844	
2560.2485	2560.2192	-0.0293	-11	71	95	LVQDVANNTNEEAGDGTTTATVLAR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Protein disulfide isomerase A3 precursor	spt|P11598	7	84	99.988	8	0	8	0	15.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
Calc. Mass	877.5094	0.0204	23	297	304	LNFAVASR			
995.5632	995.5892	0.026	26	131	140	QAGPASVPLR			
995.5632	995.5892	0.026	26	131	140	QAGPASVPLR			
1188.5354	1188.5471	0.0117	10	336	344	FVMQEEFSR			Oxidation (M)[3]
1188.5354	1188.5471	0.0117	10	336	344	FVMQEEFSR			Oxidation (M)[3]

1191.6005	1191.6256	0.0251	21	63	73	LAPEYEAAATR			
1191.6005	1191.6256	0.0251	21	63	73	LAPEYEAAATR			
1236.5127	1236.5421	0.0294	24	108	119	DGEEAGAYDGPR			
1236.5127	1236.5421	0.0294	24	108	119	DGEEAGAYDGPR	8	0	
1396.6954	1396.6975	0.0021	2	367	379	SEPIPETNEGPVK			
1593.8483	1593.8623	0.014	9	483	496	EATNPPIIQEEKPK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Protein disulfide isomerase A3 precursor	spt|P11598	8	108	100	40	97.354	21	0	18.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
877.489	877.4795	-0.0095	-11	297	304	LNFAVASR			
877.489	877.4795	-0.0095	-11	297	304	LNFAVASR			
995.5632	995.5597	-0.0035	-4	131	140	QAGPASVPLR	10	0	
995.5632	995.5597	-0.0035	-4	131	140	QAGPASVPLR			
1188.5354	1188.5244	-0.011	-9	336	344	FVMQEEFSR			Oxidation (M)[3]
1188.5354	1188.5244	-0.011	-9	336	344	FVMQEEFSR			Oxidation (M)[3]
1191.6005	1191.5995	-0.001	-1	63	73	LAPEYEAAATR	19	0	
1191.6005	1191.5995	-0.001	-1	63	73	LAPEYEAAATR			
1236.5127	1236.52	0.0073	6	108	119	DGEEAGAYDGPR	21	0	
1236.5127	1236.52	0.0073	6	108	119	DGEEAGAYDGPR			
1396.6954	1396.6801	-0.0153	-11	367	379	SEPIPETNEGPVK			
1396.6954	1396.6801	-0.0153	-11	367	379	SEPIPETNEGPVK			
1593.8483	1593.8329	-0.0154	-10	483	496	EATNPPIIQEEKPK			
1593.8483	1593.8329	-0.0154	-10	483	496	EATNPPIIQEEKPK			
1652.7472	1652.7111	-0.0361	-22	434	448	MDATANDVPSPYEVK			Oxidation (M)[1]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Protein disulfide isomerase A3 precursor	spt|P11598	16	266	100	87	100	33	81.583	32.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
877.489	877.4428	-0.0462	-53	297	304	LNFAVASR			
877.489	877.4428	-0.0462	-53	297	304	LNFAVASR	16	0	
995.5632	995.537	-0.0262	-26	131	140	QAGPASVPLR	10	0	
995.5632	995.537	-0.0262	-26	131	140	QAGPASVPLR			
997.5101	997.5075	-0.0026	-3	153	161	DASVVGFFR	8	0	
997.5101	997.5075	-0.0026	-3	153	161	DASVVGFFR			
1188.5354	1188.5184	-0.017	-14	336	344	FVMQEEFSR			Oxidation (M)[3]
1188.5354	1188.5184	-0.017	-14	336	344	FVMQEEFSR	1	0	Oxidation (M)[3]
1191.6005	1191.5948	-0.0057	-5	63	73	LAPEYEAAATR			
1191.6005	1191.5948	-0.0057	-5	63	73	LAPEYEAAATR	33	81.583	
1236.5127	1236.514	0.0013	1	108	119	DGEEAGAYDGPR			
1236.5127	1236.514	0.0013	1	108	119	DGEEAGAYDGPR	26	0	
1244.6633	1244.6436	-0.0197	-16	184	194	FAHTNVESLVK			
1244.6633	1244.6436	-0.0197	-16	184	194	FAHTNVESLVK			
1373.6736	1373.6689	-0.0047	-3	352	362	FLQEYFDGNLK			
1373.6736	1373.6689	-0.0047	-3	352	362	FLQEYFDGNLK			
1394.6587	1394.6573	-0.0014	-1	162	173	DLFSDGHSEFLK			
1396.6954	1396.6891	-0.0063	-5	367	379	SEPIPETNEGPVK			
1396.6954	1396.6891	-0.0063	-5	367	379	SEPIPETNEGPVK			
1397.5784	1397.698	0.1196	86	83	94	VDCTANTNTCNK			Carbamidomethyl (C)[3,10]
1397.7059	1397.698	-0.0079	-6	472	482	ELNDFISYLQR			
1529.7747	1529.7203	-0.0544	-36	352	363	FLQEYFDGNLKR			
1529.7747	1529.7203	-0.0544	-36	352	363	FLQEYFDGNLKR			
1593.8483	1593.8483	0	0	483	496	EATNPPIIQEEKPK			
1593.8483	1593.8483	0	0	483	496	EATNPPIIQEEKPK			

1652.7472	1652.7423	-0.0049	-3	434	448	MDATANDVPSPYEVK			Oxidation (M)[1]
1652.7662	1652.7423	-0.0239	-14	105	119	IFRDGEEAGAYDGPR	13	0	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Guanosine diphosphate dissociation inhibito	rf|NP_058784.1	14	244	100	120	100	36	95.079	33.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
938.4941	938.5244	0.0303	32	211	218	LYSESLAR	36	95.079	
938.4941	938.5244	0.0303	32	211	218	LYSESLAR			
1027.5458	1027.5732	0.0274	27	104	112	VVEGSFVYK			
1027.5458	1027.5732	0.0274	27	104	112	VVEGSFVYK			
1136.6133	1136.6481	0.0348	31	80	89	FLMANGQLVK			Oxidation (M)[3]
1141.5922	1141.6165	0.0243	21	90	98	MLLYTEVTR			Oxidation (M)[1]
1141.5922	1141.6165	0.0243	21	90	98	MLLYTEVTR	2	0	Oxidation (M)[1]
1250.5647	1250.5983	0.0336	27	437	447	KQNDVFGEADQ			
1379.5605	1379.5858	0.0253	18	424	435	MAGSAFDFENMK			Oxidation (M)[1,11]
1460.7202	1460.7483	0.0281	19	56	68	FQLLEGPPESMGR			
1476.7152	1476.7488	0.0336	23	279	290	QLICDPSYIPDR			Carbamidomethyl (C)[4]
1476.7152	1476.7488	0.0336	23	279	290	QLICDPSYIPDR	20	0	Carbamidomethyl (C)[4]
1484.6686	1484.6938	0.0252	17	157	169	TFEGVDPQTTSMR			Oxidation (M)[12]
1484.6686	1484.6938	0.0252	17	157	169	TFEGVDPQTTSMR			Oxidation (M)[12]
1535.6617	1535.6849	0.0232	15	424	436	MAGSAFDFENMKR	6	0	Oxidation (M)[1,11]
1535.6617	1535.6849	0.0232	15	424	436	MAGSAFDFENMKR			Oxidation (M)[1,11]
1722.8796	1722.9043	0.0247	14	349	364	YIAIASTTVETAEPEK			
1722.916	1722.9043	-0.0117	-7	365	379	EVEPALELLEPIDQK			
1852.8383	1852.8812	0.0429	23	194	208	TDDYLDQPCLETINR	30	77.35	Carbamidomethyl (C)[9]
1852.8383	1852.8812	0.0429	23	194	208	TDDYLDQPCLETINR			Carbamidomethyl (C)[9]
2199.0571	2199.1074	0.0503	23	310	328	NTNDANSCQIIIPQNQVNR			Carbamidomethyl (C)[8]
2199.0571	2199.1074	0.0503	23	310	328	NTNDANSCQIIIPQNQVNR	34	91.833	Carbamidomethyl (C)[8]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
RAB GDP dissociation inhibitor alpha	spt|P50398	18	296	100	140	100	35	91.74	42.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
938.4941	938.4952	0.0011	1	211	218	LYSESLAR	32	85.941	
938.4941	938.4952	0.0011	1	211	218	LYSESLAR			
1027.5458	1027.5322	-0.0136	-13	104	112	VVEGSFVYK			
1027.5458	1027.5322	-0.0136	-13	104	112	VVEGSFVYK	24	0	
1136.6133	1136.5911	-0.0222	-20	80	89	FLMANGQLVK			Oxidation (M)[3]
1136.6133	1136.5911	-0.0222	-20	80	89	FLMANGQLVK			Oxidation (M)[3]
1141.5922	1141.5731	-0.0191	-17	90	98	MLLYTEVTR			Oxidation (M)[1]
1141.5922	1141.5731	-0.0191	-17	90	98	MLLYTEVTR	3	0	Oxidation (M)[1]
1250.5647	1250.5435	-0.0212	-17	437	447	KQNDVFGEADQ			
1250.5647	1250.5435	-0.0212	-17	437	447	KQNDVFGEADQ			
1476.7151	1476.6958	-0.0193	-13	56	68	FQLLEGPPESMGR			Oxidation (M)[11]
1476.7152	1476.6958	-0.0194	-13	279	290	QLICDPSYIPDR	21	0	Carbamidomethyl (C)[4]
1484.6686	1484.6403	-0.0283	-19	157	169	TFEGVDPQTTSMR			Oxidation (M)[12]
1484.6686	1484.6403	-0.0283	-19	157	169	TFEGVDPQTTSMR			Oxidation (M)[12]
1535.6617	1535.6304	-0.0313	-20	423	435	RMAGSAFDFENMK			Oxidation (M)[2,12]
1535.6617	1535.6304	-0.0313	-20	424	436	MAGSAFDFENMKR			Oxidation (M)[1,11]
1654.8112	1654.7833	-0.0279	-17	143	156	FLVFVANFDENDPK			
1722.8796	1722.8535	-0.0261	-15	349	364	YIAIASTTVETAEPEK			
1722.8796	1722.8535	-0.0261	-15	349	364	YIAIASTTVETAEPEK			
1791.9349	1791.7239	-0.211	-118	90	103	MLLYTEVTRYLDFK			
1852.8383	1852.8303	-0.008	-4	194	208	TDDYLDQPCLETINR	29	69.028	Carbamidomethyl (C)[9]
1852.8383	1852.8303	-0.008	-4	194	208	TDDYLDQPCLETINR			Carbamidomethyl (C)[9]

2086.967	2086.9583	-0.0087	-4	119	137	VPSTETEALASNLMGMFEK			Oxidation (M)[14,16]
2086.967	2086.9583	-0.0087	-4	119	137	VPSTETEALASNLMGMFEK			Oxidation (M)[14,16]
2147.0178	2147.011	-0.0068	-3	36	54	NPYYGGESSSITPLEELYK			
2147.0178	2147.011	-0.0068	-3	36	54	NPYYGGESSSITPLEELYK			
2199.0571	2199.0669	0.0098	4	310	328	NTNDANSCQIIIPQNQVNR	35	91.74	Carbamidomethyl (C)[8]
2199.0571	2199.0669	0.0098	4	310	328	NTNDANSCQIIIPQNQVNR			Carbamidomethyl (C)[8]
2271.0896	2271.0923	0.0027	1	329	348	KSDIYVCMISYAHNVAAQGK			Carbamidomethyl (C)[7]
2271.0896	2271.0923	0.0027	1	329	348	KSDIYVCMISYAHNVAAQGK			Oxidation (M)[8]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Unnamed protein product	emb|CAA37654.1	8	138	100	53	99.827	38	95.325	20.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
833.39	833.4198	0.0298	36	276	283	APGFGDNR	14	0	
833.39	833.4198	0.0298	36	276	283	APGFGDNR			
855.4682	855.4999	0.0317	37	108	115	GANPVEIR	12	0	
855.4682	855.4999	0.0317	37	108	115	GANPVEIR			
960.5109	960.5518	0.0409	43	395	403	VTDALNATR			
960.5109	960.5518	0.0409	43	395	403	VTDALNATR			
1684.905	1684.9502	0.0452	27	404	420	AAVEEGIVLGGGCALLR			Carbamidomethyl (C)[13]
1684.905	1684.9502	0.0452	27	404	420	AAVEEGIVLGGGCALLR			Carbamidomethyl (C)[13]
1798.9004	1798.9209	0.0205	11	421	436	CIPALDSLKPANEDQK			Carbamidomethyl (C)[1]
1798.9004	1798.9209	0.0205	11	421	436	CIPALDSLKPANEDQK			Carbamidomethyl (C)[1]
1905.0552	1905.1051	0.0499	26	225	242	ISSVQSIVPALEIANAHR			
1905.0552	1905.1051	0.0499	26	225	242	ISSVQSIVPALEIANAHR			
2040.002	2040.0284	0.0264	13	345	361	IQEITEQLDITTSEYEK			
2040.002	2040.0284	0.0264	13	345	361	IQEITEQLDITTSEYEK			
2560.2485	2560.3022	0.0537	21	71	95	LVQDVANNTNEEAGDGTTTATVLAR			
2560.2485	2560.3022	0.0537	21	71	95	LVQDVANNTNEEAGDGTTTATVLAR	38	95.325	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Unnamed protein product	emb|CAA37654.1	9	138	100	24	0	24	0	20.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
833.39	833.3965	0.0065	8	276	283	APGFGDNR	10	0	
833.39	833.3965	0.0065	8	276	283	APGFGDNR			
855.4682	855.4759	0.0077	9	108	115	GANPVEIR			
855.4682	855.4759	0.0077	9	108	115	GANPVEIR	4	0	
960.5109	960.524	0.0131	14	395	403	VTDALNATR			
960.5109	960.524	0.0131	14	395	403	VTDALNATR			
961.4849	961.5095	0.0246	26	276	284	APGFGDNRK			
1684.905	1684.9135	0.0085	5	404	420	AAVEEGIVLGGGCALLR			Carbamidomethyl (C)[13]
1798.9004	1798.8812	-0.0192	-11	421	436	CIPALDSLKPANEDQK			Carbamidomethyl (C)[1]
1905.0552	1905.0764	0.0212	11	225	242	ISSVQSIVPALEIANAHR			
1905.0552	1905.0764	0.0212	11	225	242	ISSVQSIVPALEIANAHR			
2040.002	2040.0042	0.0022	1	345	361	IQEITEQLDITTSEYEK			
2040.002	2040.0042	0.0022	1	345	361	IQEITEQLDITTSEYEK			
2560.2485	2560.2559	0.0074	3	71	95	LVQDVANNTNEEAGDGTTTATVLAR			
2560.2485	2560.2559	0.0074	3	71	95	LVQDVANNTNEEAGDGTTTATVLAR	24	0	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Dihydropyrimidinase related protein-2 (DRP	spt|P47942	7	129	100	63	99.984	27	32.073	14.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
813.4213	813.4661	0.0448	55	57	63	TIEAHSR			

908.4988	908.528	0.0292	32	391	397	VFNLYPR	27	32.073	
908.4988	908.528	0.0292	32	391	397	VFNLYPR			
1015.553	1015.5897	0.0367	36	259	268	SAAEVIAQAR	22	0	
1015.553	1015.5897	0.0367	36	259	268	SAAEVIAQAR			
1310.6885	1310.7214	0.0329	25	64	75	MVIPGGIDVHTR			Oxidation (M)[1]
1310.6885	1310.7214	0.0329	25	64	75	MVIPGGIDVHTR			Oxidation (M)[1]
1682.8707	1682.9238	0.0531	32	452	467	IVLEDGTLHVTEGSGR			
1682.8707	1682.9238	0.0531	32	452	467	IVLEDGTLHVTEGSGR	4	0	
1741.8062	1741.8464	0.0402	23	375	390	MDENQFVAVTSTNAAK			Oxidation (M)[1]
1792.8348	1792.8777	0.0429	24	346	361	DNFTLIPEGTNGTEER	15	0	
1792.8348	1792.8777	0.0429	24	346	361	DNFTLIPEGTNGTEER			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Mitochondrial aldehyde dehydrogenase (Fra	trm|Q8K3V8	6	69	99.633	14	0	14	0	16.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
829.4777	829.451	-0.0267	-32	79	85	LADLIER			
902.4941	902.4804	-0.0137	-15	400	407	TIEEVVGR	9	0	
902.4941	902.4804	-0.0137	-15	400	407	TIEEVVGR			
990.5002	990.5001	-0.0001	0	318	326	VVGNPFDSR			
990.5002	990.5001	-0.0001	0	318	326	VVGNPFDSR	14	0	
1470.7627	1470.6606	-0.1021	-69	366	378	GYFIQPTVFGDVK			
1470.7627	1470.6606	-0.1021	-69	366	378	GYFIQPTVFGDVK			
1506.707	1506.7119	0.0049	3	327	339	TEQGPQVDETQFK			
1506.707	1506.7119	0.0049	3	327	339	TEQGPQVDETQFK			
3210.8169	3210.5295	-0.2874	-90	167	197	LGPALATGNVVVMKVAEQTPLTALYVANLIK			Oxidation (M)[13]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
ATPase, H transporting, lysosomal V1 subu	gi|16758754	16	365	100	200	100	57	99.919	35.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
873.4788	873.5059	0.0271	31	30	37	EQALAVSR			
873.4788	873.5059	0.0271	31	30	37	EQALAVSR	3	0	
877.4526	877.4846	0.032	36	38	44	NYLSQPR			
877.4526	877.4846	0.032	36	38	44	NYLSQPR	33	79.614	
937.4407	937.47	0.0293	31	404	412	SAIGEGMTR			Oxidation (M)[7]
1120.5303	1120.5637	0.0334	30	121	130	TPVSEDMLGR			Oxidation (M)[7]
1120.5303	1120.5637	0.0334	30	121	130	TPVSEDMLGR	23	0	Oxidation (M)[7]
1189.6323	1189.6775	0.0452	38	131	141	VFNGSGKPIDR			
1189.6323	1189.6775	0.0452	38	131	141	VFNGSGKPIDR	33	80.887	
1298.6045	1298.6547	0.0502	39	110	120	TSCEFTGDILR	25	0	Carbamidomethyl (C)[3]
1298.6045	1298.6547	0.0502	39	110	120	TSCEFTGDILR			Carbamidomethyl (C)[3]
1338.6437	1338.6945	0.0508	38	461	471	NFITQGPYENR	57	99.919	
1338.6437	1338.6945	0.0508	38	461	471	NFITQGPYENR			
1437.7373	1437.7911	0.0538	37	495	506	IPQSTLSEFYPR			
1437.7373	1437.7911	0.0538	37	495	506	IPQSTLSEFYPR	29	53.938	
1520.7954	1520.83	0.0346	23	94	108	AVVQVFEGTSGIDAK			
1556.8319	1556.8645	0.0326	21	68	81	YAEIVHLTLPDGTK			
1556.8319	1556.8645	0.0326	21	68	81	YAEIVHLTLPDGTK			
1593.8384	1593.8885	0.0501	31	494	506	RIPQSTLSEFYPR			
1593.8384	1593.8885	0.0501	31	494	506	RIPQSTLSEFYPR			
1596.9108	1596.96	0.0492	31	387	400	QIYPPINVLPSLSR			
1596.9108	1596.96	0.0492	31	387	400	QIYPPINVLPSLSR			
1712.933	1712.9806	0.0476	28	68	82	YAEIVHLTLPDGTKR			
2048.0593	2048.1025	0.0432	21	8	29	GIVNGAAPELPVPTGGPMAGAR			Oxidation (M)[18]
2052.9849	2053.0608	0.0759	37	321	337	RGFPGYMYTDLATIYER			

2384.1221	2384.0217	-0.1004	-42	110	130	TSCEFTGDILRTPVSEDMLGR			Carbamidomethyl (C)[3]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
ATPase, H transporting, lysosomal V1 subu	gi|16758754	13	313	100	198	100	53	99.781	31.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
873.4788	873.5077	0.0289	33	30	37	EQALAVSR	4	0	
873.4788	873.5077	0.0289	33	30	37	EQALAVSR			
877.4526	877.4839	0.0313	36	38	44	NYLSQPR			
877.4526	877.4839	0.0313	36	38	44	NYLSQPR	38	93.081	
937.4407	937.4719	0.0312	33	404	412	SAIGEGMTR			Oxidation (M)[7]
937.4407	937.4719	0.0312	33	404	412	SAIGEGMTR			Oxidation (M)[7]
1120.5303	1120.5604	0.0301	27	121	130	TPVSEDMLGR			Oxidation (M)[7]
1120.5303	1120.5604	0.0301	27	121	130	TPVSEDMLGR	14	0	Oxidation (M)[7]
1189.6323	1189.6759	0.0436	37	131	141	VFNGSGKPIDR	31	63.266	
1189.6323	1189.6759	0.0436	37	131	141	VFNGSGKPIDR			
1298.6045	1298.652	0.0475	37	110	120	TSCEFTGDILR			Carbamidomethyl (C)[3]
1338.6437	1338.6924	0.0487	36	461	471	NFITQGPYENR			
1338.6437	1338.6924	0.0487	36	461	471	NFITQGPYENR	53	99.781	
1437.7373	1437.7891	0.0518	36	495	506	IPQSTLSEFYPR	31	61.446	
1437.7373	1437.7891	0.0518	36	495	506	IPQSTLSEFYPR			
1520.7954	1520.8296	0.0342	22	94	108	AVVQVFEGTSGIDAK	30	58.878	
1520.7954	1520.8296	0.0342	22	94	108	AVVQVFEGTSGIDAK			
1556.8319	1556.8612	0.0293	19	68	81	YAEIVHLTLPDGTK			
1593.8384	1593.8843	0.0459	29	494	506	RIPQSTLSEFYPR			
1593.8384	1593.8843	0.0459	29	494	506	RIPQSTLSEFYPR			
1985.1252	1985.1008	-0.0244	-12	387	403	QIYPPINVLPSLSRLMK			Oxidation (M)[16]
1985.1252	1985.1008	-0.0244	-12	387	403	QIYPPINVLPSLSRLMK			Oxidation (M)[16]
2052.9849	2053.0547	0.0698	34	321	337	RGFPGYMYTDLATIYER			
2052.9849	2053.0547	0.0698	34	321	337	RGFPGYMYTDLATIYER			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
ATPase, H transporting, lysosomal V1 subu	gi|16758754	16	389	100	234	100	75	100	29.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
873.4788	873.5006	0.0218	25	30	37	EQALAVSR	21	0	
873.4788	873.5006	0.0218	25	30	37	EQALAVSR			
877.4526	877.4751	0.0225	26	38	44	NYLSQPR	27	61.054	
877.4526	877.4751	0.0225	26	38	44	NYLSQPR			
937.4407	937.4615	0.0208	22	404	412	SAIGEGMTR			Oxidation (M)[7]
1120.5303	1120.5557	0.0254	23	121	130	TPVSEDMLGR			Oxidation (M)[7]
1189.6323	1189.671	0.0387	33	131	141	VFNGSGKPIDR			
1189.6323	1189.671	0.0387	33	131	141	VFNGSGKPIDR	54	99.919	
1298.6045	1298.6458	0.0413	32	110	120	TSCEFTGDILR			Carbamidomethyl (C)[3]
1338.6437	1338.6915	0.0478	36	461	471	NFITQGPYENR	75	100	
1338.6437	1338.6915	0.0478	36	461	471	NFITQGPYENR			
1437.7373	1437.7821	0.0448	31	495	506	IPQSTLSEFYPR	56	99.957	
1437.7373	1437.7821	0.0448	31	495	506	IPQSTLSEFYPR			
1520.7954	1520.8182	0.0228	15	94	108	AVVQVFEGTSGIDAK			
1556.8319	1556.8588	0.0269	17	68	81	YAEIVHLTLPDGTK			
1593.8384	1593.8796	0.0412	26	494	506	RIPQSTLSEFYPR			
1596.9108	1596.9421	0.0313	20	387	400	QIYPPINVLPSLSR			
1712.933	1712.975	0.042	25	68	82	YAEIVHLTLPDGTKR			
1985.1252	1985.0955	-0.0297	-15	387	403	QIYPPINVLPSLSRLMK			Oxidation (M)[16]
2048.0593	2048.0923	0.033	16	8	29	GIVNGAAPELPVPTGGPMAGAR			Oxidation (M)[18]
2384.1221	2383.9868	-0.1353	-57	110	130	TSCEFTGDILRTPVSEDMLGR			Carbamidomethyl (C)[3]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Alpha-enolase	spt|P04764	14	304	100	173	100	70	100	34.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
800.3824	800.4017	0.0193	24	256	261	YDLDFK			
800.3824	800.4017	0.0193	24	256	261	YDLDFK	11	0	
806.4518	806.4669	0.0151	19	406	411	YNQILR	47	99.133	
806.4518	806.4669	0.0151	19	406	411	YNQILR			
810.4468	810.4562	0.0094	12	64	70	AVEHINK			
810.4468	810.4562	0.0094	12	64	70	AVEHINK			
815.4872	815.4864	-0.0008	-1	221	227	EALELLK			
958.5203	958.5419	0.0216	23	81	88	LNVVEQEK			
1086.6154	1086.6361	0.0207	19	80	88	KLNVVEQEK	27	20.787	
1086.6154	1086.6361	0.0207	19	80	88	KLNVVEQEK			
1143.6156	1143.6345	0.0189	17	183	192	IGAEVYHNLK	70	99.995	
1143.6156	1143.6345	0.0189	17	183	192	IGAEVYHNLK			
1406.7162	1406.7312	0.015	11	15	27	GNPTVEVDLYTAK			
1406.7162	1406.7312	0.015	11	15	27	GNPTVEVDLYTAK			
1439.7417	1439.7546	0.0129	9	269	280	YITPDQLADLYK			
1557.759	1557.7776	0.0186	12	358	371	LAQSNGWGVMVSHR			Oxidation (M)[10]
1557.759	1557.7776	0.0186	12	358	371	LAQSNGWGVMVSHR	3	0	Oxidation (M)[10]
1633.8214	1633.8322	0.0108	7	343	357	VNQIGSVTESLQACK			Carbamidomethyl (C)[14]
1633.8214	1633.8322	0.0108	7	343	357	VNQIGSVTESLQACK			Carbamidomethyl (C)[14]
1668.7455	1668.7522	0.0067	4	89	102	IDQLMIEMDGTENK	9	0	Oxidation (M)[5,8]
1668.7455	1668.7522	0.0067	4	89	102	IDQLMIEMDGTENK			Oxidation (M)[5,8]
1804.9438	1804.9741	0.0303	17	32	49	AAVPSGASTGIYEALELR			
1804.9438	1804.9741	0.0303	17	32	49	AAVPSGASTGIYEALELR	16	0	
1960.9246	1960.9404	0.0158	8	202	220	DATNVGDEGGFAPNILENK			
1960.9246	1960.9404	0.0158	8	202	220	DATNVGDEGGFAPNILENK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Guanine deaminase	trm|Q9JKB7	12	218	100	89	100	59	99.97	28.0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
885.4352	885.4564	0.0212	24	106	112	YTFPTEK			
909.588	909.5933	0.0053	6	206	213	VKPIVTPR			
909.588	909.5933	0.0053	6	206	213	VKPIVTPR	12	0	
997.5023	997.5223	0.02	20	194	201	FVSEMLQK			Oxidation (M)[5]
998.4941	998.5103	0.0162	16	428	435	FLYLGDDR			
998.4941	998.5103	0.0162	16	428	435	FLYLGDDR	18	0	
1107.568	1107.5625	-0.0055	-5	436	445	NIEEVYVGGK			
1107.568	1107.5625	-0.0055	-5	436	445	NIEEVYVGGK			
1173.6262	1173.6333	0.0071	6	394	403	DFDALLINPR			
1371.759	1371.7794	0.0204	15	371	384	LATLGGSQALGLDR			
1371.759	1371.7794	0.0204	15	371	384	LATLGGSQALGLDR			
1424.6449	1424.7676	0.1227	86	57	66	EWCFKPCEIR			Carbamidomethyl (C)[3,7]
1424.6449	1424.7676	0.1227	86	57	66	EWCFKPCEIR			Carbamidomethyl (C)[3,7]
1436.7267	1436.7267	0	0	42	53	IVFLEESSQQEK			
1544.7227	1544.7362	0.0135	9	114	126	FQSTDVAEEVYTR	59	99.97	
1544.7227	1544.7362	0.0135	9	114	126	FQSTDVAEEVYTR			
1598.7189	1598.7037	-0.0152	-10	169	181	VCMDLNNTVPEYK			Carbamidomethyl (C)[2]
1712.8351	1712.8419	0.0068	4	232	245	THDLYIQSHISENR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage

Guanine deaminase	trm|Q9JKB7	13	265	100	128	100	53	99.8	29.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
885.4352	885.4595	0.0243	27	106	112	YTFPTEK			
909.588	909.5983	0.0103	11	206	213	VKPIVTPR			
909.588	909.5983	0.0103	11	206	213	VKPIVTPR			
997.5023	997.5253	0.023	23	194	201	FVSEMLQK			Oxidation (M)[5]
997.5023	997.5253	0.023	23	194	201	FVSEMLQK			Oxidation (M)[5]
998.4941	998.5149	0.0208	21	428	435	FLYLGDDR	25	0	
998.4941	998.5149	0.0208	21	428	435	FLYLGDDR			
1058.6357	1058.6479	0.0122	12	6	14	TPQLALIFR			
1107.568	1107.5677	-0.0003	0	436	445	NIEEVYVGGK	12	0	
1107.568	1107.5677	-0.0003	0	436	445	NIEEVYVGGK			
1173.6262	1173.6469	0.0207	18	394	403	DFDALLINPR	26	0	
1173.6262	1173.6469	0.0207	18	394	403	DFDALLINPR			
1371.759	1371.7803	0.0213	16	371	384	LATLGGSQALGLDR	12	0	
1371.759	1371.7803	0.0213	16	371	384	LATLGGSQALGLDR			
1436.7267	1436.7289	0.0022	2	42	53	IVFLEESSQQEK			
1436.7267	1436.7289	0.0022	2	42	53	IVFLEESSQQEK	10	0	
1544.7227	1544.7402	0.0175	11	114	126	FQSTDVAEEVYTR	53	99.8	
1544.7227	1544.7402	0.0175	11	114	126	FQSTDVAEEVYTR			
1598.7189	1598.7087	-0.0102	-6	169	181	VCMDLNNTVPEYK			Oxidation (M)[3]
1712.8351	1712.853	0.0179	10	232	245	THDLYIQSHISENR			
1712.8351	1712.853	0.0179	10	232	245	THDLYIQSHISENR			
1814.892	1814.8871	-0.0049	-3	260	274	NYTDVYDKNNLLTNK			
1814.892	1814.8871	-0.0049	-3	260	274	NYTDVYDKNNLLTNK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Guanosine diphosphate dissociation inhibit	cra|rCP13240.1	11	118	100	14	0	14	0	26.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
938.4941	938.516	0.0219	23	211	218	LYSESLAR			
938.4941	938.516	0.0219	23	211	218	LYSESLAR			
1126.5674	1126.5741	0.0067	6	58	68	LPGQPPASMGR			Oxidation (M)[9]
1126.5674	1126.5741	0.0067	6	58	68	LPGQPPASMGR			Oxidation (M)[9]
1323.6949	1323.6938	-0.0011	-1	58	70	LPGQPPASMGRGR			
1351.6852	1351.6991	0.0139	10	391	402	DLGTDSQIFISR			
1351.6852	1351.6991	0.0139	10	391	402	DLGTDSQIFISR			
1401.7307	1401.7334	0.0027	2	56	68	FKLPGQPPASMGR			Oxidation (M)[11]
1401.7307	1401.7334	0.0027	2	56	68	FKLPGQPPASMGR	14	0	Oxidation (M)[11]
1493.7417	1493.7529	0.0112	7	279	290	QLICDPSYVKDR			Carbamidomethyl (C)[4]
1493.7417	1493.7529	0.0112	7	279	290	QLICDPSYVKDR			Carbamidomethyl (C)[4]
1638.6774	1638.6731	-0.0043	-3	423	435	RMTGSEFDFEEMK			Oxidation (M)[2,12]
1638.6774	1638.6731	-0.0043	-3	424	436	MTGSEFDFEEMKR			Oxidation (M)[1,11]
1899.7848	1899.7953	0.0105	6	194	208	TDDYLDQPCCETINR			Carbamidomethyl (C)[9,10]
2199.0571	2199.0649	0.0078	4	310	328	NTNDANSCQIIIPQNQVNR			Carbamidomethyl (C)[8]
2199.0571	2199.0649	0.0078	4	310	328	NTNDANSCQIIIPQNQVNR			Carbamidomethyl (C)[8]
2384.2417	2383.9634	-0.2783	-117	116	137	IYKVPSTEAEALASSLMGLFEK			
2384.2417	2383.9634	-0.2783	-117	116	137	IYKVPSTEAEALASSLMGLFEK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Similar to translation initiation factor eIF-4A	rf|XP_221325.2	8	97	100	16	0	16	0	19.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
831.4107	831.4429	0.0322	39	355	360	ENYIHR			
831.4107	831.4429	0.0322	39	355	360	ENYIHR			

910.4451	910.4615	0.0164	18	163	169	VFDMLNR			Oxidation (M)[4]
910.4451	910.4615	0.0164	18	163	169	VFDMLNR			Oxidation (M)[4]
1066.5463	1066.5662	0.0199	19	163	170	VFDMLNRR			Oxidation (M)[4]
1068.5472	1068.5743	0.0271	25	249	256	QFYINVER			
1068.5472	1068.5743	0.0271	25	249	256	QFYINVER			
1394.691	1394.7031	0.0121	9	70	83	GYDVIAQAQSGTGK			
1394.691	1394.7031	0.0121	9	70	83	GYDVIAQAQSGTGK			
1544.8544	1544.8807	0.0263	17	148	162	LQAEAPHIVVGTPGR	16	0	
1544.8544	1544.8807	0.0263	17	148	162	LQAEAPHIVVGTPGR			
1579.7057	1579.701	-0.0047	-3	297	310	DFTVSALHGDMDQK			Oxidation (M)[11]
1827.9387	1827.9645	0.0258	14	47	62	GIYAYGFEKPSAIQQR			
1827.9387	1827.9645	0.0258	14	47	62	GIYAYGFEKPSAIQQR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Guanine deaminase	trm|Q9JKB7	6	120	100	51	99.727	36	91.9	14.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
998.4941	998.5274	0.0333	33	428	435	FLYLGDDR	15	0	
998.4941	998.5274	0.0333	33	428	435	FLYLGDDR			
1107.568	1107.5858	0.0178	16	436	445	NIEEVYVGGK			
1371.759	1371.785	0.026	19	371	384	LATLGGSQALGLDR			
1371.759	1371.785	0.026	19	371	384	LATLGGSQALGLDR			
1424.6449	1424.7695	0.1246	87	57	66	EWCFKPCEIR			Carbamidomethyl (C)[3,7]
1436.7267	1436.7412	0.0145	10	42	53	IVFLEESSQQEK			
1436.7267	1436.7412	0.0145	10	42	53	IVFLEESSQQEK			
1544.7227	1544.751	0.0283	18	114	126	FQSTDVAEEVYTR			
1544.7227	1544.751	0.0283	18	114	126	FQSTDVAEEVYTR	36	91.9	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Creatine kinase	gb|AAA40932.1	12	322	100	221	100	66	99.992	38.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1031.5554	1031.5774	0.022	21	359	366	LLIEMEQR			
1047.5503	1047.5715	0.0212	20	359	366	LLIEMEQR	24	0	Oxidation (M)[5]
1047.5503	1047.5715	0.0212	20	359	366	LLIEMEQR			Oxidation (M)[5]
1159.5491	1159.5751	0.026	22	2	11	PFSNSHNTQK			
1159.5491	1159.5751	0.026	22	2	11	PFSNSHNTQK			
1230.5507	1230.5891	0.0384	31	139	148	GFCLPPHCSR			Carbamidomethyl (C)[3,8]
1230.5507	1230.5891	0.0384	31	139	148	GFCLPPHCSR	18	0	Carbamidomethyl (C)[3,8]
1232.6157	1232.6265	0.0108	9	87	96	DLFDPIIEDR	14	0	
1232.6157	1232.6265	0.0108	9	87	96	DLFDPIIEDR			
1254.5498	1254.5713	0.0215	17	97	107	HGGYQPSDEHK			
1254.5498	1254.5713	0.0215	17	97	107	HGGYQPSDEHK	11	0	
1303.7256	1303.7584	0.0328	25	33	43	VLTPELYAELR	29	57.511	
1303.7256	1303.7584	0.0328	25	33	43	VLTPELYAELR			
1602.8334	1602.848	0.0146	9	157	172	LAVEALSSLDGDLSGR			
1698.8367	1698.8489	0.0122	7	367	381	LEQGQPIDDLMPAQK	58	99.95	Oxidation (M)[11]
1698.8367	1698.8489	0.0122	7	367	381	LEQGQPIDDLMPAQK			Oxidation (M)[11]
1964.9308	1964.9641	0.0333	17	321	341	GTGGVDTAAVGGVFDVSNADR			
1964.9308	1964.9641	0.0333	17	321	341	GTGGVDTAAVGGVFDVSNADR	66	99.992	
2121.0317	2121.052	0.0203	10	320	341	RGTGGVDTAAVGGVFDVSNADR	2	0	
2121.0317	2121.052	0.0203	10	320	341	RGTGGVDTAAVGGVFDVSNADR			
2201.9556	2201.9763	0.0207	9	14	32	FPAEDEFPDLSSHNNHMAK			Oxidation (M)[17]
2518.1692	2518.1792	0.01	4	108	130	TDLNPDNLQGGDDLDPNYVLSSR			
2518.1692	2518.1792	0.01	4	108	130	TDLNPDNLQGGDDLDPNYVLSSR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
NAD+-specific isocitrate dehydrogenase a-s	trm|Q99NA5	9	155	100	68	99.997	29	75.65	26.0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1028.516	1028.5249	0.0089	9	59	66	APIQWEER	29	75.65	
1028.516	1028.5249	0.0089	9	59	66	APIQWEER			
1041.5687	1041.5568	-0.0119	-11	67	77	NVTAIQGPGGK			
1054.5238	1054.5187	-0.0051	-5	206	214	MSDGLFLQK			Oxidation (M)[1]
1123.5817	1123.5795	-0.0022	-2	327	336	IEAACFATIK			Carbamidomethyl (C)[5]
1126.5463	1126.5609	0.0146	13	317	326	HMGLFDHAAK			
1126.5463	1126.5609	0.0146	13	317	326	HMGLFDHAAK			
1142.5411	1142.535	-0.0061	-5	317	326	HMGLFDHAAK			Oxidation (M)[2]
1216.5996	1216.6134	0.0138	11	179	188	IAEFAFEYAR			
1216.5996	1216.6134	0.0138	11	179	188	IAEFAFEYAR	29	72.742	
1316.5245	1316.5311	0.0066	5	351	360	CSDFTEEICR			Carbamidomethyl (C)[1,9]
1391.7529	1391.7576	0.0047	3	135	146	TPYTDVNIVTIR			
1391.7529	1391.7576	0.0047	3	135	146	TPYTDVNIVTIR	10	0	
1606.8734	1606.8694	-0.004	-2	101	115	TPIAAGHPSMNLLLR			Oxidation (M)[10]
1606.8734	1606.8694	-0.004	-2	101	115	TPIAAGHPSMNLLLR			Oxidation (M)[10]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Guanine nucleotide binding protein, alpha o	cra|rCP51914	6	177	100	118	100	70	99.997	13.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
891.4682	891.4983	0.0301	34	198	205	LFDVGGQR			
891.4682	891.4983	0.0301	34	198	205	LFDVGGQR	27	24.242	
1380.7158	1380.744	0.0282	20	181	192	TTGIVETHFTFK			
1380.7158	1380.744	0.0282	20	181	192	TTGIVETHFTFK			
1445.6907	1445.7213	0.0306	21	54	66	IIHEDGFSGEDVK			
1445.6907	1445.7213	0.0306	21	54	66	IIHEDGFSGEDVK	11	0	
1597.8624	1597.7501	-0.1123	-70	258	270	WFTDTSIILFLNK			
1597.8624	1597.7501	-0.1123	-70	258	270	WFTDTSIILFLNK			
1599.7319	1599.7551	0.0232	15	86	99	AMDTLGVEYGDKER			Oxidation (M)[2]
1599.7319	1599.7551	0.0232	15	86	99	AMDTLGVEYGDKER	9	0	Oxidation (M)[2]
1689.8442	1689.8916	0.0474	28	162	176	IGAADYQPTEQDILR	70	99.997	
1689.8442	1689.8916	0.0474	28	162	176	IGAADYQPTEQDILR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Guanine nucleotide binding protein, alpha o	cra|rCP51914	8	253	100	173	100	60	99.967	22.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
891.4682	891.5044	0.0362	41	198	205	LFDVGGQR	47	99.307	
891.4682	891.5044	0.0362	41	198	205	LFDVGGQR			
1314.5883	1314.6199	0.0316	24	86	97	AMDTLGVEYGDK			Oxidation (M)[2]
1314.5883	1314.6199	0.0316	24	86	97	AMDTLGVEYGDK			Oxidation (M)[2]
1380.7158	1380.7542	0.0384	28	181	192	TTGIVETHFTFK			
1380.7158	1380.7542	0.0384	28	181	192	TTGIVETHFTFK			
1445.6907	1445.731	0.0403	28	54	66	IIHEDGFSGEDVK	53	99.843	
1445.6907	1445.731	0.0403	28	54	66	IIHEDGFSGEDVK			
1597.8624	1597.7494	-0.113	-71	258	270	WFTDTSIILFLNK			
1597.8624	1597.7494	-0.113	-71	258	270	WFTDTSIILFLNK			
1599.7319	1599.7639	0.032	20	86	99	AMDTLGVEYGDKER			Oxidation (M)[2]
1599.7319	1599.7639	0.032	20	86	99	AMDTLGVEYGDKER	14	0	Oxidation (M)[2]
1689.8442	1689.8964	0.0522	31	162	176	IGAADYQPTEQDILR			
1689.8442	1689.8964	0.0522	31	162	176	IGAADYQPTEQDILR	60	99.967	

2005.8551	2005.8855	0.0304	15	113	129	MEDTEPFSAELLSAMMR			Oxidation (M)[1,15,16]
2005.8551	2005.8855	0.0304	15	113	129	MEDTEPFSAELLSAMMR			Oxidation (M)[1,15,16]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
NAD+-specific isocitrate dehydrogenase a-s	trm|Q99NA5	6	124	100	72	99.999	33	86.781	17.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1028.516	1028.5465	0.0305	30	59	66	APIQWEER			
1028.516	1028.5465	0.0305	30	59	66	APIQWEER	21	0	
1142.5411	1142.5609	0.0198	17	317	326	HMGLFDHAAK			Oxidation (M)[2]
1216.5996	1216.6373	0.0377	31	179	188	IAEFAFEYAR	33	86.781	
1216.5996	1216.6373	0.0377	31	179	188	IAEFAFEYAR			
1316.5245	1316.5613	0.0368	28	351	360	CSDFTEEICR			Carbamidomethyl (C)[1,9]
1316.5245	1316.5613	0.0368	28	351	360	CSDFTEEICR			Carbamidomethyl (C)[1,9]
1391.7529	1391.7827	0.0298	21	135	146	TPYTDVNIVTIR			
1391.7529	1391.7827	0.0298	21	135	146	TPYTDVNIVTIR	19	0	
1606.8734	1606.896	0.0226	14	101	115	TPIAAGHPSMNLLLR			Oxidation (M)[10]
1606.8734	1606.896	0.0226	14	101	115	TPIAAGHPSMNLLLR			Oxidation (M)[10]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
NG,NG-dimethylarginine dimethylaminohyd	spt|O08557	8	174	100	75	100	34	87.688	32.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
831.4947	831.4919	-0.0028	-3	230	236	GHVLLHR			
929.4509	929.4608	0.0099	11	19	26	APPESLCR			Carbamidomethyl (C)[7]
929.4509	929.4608	0.0099	11	19	26	APPESLCR	10	0	Carbamidomethyl (C)[7]
1137.5171	1137.5289	0.0118	10	32	41	SQGEEVDFAR	34	87.688	
1137.5171	1137.5289	0.0118	10	32	41	SQGEEVDFAR			
1150.5262	1150.5298	0.0036	3	237	246	TPEEYPESAK			
1177.5089	1177.5065	-0.0024	-2	199	207	IMQQMSDHR			Oxidation (M)[2,5]
1177.5089	1177.5065	-0.0024	-2	199	207	IMQQMSDHR	0	0	Oxidation (M)[2,5]
1679.7871	1679.7964	0.0093	6	120	135	DENATLDGGDVLFTGR			
1679.7871	1679.7964	0.0093	6	120	135	DENATLDGGDVLFTGR	31	75.434	
1714.901	1714.8903	-0.0107	-6	159	174	DYAVSTVPVADSLHLK			
1714.901	1714.8903	-0.0107	-6	159	174	DYAVSTVPVADSLHLK			
1868.9786	1868.9707	-0.0079	-4	251	266	LKDHLLIPVSNSEMEK			Oxidation (M)[14]
1868.9786	1868.9707	-0.0079	-4	251	266	LKDHLLIPVSNSEMEK			Oxidation (M)[14]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Unnamed protein product	emb|CAA37654.1	5	80	99.967	27	31.05	27	31.05	19.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
829.4315	829.4695	0.038	46	207	214	GGWGISPR			
951.5118	951.5261	0.0143	15	296	303	GEPHVTRR			
1340.6633	1340.6902	0.0269	20	284	294	YSFLQFDPAPR	27	31.05	
1340.6633	1340.6902	0.0269	20	284	294	YSFLQFDPAPR			
1791.837	1791.8184	-0.0186	-10	122	135	QITQVYGFYDECLR			Carbamidomethyl (C)[12]
1808.7795	1808.7812	0.0017	1	75	89	SPDTNYLFMGDYVDR			Oxidation (M)[9]
1808.7795	1808.7812	0.0017	1	75	89	SPDTNYLFMGDYVDR			Oxidation (M)[9]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Malate dehydrogenase 1, NAD (Soluble)	trm|Q6PCV2	9	194	100	91	100	55	99.858	27.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
803.4257	803.4472	0.0215	27	111	118	SQGAALEK			
803.4257	803.4472	0.0215	27	111	118	SQGAALEK			
811.442	811.4474	0.0054	7	249	255	AISDHIR			
811.442	811.4474	0.0054	7	249	255	AISDHIR	17	0	
917.4938	917.4971	0.0033	4	171	179	LGVTADDVK			
935.4866	935.4933	0.0067	7	311	318	EKMDLTAK			
1026.4673	1026.4871	0.0198	19	150	157	ENFSCLTR			Carbamidomethyl (C)[5]
1026.4673	1026.4871	0.0198	19	150	157	ENFSCLTR			Carbamidomethyl (C)[5]
1178.6165	1178.6331	0.0166	14	221	230	GEFITTVQQR			
1178.6165	1178.6331	0.0166	14	221	230	GEFITTVQQR	55	99.858	
1387.725	1387.7142	-0.0108	-8	80	92	DLDVAVLVGSMPR			Oxidation (M)[11]
1393.7111	1393.7209	0.0098	7	299	310	FVEGLPINDFSR			
1393.7111	1393.7209	0.0098	7	299	310	FVEGLPINDFSR	20	0	
1757.9214	1757.9026	-0.0188	-11	126	142	VIVVGNPANTNCLTASK			Carbamidomethyl (C)[12]
1757.9214	1757.9026	-0.0188	-11	126	142	VIVVGNPANTNCLTASK			Carbamidomethyl (C)[12]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Pyruvate dehydrogenase (Lipoamide) beta	trm|Q6AY95	9	116	100	38	94.48	22	0	27.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
902.5345	902.4565	-0.078	-86	220	227	DFLIPIGK			
902.5345	902.4565	-0.078	-86	220	227	DFLIPIGK			
1255.6892	1255.6935	0.0043	3	337	347	ILEDNSIPQVK			
1255.6892	1255.6935	0.0043	3	337	347	ILEDNSIPQVK			
1432.7511	1432.7002	-0.0509	-36	1	14	MAGVAGLVRGLCGR			Carbamidomethyl (C)[12]
1533.6849	1533.713	0.0281	18	37	49	EAINQGMDEELER	8	0	
1533.6849	1533.713	0.0281	18	37	49	EAINQGMDEELER			
1549.6798	1549.7004	0.0206	13	37	49	EAINQGMDEELER			Oxidation (M)[7]
1549.6798	1549.7004	0.0206	13	37	49	EAINQGMDEELER	22	0	Oxidation (M)[7]
1763.8785	1763.8956	0.0171	10	309	324	IMEGPAFNFLDAPAVR	16	0	Oxidation (M)[2]
1763.8785	1763.8956	0.0171	10	309	324	IMEGPAFNFLDAPAVR			Oxidation (M)[2]
1801.9006	1801.9089	0.0083	5	53	68	VFLLGEEVAQYDGAYK			
1835.9241	1835.9368	0.0127	7	270	285	TIRPMDIEAIEASVMK			Oxidation (M)[5,15]
1835.9241	1835.9368	0.0127	7	270	285	TIRPMDIEAIEASVMK			Oxidation (M)[5,15]
1857.9568	1857.9602	0.0034	2	130	145	TYYMSAGLQPVPIVFR			Oxidation (M)[4]
1857.9568	1857.9602	0.0034	2	130	145	TYYMSAGLQPVPIVFR			Oxidation (M)[4]
1921.8444	1921.8593	0.0149	8	37	52	EAINQGMDEELERDEK			Oxidation (M)[7]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Similar to HSPC263	rf|XP_215178.2	8	120	100	25	0	25	0	29.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
829.4566	829.4819	0.0253	31	103	108	KYSYIR			
829.4566	829.4819	0.0253	31	104	109	YSYIRK			
1050.5942	1050.6223	0.0281	27	202	210	LLTSGYLQR			
1050.5942	1050.6223	0.0281	27	202	210	LLTSGYLQR			
1238.5952	1238.6281	0.0329	27	214	223	FFEHFIEGGR			
1238.5952	1238.6281	0.0329	27	214	223	FFEHFIEGGR	7	0	
1285.5742	1285.6001	0.0259	20	110	119	TRPDGNCFYR	4	0	Carbamidomethyl (C)[7]
1285.5742	1285.6001	0.0259	20	110	119	TRPDGNCFYR			Carbamidomethyl (C)[7]
1515.6598	1515.6704	0.0106	7	85	96	EYAEDDNIYQQK			
1515.6598	1515.6704	0.0106	7	85	96	EYAEDDNIYQQK			
1723.9337	1723.969	0.0353	20	62	76	IQQEIAVQNPLVSER			
1723.9337	1723.969	0.0353	20	62	76	IQQEIAVQNPLVSER	25	0	
1839.8507	1839.8657	0.015	8	264	281	GEGGTTNPHVFPEGSEPK			
1839.8507	1839.8657	0.015	8	264	281	GEGGTTNPHVFPEGSEPK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Guanine nucleotide binding protein, beta po	cra|rCP49190	7	120	100	34	78.756	34	78.756	17.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
804.4509	804.4882	0.0373	46	43	48	IQMRTR			
804.4509	804.4882	0.0373	46	43	48	IQMRTR			
873.4424	873.4664	0.024	27	9	15	QEAEQLR			
873.4424	873.4664	0.024	27	9	15	QEAEQLR			
916.4958	916.5021	0.0063	7	130	137	EGNVRVSR			
916.4958	916.5021	0.0063	7	130	137	EGNVRVSR			
1009.5173	1009.5446	0.0273	27	305	314	AGVLAGHDNR			
1009.5173	1009.5446	0.0273	27	305	314	AGVLAGHDNR	34	78.756	
1352.6052	1352.632	0.0268	20	58	68	IYAMHWGTDSR	12	0	Oxidation (M)[4]
1352.6052	1352.632	0.0268	20	58	68	IYAMHWGTDSR			Oxidation (M)[4]
1384.7291	1384.6259	-0.1032	-75	9	19	QEAEQLRNQIR			
1384.7291	1384.6259	-0.1032	-75	9	19	QEAEQLRNQIR			
1549.6886	1549.7227	0.0341	22	138	150	ELPGHTGYLSCCR			Carbamidomethyl (C)[11,12]
1549.6886	1549.7227	0.0341	22	138	150	ELPGHTGYLSCCR			Carbamidomethyl (C)[11,12]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Similar to Swiprosin 1	rf|XP_216579.2	7	173	100	81	100	42	98.339	29.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1134.663	1134.6572	-0.0058	-5	123	133	LGAPQTHLGLK			
1536.7177	1536.7415	0.0238	15	206	217	FEEEIKAEQEER			
1536.7177	1536.7415	0.0238	15	206	217	FEEEIKAEQEER	13	0	
1558.6577	1558.6595	0.0018	1	134	146	SMIQEVDEDFDSK			Oxidation (M)[2]
1568.7664	1568.7914	0.025	16	62	76	ADLNQGIGEPQSPSR			
1568.7664	1568.7914	0.025	16	62	76	ADLNQGIGEPQSPSR	35	92.215	
1724.8674	1724.8868	0.0194	11	61	76	RADLNQGIGEPQSPSR	42	98.339	
1724.8674	1724.8868	0.0194	11	62	77	ADLNQGIGEPQSPSRR			
1736.8926	1736.9141	0.0215	12	159	175	AAAGELQEDSGLHVLAR			
1736.8926	1736.9141	0.0215	12	159	175	AAAGELQEDSGLHVLAR	4	0	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Annexin A5 (Annexin V)	spt|P14668	12	233	100	76	100	26	15.009	43.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
920.5563	920.5837	0.0274	30	191	198	FITILGTR	18	0	
920.5563	920.5837	0.0274	30	191	198	FITILGTR			
992.5046	992.5358	0.0312	31	48	55	QQIAEEFK			
992.5046	992.5358	0.0312	31	48	55	QQIAEEFK	5	0	
1001.5989	1001.6309	0.032	32	106	114	VLTEIIASR			
1001.5989	1001.6309	0.032	32	106	114	VLTEIIASR	12	0	
1106.584	1106.6169	0.0329	30	274	282	SEIDLFNIR			
1126.5851	1126.5922	0.0071	6	95	105	HALKGAGTDEK			
1126.5851	1126.5922	0.0071	6	95	105	HALKGAGTDEK			
1143.6918	1143.7184	0.0266	23	77	86	LIVALMKPSR			Oxidation (M)[6]
1143.6918	1143.7184	0.0266	23	77	86	LIVALMKPSR			Oxidation (M)[6]
1155.5753	1155.6108	0.0355	31	258	268	GAGTDDHTLIR			
1155.5753	1155.6108	0.0355	31	258	268	GAGTDDHTLIR	20	0	
1172.682	1172.7036	0.0216	18	149	158	MLVVLLQANR			Oxidation (M)[1]
1172.682	1172.7036	0.0216	18	149	158	MLVVLLQANR			Oxidation (M)[1]
1258.5698	1258.6099	0.0401	32	4	15	GTVTDFSGFDGR	26	15.009	

1258.5698	1258.6099	0.0401	32	4	15	GTVTDFSGFDGR			
1424.7202	1424.7902	0.07	49	56	67	TLFGRDLVNDMK			Oxidation (M)[11]
1818.8578	1818.892	0.0342	19	210	224	YMTISGFQIEETIDR			Oxidation (M)[2]
2887.2175	2887.2476	0.0301	10	124	148	QAYEEEYGSNLEDDVVGDTSGYYQR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Guanine nucleotide binding protein, beta po	cra|rCP49190	7	154	100	102	100	62	99.973	17.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
804.4509	804.4944	0.0435	54	43	48	IQMRTR			
804.4509	804.4944	0.0435	54	43	48	IQMRTR			
873.4424	873.4691	0.0267	31	9	15	QEAEQLR			
873.4424	873.4691	0.0267	31	9	15	QEAEQLR	29	54.248	
916.4958	916.5026	0.0068	7	130	137	EGNVRVSR	7	0	
916.4958	916.5026	0.0068	7	130	137	EGNVRVSR			
1009.5173	1009.5516	0.0343	34	305	314	AGVLAGHDNR	62	99.973	
1009.5173	1009.5516	0.0343	34	305	314	AGVLAGHDNR			
1352.6052	1352.6326	0.0274	20	58	68	IYAMHWGTDSR	11	0	Oxidation (M)[4]
1352.6052	1352.6326	0.0274	20	58	68	IYAMHWGTDSR			Oxidation (M)[4]
1384.7291	1384.6261	-0.103	-74	9	19	QEAEQLRNQIR			
1384.7291	1384.6261	-0.103	-74	9	19	QEAEQLRNQIR			
1549.6886	1549.7334	0.0448	29	138	150	ELPGHTGYLSCCR			Carbamidomethyl (C)[11,12]
1549.6886	1549.7334	0.0448	29	138	150	ELPGHTGYLSCCR			Carbamidomethyl (C)[11,12]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Similar to GAS2-related protein	rf|XP_220783.1	7	62	97.984			12	0	4.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1031.5156	1031.6298	0.1142	111	36	43	EDLAEWLR			
1126.6514	1126.5868	-0.0646	-57	246	254	ILRSHVMVR			Oxidation (M)[7]
1126.6514	1126.5868	-0.0646	-57	246	254	ILRSHVMVR			Oxidation (M)[7]
1258.6875	1258.6108	-0.0767	-61	2	12	SQHVGHGRKPR			
1258.7188	1258.6108	-0.108	-86	146	156	SVVLCLLELGR	12	0	Carbamidomethyl (C)[5]
1430.7598	1430.7333	-0.0265	-19	802	817	ATLGGTGGDVNGVGKK			
2384.218	2383.9966	-0.2214	-93	613	634	SQAIPRSGVYVPSLGGMWPEPR			
2717.365	2717.1282	-0.2368	-87	87	111	VQKIPMPQVGVFCNGAAQPGTFQAR			Oxidation (M)[6]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Tyrosine 3-monooxgenase/tryptophan 5-mo	rf|NP_062250.1	6	164	100	123	100	85	100	22.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
816.421	816.4495	0.0285	35	13	19	LAEQAER			
816.421	816.4495	0.0285	35	13	19	LAEQAER	19	0	
903.5145	903.5425	0.028	31	62	69	VISSIEQK			
903.5145	903.5425	0.028	31	62	69	VISSIEQK			
948.4243	948.462	0.0377	40	126	132	MKGDYYR			Oxidation (M)[1]
948.4243	948.462	0.0377	40	126	132	MKGDYYR			Oxidation (M)[1]
1080.5571	1080.5905	0.0334	31	133	142	YLAEVATGEK			
1080.5571	1080.5905	0.0334	31	133	142	YLAEVATGEK	20	0	
1134.5426	1134.578	0.0354	31	153	162	AYSEAHEISK			
1643.7871	1643.8422	0.0551	34	29	42	NVTELNEPLSNEER	85	100	
1643.7871	1643.8422	0.0551	34	29	42	NVTELNEPLSNEER			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage

Similar to RhoGDI-1	rf|XP_340951.1	6	173	100	113	100	46	99.167	33.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
980.4948	980.54	0.0452	46	128	134	YIQHTYR	46	99.167	
980.4948	980.54	0.0452	46	128	134	YIQHTYR			
1261.5518	1261.5953	0.0435	34	142	152	TDYMVGSYGPR			Oxidation (M)[4]
1261.5518	1261.5953	0.0435	34	142	152	TDYMVGSYGPR	16	0	Oxidation (M)[4]
1617.7577	1617.8046	0.0469	29	139	152	IDKTDYMVGSYGPR			Oxidation (M)[7]
1617.7577	1617.8046	0.0469	29	139	152	IDKTDYMVGSYGPR			Oxidation (M)[7]
1650.9174	1650.9772	0.0598	36	59	74	VAVSADPNVPNVIVTR			
1650.9174	1650.9772	0.0598	36	59	74	VAVSADPNVPNVIVTR	35	90.506	
1799.8043	1799.8522	0.0479	27	153	167	AEEYEFLTPMEEAPK	16	0	Oxidation (M)[10]
1799.8043	1799.8522	0.0479	27	153	167	AEEYEFLTPMEEAPK			Oxidation (M)[10]
1917.9399	1918.007	0.0671	35	34	49	SIQEIQELDKDDESLR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Ubiquitin carboxyl-terminal hydrolase isozyn	spt|Q00981	6	96	100	44	99.553	32	91.449	37.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
886.4893	886.5276	0.0383	43	20	27	LGVAGQWR	13	0	
886.4893	886.5276	0.0383	43	20	27	LGVAGQWR			
981.4887	981.5199	0.0312	32	116	123	QFLSETEK			
981.4887	981.5199	0.0312	32	116	123	QFLSETEK			
1484.7955	1484.8298	0.0343	23	66	78	QIEELKGQEVSPK			
1484.7955	1484.8298	0.0343	23	66	78	QIEELKGQEVSPK			
1863.9012	1863.9526	0.0514	28	1	15	MQLKPMEINPEMLNK			Oxidation (M)[1,6,12]
1983.8937	1983.9548	0.0611	31	136	153	NEAIQAAHDSVAQEGQCR	32	91.449	Carbamidomethyl (C)[17]
1983.8937	1983.9548	0.0611	31	136	153	NEAIQAAHDSVAQEGQCR			Carbamidomethyl (C)[17]
2230.0444	2230.0852	0.0408	18	179	199	MPFPVNHGASSEDSLLQDAAK			Oxidation (M)[1]
2230.0444	2230.0852	0.0408	18	179	199	MPFPVNHGASSEDSLLQDAAK			Oxidation (M)[1]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Ubiquitin carboxyl-terminal hydrolase isozyn	spt|Q00981	6	129	100	66	99.996	28	78.515	37.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
886.4893	886.5231	0.0338	38	20	27	LGVAGQWR			
886.4893	886.5231	0.0338	38	20	27	LGVAGQWR	10	0	
981.4887	981.5192	0.0305	31	116	123	QFLSETEK	15	0	
981.4887	981.5192	0.0305	31	116	123	QFLSETEK			
1484.7955	1484.829	0.0335	23	66	78	QIEELKGQEVSPK	22	15.833	
1484.7955	1484.829	0.0335	23	66	78	QIEELKGQEVSPK			
1863.9012	1863.9303	0.0291	16	1	15	MQLKPMEINPEMLNK			Oxidation (M)[1,6,12]
1863.9012	1863.9303	0.0291	16	1	15	MQLKPMEINPEMLNK			Oxidation (M)[1,6,12]
1983.8937	1983.9504	0.0567	29	136	153	NEAIQAAHDSVAQEGQCR			Carbamidomethyl (C)[17]
1983.8937	1983.9504	0.0567	29	136	153	NEAIQAAHDSVAQEGQCR	28	78.515	Carbamidomethyl (C)[17]
2230.0444	2230.0916	0.0472	21	179	199	MPFPVNHGASSEDSLLQDAAK			Oxidation (M)[1]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
NADH-ubiquinone oxidoreductase 24 kDa s	spt|P19234	4	65	99.078	20	0	20	0	19.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
872.4009	872.421	0.0201	23	61	67	NYPEGHR	20	0	
872.4009	872.421	0.0201	23	61	67	NYPEGHR			
1254.6875	1254.6981	0.0106	8	93	103	VAEVLQVPPMR			Oxidation (M)[10]
1254.6875	1254.6981	0.0106	8	93	103	VAEVLQVPPMR			Oxidation (M)[10]

1276.6379	1276.6654	0.0275	22	136	146	DSDSILETLQR			
2398.0105	2398.0085	-0.002	-1	35	54	DTPENNPDTPFDFTPENYER			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Similar to heme-binding protein	rf|XP_342776.1	4	87	99.994	47	99.558	28	61.958	18.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1026.4375	1026.4305	-0.007	-7	27	34	EDVSYEER			
1026.4375	1026.4305	-0.007	-7	27	34	EDVSYEER	19	0	
1373.6808	1373.7048	0.024	17	141	152	EADYVAHATQLR	28	61.958	
1373.6808	1373.7048	0.024	17	141	152	EADYVAHATQLR			
1789.933	1789.9598	0.0268	15	41	56	FATVEVTDKPVDEALR			
1926.9556	1926.9615	0.0059	3	104	121	IPNQFQGSPPTPSDQSVK			
1926.9556	1926.9615	0.0059	3	104	121	IPNQFQGSPPTPSDQSVK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Peroxiredoxin 6	spt|O35244	5	82	99.981	14	0	14	0	24.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
906.4679	906.5043	0.0364	40	155	161	NFDEILR			
906.4679	906.5043	0.0364	40	155	161	NFDEILR			
1191.6732	1191.7178	0.0446	37	144	154	LSILYPATTGR			
1191.6732	1191.7178	0.0446	37	144	154	LSILYPATTGR			
1328.7208	1328.7566	0.0358	27	97	107	LPFPIIDDKDR			
1328.7208	1328.7566	0.0358	27	97	107	LPFPIIDDKDR			
1363.6488	1363.6709	0.0221	16	84	96	DINAYNGAAPTEK			
1363.6488	1363.6709	0.0221	16	84	96	DINAYNGAAPTEK	14	0	
1395.6573	1395.6998	0.0425	30	41	52	DFTPVCTTELGR			Carbamidomethyl (C)[6]
1395.6573	1395.6998	0.0425	30	41	52	DFTPVCTTELGR			Carbamidomethyl (C)[6]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Peroxiredoxin 6	spt|O35244	5	71	99.74					24.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
906.4679	906.5007	0.0328	36	155	161	NFDEILR			
906.4679	906.5007	0.0328	36	155	161	NFDEILR			
1191.6732	1191.712	0.0388	33	144	154	LSILYPATTGR			
1191.6732	1191.712	0.0388	33	144	154	LSILYPATTGR			
1328.7208	1328.7632	0.0424	32	97	107	LPFPIIDDKDR			
1363.6488	1363.6837	0.0349	26	84	96	DINAYNGAAPTEK			
1363.6488	1363.6837	0.0349	26	84	96	DINAYNGAAPTEK			
1395.6573	1395.6978	0.0405	29	41	52	DFTPVCTTELGR			Carbamidomethyl (C)[6]
1395.6573	1395.6978	0.0405	29	41	52	DFTPVCTTELGR			Carbamidomethyl (C)[6]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Tyrosine 3-monooxgenase/tryptophan 5-mo	rf|NP_062250.1	6	241	100	201	100	100	100	25.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
816.421	816.45	0.029	36	14	20	LAEQAER			
816.421	816.45	0.029	36	14	20	LAEQAER	41	96.086	
903.5145	903.5443	0.0298	33	63	70	VISSIEQK			
903.5145	903.5443	0.0298	33	63	70	VISSIEQK	25	0	
1124.5518	1124.5887	0.0369	33	161	169	EMQPTHPIR	19	0	Oxidation (M)[2]
1124.5518	1124.5887	0.0369	33	161	169	EMQPTHPIR			Oxidation (M)[2]

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1182.5637	1182.6002	0.0365	31	130	140	YLSEVASGDNK	1	0	
1182.5637	1182.6002	0.0365	31	130	140	YLSEVASGDNK			
1252.6467	1252.6851	0.0384	31	160	169	KEMQPTHPIR			Oxidation (M)[3]
1252.6467	1252.6851	0.0384	31	160	169	KEMQPTHPIR	16	0	Oxidation (M)[3]
1598.7405	1598.8007	0.0602	38	30	43	AVTEQGHELSNEER			
1598.7405	1598.8007	0.0602	38	30	43	AVTEQGHELSNEER	100	100	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Tropomyosin isoform 6	cra|rCP42035	10	247	100	139	100	35	90.121	27.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
802.4417	802.4799	0.0382	48	163	169	NVTNNLK			
832.441	832.4799	0.0389	47	98	104	ALKDEEK			
894.4679	894.5054	0.0375	42	125	131	KYEEVAR	32	77.37	
894.4679	894.5054	0.0375	42	126	132	YEEVARK			
940.4482	940.49	0.0418	44	117	124	HIAEEADR	20	0	
940.4482	940.49	0.0418	44	117	124	HIAEEADR			
1182.5525	1182.5864	0.0339	29	182	190	EDKYEEEIK			
1182.5525	1182.5864	0.0339	29	182	190	EDKYEEEIK			
1243.6528	1243.7018	0.049	39	56	65	IQLVEEELDR			
1243.6528	1243.7018	0.049	39	56	65	IQLVEEELDR			
1316.644	1316.6957	0.0517	39	43	54	EQAEAEVASLNR	28	43.935	
1316.644	1316.6957	0.0517	39	43	54	EQAEAEVASLNR			
1642.8031	1642.8552	0.0521	32	14	27	IQVLQQQADDAEER			
1642.8031	1642.8552	0.0521	32	14	27	IQVLQQQADDAEER	35	90.121	
1770.8981	1770.9525	0.0544	31	13	27	KIQVLQQQADDAEER			
1770.8981	1770.9525	0.0544	31	13	27	KIQVLQQQADDAEER	24	0	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Lactate dehydrogenase B	rf|NP_036727.1	8	217	100	122	100	50	99.59	26.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
833.3747	833.415	0.0403	48	101	107	QQEGESR			
833.3747	833.415	0.0403	48	101	107	QQEGESR			
913.5828	913.6253	0.0425	47	92	100	IVVVTAGVR	42	97.278	
913.5828	913.6253	0.0425	47	92	100	IVVVTAGVR			
959.5519	959.5823	0.0304	32	300	308	GLTSVINQK			
1186.6426	1186.699	0.0564	48	309	318	LKDDEVAQLR	50	99.59	
1186.6426	1186.699	0.0564	48	309	318	LKDDEVAQLR			
1248.6001	1248.6606	0.0605	48	159	170	VIGSGCNLDSAR	30	58.226	Carbamidomethyl (C)[6]
1248.6001	1248.6606	0.0605	48	159	170	VIGSGCNLDSAR			Carbamidomethyl (C)[6]
1510.7748	1510.8196	0.0448	30	78	91	IVADKDYSVTANSK			
1510.8185	1510.8196	0.0011	1	234	246	MVVDSAYEVIKLK			Oxidation (M)[1]
1666.8646	1666.9014	0.0368	22	8	23	LIAPVADDETAVPNNK			
1666.8646	1666.9014	0.0368	22	8	23	LIAPVADDETAVPNNK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Malate dehydrogenase 1, NAD (Soluble)	trm|Q6PCV2	7	152	100	78	100	28	55.428	22.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
811.442	811.4243	-0.0177	-22	249	255	AISDHIR	28	48.351	
811.442	811.4243	-0.0177	-22	249	255	AISDHIR			
935.4866	935.4739	-0.0127	-14	311	318	EKMDLTAK			
1026.4673	1026.4673	0	0	150	157	ENFSCLTR			Carbamidomethyl (C)[5]
1026.4673	1026.4673	0	0	150	157	ENFSCLTR			Carbamidomethyl (C)[5]

1178.6165	1178.6185	0.002	2	221	230	GEFITTVQQR			
1178.6165	1178.6185	0.002	2	221	230	GEFITTVQQR	28	55.428	
1387.725	1387.7142	-0.0108	-8	80	92	DLDVAVLVGSMPR			Oxidation (M)[11]
1393.7111	1393.7131	0.002	1	299	310	FVEGLPINDFSR	22	0	
1393.7111	1393.7131	0.002	1	299	310	FVEGLPINDFSR			
1757.9214	1757.9094	-0.012	-7	126	142	VIVVGNPANTNCLTASK			Carbamidomethyl (C)[12]
1757.9214	1757.9094	-0.012	-7	126	142	VIVVGNPANTNCLTASK			Carbamidomethyl (C)[12]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Tubulin beta chain 15	pir|A25113	11	262	100	141	100	39	93.593	25.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
808.3471	808.3889	0.0418	52	157	162	EEYPDR			
808.3471	808.3889	0.0418	52	157	162	EEYPDR	10	0	
1028.5194	1028.5743	0.0549	53	351	359	TAVCDIPPR	32	73.23	Carbamidomethyl (C)[4]
1028.5194	1028.5743	0.0549	53	351	359	TAVCDIPPR			Carbamidomethyl (C)[4]
1077.5323	1077.5872	0.0549	51	155	162	IREEYPDR	39	93.593	
1077.5323	1077.5872	0.0549	51	155	162	IREEYPDR			
1097.4172	1097.4594	0.0422	38	298	306	NMMAACDPR			Oxidation (M)[2,3]
1097.4172	1097.4594	0.0422	38	298	306	NMMAACDPR	7	0	Carbamidomethyl (C)[6]
1130.5953	1130.6533	0.058	51	242	251	FPGQLNADLR			
1130.5953	1130.6533	0.058	51	242	251	FPGQLNADLR	20	0	
1159.6292	1159.6742	0.045	39	253	262	LAVNMVPFPR			Oxidation (M)[5]
1159.6292	1159.6742	0.045	39	253	262	LAVNMVPFPR	7	0	Oxidation (M)[5]
1245.5933	1245.6454	0.0521	42	381	390	ISEQFTAMFR	8	0	Oxidation (M)[8]
1245.5933	1245.6454	0.0521	42	381	390	ISEQFTAMFR			Oxidation (M)[8]
1355.6589	1355.7047	0.0458	34	47	58	INVYYNEAAGNK			
1355.6589	1355.7047	0.0458	34	47	58	INVYYNEAAGNK	30	57.768	
1462.6842	1462.7289	0.0447	31	325	336	EVDEQMLNVQNK			Oxidation (M)[6]
1462.6842	1462.7289	0.0447	31	325	336	EVDEQMLNVQNK	10	0	Oxidation (M)[6]
1631.8309	1631.8795	0.0486	30	63	77	AILVDLEPGTMDSVR	8	0	Oxidation (M)[11]
1631.8309	1631.8795	0.0486	30	63	77	AILVDLEPGTMDSVR			Oxidation (M)[11]
1822.9229	1822.9856	0.0627	34	3	19	EIVHIQAGQCGNQIGAK			Carbamidomethyl (C)[10]
1822.9229	1822.9856	0.0627	34	3	19	EIVHIQAGQCGNQIGAK			Carbamidomethyl (C)[10]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Tubulin beta chain 15	pir|A25113	11	226	100	116	100	38	92.025	25.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
808.3471	808.3696	0.0225	28	157	162	EEYPDR			
808.3471	808.3696	0.0225	28	157	162	EEYPDR	25	0	
1028.5194	1028.5576	0.0382	37	351	359	TAVCDIPPR	27	0	Carbamidomethyl (C)[4]
1028.5194	1028.5576	0.0382	37	351	359	TAVCDIPPR			Carbamidomethyl (C)[4]
1077.5323	1077.5656	0.0333	31	155	162	IREEYPDR	38	92.025	
1077.5323	1077.5656	0.0333	31	155	162	IREEYPDR			
1097.4172	1097.4398	0.0226	21	298	306	NMMAACDPR	6	0	Oxidation (M)[2,3]
1097.4172	1097.4398	0.0226	21	298	306	NMMAACDPR			Carbamidomethyl (C)[6]
1130.5953	1130.6327	0.0374	33	242	251	FPGQLNADLR	16	0	
1130.5953	1130.6327	0.0374	33	242	251	FPGQLNADLR			
1159.6292	1159.6541	0.0249	21	253	262	LAVNMVPFPR			Oxidation (M)[5]
1159.6292	1159.6541	0.0249	21	253	262	LAVNMVPFPR	9	0	Oxidation (M)[5]
1245.5933	1245.625	0.0317	25	381	390	ISEQFTAMFR			Oxidation (M)[8]
1245.5933	1245.625	0.0317	25	381	390	ISEQFTAMFR			Oxidation (M)[8]
1355.6589	1355.6829	0.024	18	47	58	INVYYNEAAGNK			
1355.6589	1355.6829	0.024	18	47	58	INVYYNEAAGNK			
1462.6842	1462.7075	0.0233	16	325	336	EVDEQMLNVQNK			Oxidation (M)[6]

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1462.6842	1462.7075	0.0233	16	325	336	EVDEQMLNVQNK			Oxidation (M)[6]
1631.8309	1631.8573	0.0264	16	63	77	AILVDLEPGTMDSVR			Oxidation (M)[11]
1631.8309	1631.8573	0.0264	16	63	77	AILVDLEPGTMDSVR	10	0	Oxidation (M)[11]
1822.9229	1822.9528	0.0299	16	3	19	EIVHIQAGQCGNQIGAK			Carbamidomethyl (C)[10]
1822.9229	1822.9528	0.0299	16	3	19	EIVHIQAGQCGNQIGAK			Carbamidomethyl (C)[10]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Tubulin beta chain 15	pir|A25113	9	141	100	63	99.976	29	45.402	19.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
808.3471	808.3726	0.0255	32	157	162	EEYPDR			
808.3471	808.3726	0.0255	32	157	162	EEYPDR			
1028.5194	1028.5568	0.0374	36	351	359	TAVCDIPPR			Carbamidomethyl (C)[4]
1028.5194	1028.5568	0.0374	36	351	359	TAVCDIPPR	23	0	Carbamidomethyl (C)[4]
1077.5323	1077.5574	0.0251	23	155	162	IREEYPDR			
1077.5323	1077.5574	0.0251	23	155	162	IREEYPDR	29	45.402	
1097.4172	1097.4406	0.0234	21	298	306	NMMAACDPR			Oxidation (M)[2,3]
1130.5953	1130.6309	0.0356	31	242	251	FPGQLNADLR	11	0	
1130.5953	1130.6309	0.0356	31	242	251	FPGQLNADLR			
1245.5933	1245.6185	0.0252	20	381	390	ISEQFTAMFR			Oxidation (M)[8]
1245.5933	1245.6185	0.0252	20	381	390	ISEQFTAMFR			Oxidation (M)[8]
1355.6589	1355.6759	0.017	13	47	58	INVYYNEAAGNK			
1355.6589	1355.6759	0.017	13	47	58	INVYYNEAAGNK			
1462.6842	1462.6948	0.0106	7	325	336	EVDEQMLNVQNK			Oxidation (M)[6]
1462.6842	1462.6948	0.0106	7	325	336	EVDEQMLNVQNK			Oxidation (M)[6]
1822.9229	1822.9365	0.0136	7	3	19	EIVHIQAGQCGNQIGAK			Carbamidomethyl (C)[10]
1822.9229	1822.9365	0.0136	7	3	19	EIVHIQAGQCGNQIGAK			Carbamidomethyl (C)[10]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Actin-beta	pir|ATRTC	11	300	100	179	100	94	100	32.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
800.5352	800.5504	0.0152	19	62	68	RGILTLK			
800.5352	800.5504	0.0152	19	62	68	RGILTLK			
976.4482	976.486	0.0378	39	19	28	AGFAGDDAPR	45	98.847	
976.4482	976.486	0.0378	39	19	28	AGFAGDDAPR			
1132.527	1132.567	0.04	35	197	206	GYSFTTTAER	41	96.994	
1132.527	1132.567	0.04	35	197	206	GYSFTTTAER			
1177.6133	1177.6304	0.0171	15	316	326	EITALAPSTMK			Oxidation (M)[10]
1198.5222	1198.5483	0.0261	22	51	61	DSYVGDEAQSK			
1198.7054	1198.5483	-0.1571	-131	29	39	AVFPSIVGRPR			
1203.5609	1203.5763	0.0154	13	40	50	HQGVMVGMGQK			Oxidation (M)[5,8]
1203.5609	1203.5763	0.0154	13	40	50	HQGVMVGMGQK			Oxidation (M)[5,8]
1516.7026	1516.7467	0.0441	29	360	372	QEYDESGPSIVHR			
1516.7026	1516.7467	0.0441	29	360	372	QEYDESGPSIVHR	94	100	
1548.8125	1548.7407	-0.0718	-46	313	326	MQKEITALAPSTMK			
1548.8125	1548.7407	-0.0718	-46	313	326	MQKEITALAPSTMK			
1790.8918	1790.9406	0.0488	27	239	254	SYELPDGQVITIGNER			
1790.8918	1790.9406	0.0488	27	239	254	SYELPDGQVITIGNER			
1954.0643	1954.0962	0.0319	16	96	113	VAPEEHPVLLTEAPLNPK			
1954.0643	1954.0962	0.0319	16	96	113	VAPEEHPVLLTEAPLNPK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Tyrosine 3-monooxgenase/tryptophan 5-mo	rf|NP_062250.1	10	172	100	68	99.994	46	99.019	38.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
816.421	816.4512	0.0302	37	13	19	LAEQAER			
816.421	816.4512	0.0302	37	13	19	LAEQAER	22	0	
917.5302	917.5606	0.0304	33	62	69	IISSIEQK			
917.5302	917.5606	0.0304	33	62	69	IISSIEQK			
922.4199	922.4658	0.0459	50	124	130	MKGDYHR			Oxidation (M)[1]
1237.6536	1237.6909	0.0373	30	107	118	HLIPAANTGESK			
1256.5906	1256.6464	0.0558	44	131	141	YLAEFATGNDR			
1256.5906	1256.6464	0.0558	44	131	141	YLAEFATGNDR	46	99.019	
1291.5544	1291.5896	0.0352	27	20	29	YDEMVESMKK			Oxidation (M)[4,8]
1384.6855	1384.7383	0.0528	38	131	142	YLAEFATGNDRK			
1384.6855	1384.7383	0.0528	38	131	142	YLAEFATGNDRK			
1463.7046	1463.7445	0.0399	27	30	42	VAGMDVELTVEER			Oxidation (M)[4]
1463.7046	1463.7445	0.0399	27	30	42	VAGMDVELTVEER			Oxidation (M)[4]
1476.7437	1476.7545	0.0108	7	95	106	LICCDILDVLDK			Carbamidomethyl (C)[3,4]
1476.7437	1476.7545	0.0108	7	95	106	LICCDILDVLDK			Carbamidomethyl (C)[3,4]
1819.9371	1819.9891	0.052	29	154	170	AASDIAMTELPPTHPIR			
1835.932	1835.9742	0.0422	23	154	170	AASDIAMTELPPTHPIR			Oxidation (M)[7]
1835.932	1835.9742	0.0422	23	154	170	AASDIAMTELPPTHPIR			Oxidation (M)[7]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
SNAP-25b	gb|AAA99826.1	6	79	99.962	29	63.787	15	0	21.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
817.4315	817.5255	0.094	115	23	29	ASHSFLR	10	0	
817.4315	817.5255	0.094	115	23	29	ASHSFLR	15	0	
817.4315	817.5255	0.094	115	23	29	ASHSFLR			
821.4263	821.5228	0.0965	117	30	37	GLFGGNTR			
821.4263	821.5228	0.0965	117	30	37	GLFGGNTR			
853.405	853.5078	0.1028	120	314	320	EFDSISR			
853.405	853.5078	0.1028	120	314	320	EFDSISR			
1482.7587	1482.9036	0.1449	98	217	229	VAAYAAQLEQYQK			
1508.6362	1508.7842	0.148	98	277	288	YEEMFPAFTDSR	14	0	Oxidation (M)[4]
1508.6362	1508.7842	0.148	98	277	288	YEEMFPAFTDSR			Oxidation (M)[4]
1508.6362	1508.7842	0.148	98	277	288	YEEMFPAFTDSR	14	0	Oxidation (M)[4]
2060.9771	2061.1677	0.1906	92	296	313	LLEAHEEQNSEAYTEAVK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
alpha-soluble NSF attachment protein - rat	pir|S58285	8	128	100	50	99.791	37	95.862	31.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
869.3999	869.5105	0.1106	127	265	271	EYDSISR			
1175.5538	1175.6876	0.1338	114	286	295	TIQGDEEDLR			
1175.5538	1175.6876	0.1338	114	286	295	TIQGDEEDLR	9	0	
1184.5616	1184.6921	0.1305	110	107	116	AIEIYTDMGR	12	0	Oxidation (M)[8]
1184.5616	1184.6921	0.1305	110	107	116	AIEIYTDMGR			Oxidation (M)[8]
1253.583	1253.7241	0.1411	113	38	47	IEEACEIYAR	13	0	Carbamidomethyl (C)[5]
1253.583	1253.7241	0.1411	113	38	47	IEEACEIYAR			Carbamidomethyl (C)[5]
1418.6943	1418.8419	0.1476	104	7	19	QAEAMALLAEAER			Oxidation (M)[5]
1418.6943	1418.8419	0.1476	104	7	19	QAEAMALLAEAER			Oxidation (M)[5]
1460.6692	1460.8208	0.1516	104	228	239	YEELFPAFSDSR			
1460.6692	1460.8208	0.1516	104	228	239	YEELFPAFSDSR	26	42.345	
1460.6692	1460.8208	0.1516	104	228	239	YEELFPAFSDSR	37	95.862	
1558.7173	1558.879	0.1617	104	141	153	AIAHYEQSADYYK			
2090.9875	2091.1851	0.1976	95	247	264	LLEAHEEQNVDSYTESVK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Heat shock protein 73	rf|NP_077327.1	15	246	100	136	100	59	99.99	35.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
861.4424	861.4445	0.0021	2	252	258	DISENKR			
1197.6626	1197.6552	-0.0074	-6	459	469	FELTGIPPAPR			
1199.6742	1199.6726	-0.0016	-1	160	171	DAGTIAGLNVLR			
1228.6281	1228.6282	0.0001	0	26	36	VEIIANDQGNR			
1253.6161	1253.6172	0.0011	1	302	311	FEELNADLFR	40	99.26	
1253.6161	1253.6172	0.0011	1	302	311	FEELNADLFR			
1426.6631	1426.6639	0.0008	1	77	88	RFDDAVVQSDMK			Oxidation (M)[11]
1481.807	1481.8042	-0.0028	-2	329	342	SQIHDIVLVGGSTR			
1487.7013	1487.7012	-0.0001	0	37	49	TTPSYVAFTDTER			
1665.79	1665.7821	-0.0079	-5	57	71	NQVAMNPTNTVFDAK			Oxidation (M)[5]
1691.7256	1691.7229	-0.0027	-2	221	236	STAGDTHLGGEDFDNR			
1691.7256	1691.7229	-0.0027	-2	221	236	STAGDTHLGGEDFDNR	59	99.992	
1745.809	1745.8019	-0.0071	-4	584	597	NQTAEKEEFEHQQK			
1981.9978	1981.9958	-0.002	-1	138	155	TVTNAVVTVPAYFNDSQR			
1981.9978	1981.9958	-0.002	-1	138	155	TVTNAVVTVPAYFNDSQR	38	98.814	
2774.3267	2774.3206	-0.0061	-2	424	447	QTQTFTTYSDNQPGVLIQVYEGER			
2921.3708	2921.3591	-0.0117	-4	78	102	FDDAVVQSDMKHWPFMVVNDAGRPK			Oxidation (M)[10,16]
3346.499	3346.7026	0.2036	61	610	646	LYQSAGGMPGGMPGGFPGGGAPPSGGASSGPTIEEVD			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
ATPase, H transporting, lysosomal V1 subu	gi|16758754	16	135	100	22	68.499	22	68.499	37.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
873.4788	873.5046	0.0258	30	30	37	EQALAVSR			
877.4526	877.4496	-0.003	-3	38	44	NYLSQPR			
1120.5303	1120.5336	0.0033	3	121	130	TPVSEDMLGR			Oxidation (M)[7]
1189.6323	1189.6432	0.0109	9	131	141	VFNGSGKPIDR			
1298.6045	1298.6169	0.0124	10	110	120	TSCEFTGDILR			Carbamidomethyl (C)[3]
1338.6437	1338.6473	0.0036	3	461	471	NFITQGPYENR			
1338.6437	1338.6473	0.0036	3	461	471	NFITQGPYENR	22	68.499	
1437.7373	1437.7429	0.0056	4	495	506	IPQSTLSEFYPR			
1556.8319	1556.8275	-0.0044	-3	68	81	YAEIVHLTLPDGTK			
1593.8384	1593.8401	0.0017	1	494	506	RIPQSTLSEFYPR			
1596.9108	1596.9133	0.0025	2	387	400	QIYPPINVLPSLSR			
1647.9427	1647.9185	-0.0242	-15	49	64	TVSGVNGPLVILDHVK			
1706.9113	1706.9103	-0.001	-1	472	485	TVYETLDIGWQLLR			
1912.8785	1912.88	0.0015	1	322	337	GFPGYMYTDLATIYER			Oxidation (M)[6]
1969.1304	1969.0571	-0.0733	-37	387	403	QIYPPINVLPSLSRLMK			
1985.1252	1985.059	-0.0662	-33	387	403	QIYPPINVLPSLSRLMK			Oxidation (M)[16]
2048.0593	2048.0527	-0.0066	-3	8	29	GIVNGAAPELPVPTGGPMAGAR			Oxidation (M)[18]
2178.1487	2178.1467	-0.002	-1	189	208	IPIFSAAGLPHNEIAAQICR			Carbamidomethyl (C)[19]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Alpha enolase	spt|P04764	12	131	100	28	87.046	28	87.046	34.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
806.4518	806.4489	-0.0029	-4	406	411	YNQILR			
840.4474	840.4874	0.04	48	422	428	FAGRSFR			
904.4622	904.4297	-0.0325	-36	412	419	IEEELGSK			
1143.6156	1143.6099	-0.0057	-5	183	192	IGAEVYHNLK			
1143.6156	1143.6099	-0.0057	-5	183	192	IGAEVYHNLK			

1406.7162	1406.6981	-0.0181	-13	15	27	GNPTVEVDLYTAK			
1439.7417	1439.7305	-0.0112	-8	269	280	YITPDQLADLYK			
1557.759	1557.7472	-0.0118	-8	358	371	LAQSNGWGVMVSHR			Oxidation (M)[10]
1804.9438	1804.9427	-0.0011	-1	32	49	AAVPSGASTGIYEALELR	28	87.046	
1804.9438	1804.9427	-0.0011	-1	32	49	AAVPSGASTGIYEALELR			
1928.9608	1928.9543	-0.0065	-3	162	178	LAMQEFMILPVGASSFR			Oxidation (M)[3,7]
2047.0706	2047.0757	0.0051	2	306	325	FTATAGIQVVGDDLTVTNPK			
2208.0278	2208.0503	0.0225	10	233	252	AGYTDQVVIGMDVAASEFYR			Oxidation (M)[11]
2662.3181	2662.375	0.0569	21	228	252	SAIAKAGYTDQVVIGMDVAASEFYR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
NADH ubiquinone oxidoreductase	spt|Q66HF1	13	113	100	39	99.191	23	63.702	24.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
898.4927	898.4843	-0.0084	-9	512	518	VMNILHR			Oxidation (M)[2]
980.5887	980.5858	-0.0029	-3	608	617	VAVTPPGLAR			
1064.5524	1064.5524	0	0	409	417	FEAPLFNAR			
1064.5524	1064.5524	0	0	409	417	FEAPLFNAR	23	63.702	
1083.6156	1083.6133	-0.0023	-2	646	655	LGEVSPNLVR			
1401.7882	1401.7622	-0.026	-19	471	483	KPMVVLGSSALQR			Oxidation (M)[3]
1403.7893	1403.7827	-0.0066	-5	429	441	VALIGSPVDLTYR			
1403.7893	1403.7827	-0.0066	-5	429	441	VALIGSPVDLTYR	17	0	
1505.8145	1505.8064	-0.0081	-5	544	557	LLFLLGADGGCITR			Carbamidomethyl (C)[11]
1558.786	1558.7782	-0.0078	-5	451	464	ILQDIASGNHEFSK			
1608.7864	1608.7776	-0.0088	-5	185	200	FASEIAGVDDLGTTGR			
1611.8013	1611.7917	-0.0096	-6	312	325	GLLTYTSWEDALSR			
2008.9855	2008.9858	0.0003	0	248	266	TESIDVMDAVGSNIVVSTR			Oxidation (M)[7]
2071.1545	2071.1531	-0.0014	-1	519	538	IASQVAALDLGYKPGVEAIR			
2075.1018	2075.1086	0.0068	3	625	643	ALSEIAGITLPYDTLDQVR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
NADH ubiquinone oxidoreductase	spt|Q66HF1	12	117	100	53	99.969	31	94.265	20.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
816.4396	816.4338	-0.0058	-7	56	62	VGMQIPR			Oxidation (M)[3]
980.5887	980.5939	0.0052	5	608	617	VAVTPPGLAR			
1064.5524	1064.5625	0.0101	9	409	417	FEAPLFNAR			
1064.5524	1064.5625	0.0101	9	409	417	FEAPLFNAR	23	61.761	
1083.6156	1083.6208	0.0052	5	646	655	LGEVSPNLVR			
1401.7882	1401.7874	-0.0008	-1	471	483	KPMVVLGSSALQR			Oxidation (M)[3]
1403.7893	1403.797	0.0077	5	429	441	VALIGSPVDLTYR			
1505.8145	1505.8259	0.0114	8	544	557	LLFLLGADGGCITR			Carbamidomethyl (C)[11]
1558.786	1558.7866	0.0006	0	451	464	ILQDIASGNHEFSK			
1608.7864	1608.7937	0.0073	5	185	200	FASEIAGVDDLGTTGR	31	94.265	
1608.7864	1608.7937	0.0073	5	185	200	FASEIAGVDDLGTTGR			
1942.0579	1941.9376	-0.1203	-62	540	557	NPPKLLFLLGADGGCITR			Carbamidomethyl (C)[15]
2071.1545	2071.156	0.0015	1	519	538	IASQVAALDLGYKPGVEAIR			
2075.1018	2075.1094	0.0076	4	625	643	ALSEIAGITLPYDTLDQVR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
RAB GDP dissociation inhibitor alpha	spt|P50398	10	79	99.956	12	0	13	0	26.0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
938.4941	938.4999	0.0058	6	211	218	LYSESLAR			
1141.5922	1141.5793	-0.0129	-11	90	98	MLLYTEVTR			Oxidation (M)[1]

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1476.7151	1476.6986	-0.0165	-11	56	68	FQLLEGPPESMGR			Oxidation (M)[11]
1476.7152	1476.6986	-0.0166	-11	279	290	QLICDPSYIPDR	13	0	Carbamidomethyl (C)[4]
1484.6686	1484.6483	-0.0203	-14	157	169	TFEGVDPQTTSMR			Oxidation (M)[12]
1535.6617	1535.6385	-0.0232	-15	424	436	MAGSAFDFENMKR			Oxidation (M)[1,11]
1852.8383	1852.8309	-0.0074	-4	194	208	TDDYLDQPCLETINR			Carbamidomethyl (C)[9]
2141.1064	2141.1023	-0.0041	-2	222	240	SPYLYPLYGLGELPQGFAR			
2199.0571	2199.0647	0.0076	3	310	328	NTNDANSCQIIIPQNQVNR			Carbamidomethyl (C)[8]
2211.0784	2211.1025	0.0241	11	119	138	VPSTETEALASNLMGMFEKR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Dihydropyrimidinase related protein-2 (DRP	spt|P47942	10	85	99.989					26.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
908.4988	908.5001	0.0013	1	391	397	VFNLYPR			
1015.553	1015.5546	0.0016	2	259	268	SAAEVIAQAR			
1310.6885	1310.6705	-0.018	-14	64	75	MVIPGGIDVHTR			Oxidation (M)[1]
1682.8707	1682.8474	-0.0233	-14	452	467	IVLEDGTLHVTEGSGR			
1682.8707	1682.8474	-0.0233	-14	452	467	IVLEDGTLHVTEGSGR			
1792.8348	1792.8163	-0.0185	-10	346	361	DNFTLIPEGTNGTEER			
1911.0222	1910.9924	-0.0298	-16	174	189	FQLTDSQIYEVLSVIR			
2169.0684	2169.0654	-0.003	-1	533	552	NLHQSGFSLSGAQIDDNIPR			
2297.144	2297.1951	0.0511	22	369	390	AVVTGKMDENQFVAVTSTNAAK			Oxidation (M)[7]
2377.1741	2377.1675	-0.0066	-3	190	211	DIGAIAQVHAENGDIIAEEQQR			
2748.489	2748.3606	-0.1284	-47	441	467	GSPLVVISQGKIVLEDGTLHVTEGSGR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
RAB GDP dissociation inhibitor alpha	spt|P50398	11	90	99.996	20	32.249	21	45.733	30.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
938.4941	938.4986	0.0045	5	211	218	LYSESLAR			
1141.5922	1141.5775	-0.0147	-13	90	98	MLLYTEVTR			Oxidation (M)[1]
1476.7151	1476.6938	-0.0213	-14	56	68	FQLLEGPPESMGR			Oxidation (M)[11]
1476.7152	1476.6938	-0.0214	-14	279	290	QLICDPSYIPDR	21	45.733	Carbamidomethyl (C)[4]
1484.6686	1484.6429	-0.0257	-17	157	169	TFEGVDPQTTSMR			Oxidation (M)[12]
1535.6617	1535.6338	-0.0279	-18	424	436	MAGSAFDFENMKR			Oxidation (M)[1,11]
1852.8383	1852.8224	-0.0159	-9	194	208	TDDYLDQPCLETINR			Carbamidomethyl (C)[9]
2141.1064	2141.1008	-0.0056	-3	222	240	SPYLYPLYGLGELPQGFAR			
2199.0571	2199.0579	0.0008	0	310	328	NTNDANSCQIIIPQNQVNR			Carbamidomethyl (C)[8]
2211.0784	2211.104	0.0256	12	119	138	VPSTETEALASNLMGMFEKR			
2303.1189	2303.1267	0.0078	3	36	55	NPYYGGESSSITPLEELYKR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Actin-beta	pir|ATRTC	11	350	100	255	100	103	100	47.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
800.5352	800.5499	0.0147	18	62	68	RGILTLK			
976.4482	976.455	0.0068	7	19	28	AGFAGDDAPR			
1132.527	1132.5284	0.0014	1	197	206	GYSFTTTAER	53	99.956	
1132.527	1132.5284	0.0014	1	197	206	GYSFTTTAER			
1198.7054	1198.6967	-0.0087	-7	29	39	AVFPSIVGRPR			
1515.7491	1515.7312	-0.0179	-12	85	95	IWHHTFYNELR			
1516.7026	1516.6971	-0.0055	-4	360	372	QEYDESGPSIVHR			
1516.7026	1516.6971	-0.0055	-4	360	372	QEYDESGPSIVHR	99	100	
1790.8918	1790.8792	-0.0126	-7	239	254	SYELPDGQVITIGNER	103	100	
1790.8918	1790.8792	-0.0126	-7	239	254	SYELPDGQVITIGNER			

1954.0643	1954.0457	-0.0186	-10	96	113	VAPEEHPVLLTEAPLNPK			
2215.0698	2215.0786	0.0088	4	292	312	DLYANTVLSGGTTMYPGIADR			
2231.0649	2231.0725	0.0076	3	292	312	DLYANTVLSGGTTMYPGIADR			Oxidation (M)[14]
2746.4272	2746.353	-0.0742	-27	336	359	KYSVWIGGSILASLSTFQQMWISK			Oxidation (M)[20]
3808.969	3808.9941	0.0251	7	148	183	TTGIVMDSGDGVTHTVPIYEGYALPHAILRLDLAGR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Tyrosine 3-monooxgenase/tryptophan 5-mo	rf|NP_062250.1	11	171	100	74	100	74	100	45.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
816.421	816.4277	0.0067	8	13	19	LAEQAER			
903.5145	903.5118	-0.0027	-3	62	69	VISSIEQK			
907.5247	907.5196	-0.0051	-6	43	50	NLLSVAYK			
948.4243	948.4242	-0.0001	0	126	132	MKGDYYR			Oxidation (M)[1]
1080.5571	1080.5518	-0.0053	-5	133	142	YLAEVATGEK			
1105.5847	1105.5801	-0.0046	-4	143	152	RATVVESSEK			
1134.5426	1134.5349	-0.0077	-7	153	162	AYSEAHEISK			
1205.6559	1205.6426	-0.0133	-11	218	227	DSTLIMQLLR	12	0	Oxidation (M)[6]
1205.6559	1205.6426	-0.0133	-11	218	227	DSTLIMQLLR			Oxidation (M)[6]
1245.6157	1245.5728	-0.0429	-34	163	172	EHMQPTHPIR			
1643.7871	1643.7736	-0.0135	-8	29	42	NVTELNEPLSNEER			
1643.7871	1643.7736	-0.0135	-8	29	42	NVTELNEPLSNEER	74	100	
2130.9714	2130.968	-0.0034	-2	199	217	TAFDDAIAELDTLNEDSYK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
SNAP-25B	dbj|BAA20152.1	7	63	98.47					7.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
831.4431	831.4389	-0.0042	-5	127	133	RVTNDAR			
1224.6041	1224.5969	-0.0072	-6	116	126	EQMAISGGFIR			Oxidation (M)[3]
1434.6707	1434.6763	0.0056	4	9	21	ADQLADESLESTR			
1434.6707	1434.6763	0.0056	4	9	21	ADQLADESLESTR			
1590.7719	1590.7694	-0.0025	-2	9	22	ADQLADESLESTRR			
1676.8159	1676.8147	-0.0012	-1	37	50	TLVMLDEQGEQLER			Oxidation (M)[4]
1676.8159	1676.8147	-0.0012	-1	37	50	TLVMLDEQGEQLER			Oxidation (M)[4]
1776.7639	1776.7711	0.0072	4	153	167	HMALDMGNEIDTQNR			Oxidation (M)[2,6]
2176.0186	2176.0164	-0.0022	-1	134	152	ENEMDENLEQVSGIIGNLR			Oxidation (M)[4]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Prohibitin	rf|XP_346517.1	8	181	100	109	100	59	99.99	27.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1058.5225	1058.5286	0.0061	6	182	190	QVAQQEAER			
1062.5062	1062.5199	0.0137	13	144	152	QVSDDLTER			
1149.5898	1149.5944	0.0046	4	129	138	FDAGELITQR			
1149.5898	1149.5944	0.0046	4	129	138	FDAGELITQR	50	99.906	
1185.6586	1185.6642	0.0056	5	79	88	DLQNVNITLR			
1396.8423	1396.8464	0.0041	3	89	100	ILFRPVASQLPR			
1460.6539	1460.6602	0.0063	4	101	112	IYTSIGEDYDER	59	99.99	
1460.6539	1460.6602	0.0063	4	101	112	IYTSIGEDYDER			
1478.7485	1478.7445	-0.004	-3	236	248	LEAAEDIAYQLSR			
1606.8435	1606.8468	0.0033	2	235	248	KLEAAEDIAYQLSR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage

Actin-beta	pir|ATRTC	12	349	100	249	100	86	100	40.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
800.5352	800.5437	0.0085	11	62	68	RGILTLK			
976.4482	976.4531	0.0049	5	19	28	AGFAGDDAPR			
1132.527	1132.5366	0.0096	8	197	206	GYSFTTTAER	59	99.991	
1132.527	1132.5366	0.0096	8	197	206	GYSFTTTAER			
1198.7054	1198.7036	-0.0018	-2	29	39	AVFPSIVGRPR			
1203.5609	1203.5533	-0.0076	-6	40	50	HQGVMVGMGQK			Oxidation (M)[5,8]
1515.7491	1515.7489	-0.0002	0	85	95	IWHHTFYNELR			
1516.7026	1516.7177	0.0151	10	360	372	QEYDESGPSIVHR			
1516.7026	1516.7177	0.0151	10	360	372	QEYDESGPSIVHR	84	100	
1790.8918	1790.892	0.0002	0	239	254	SYELPDGQVITIGNER	86	100	
1790.8918	1790.892	0.0002	0	239	254	SYELPDGQVITIGNER			
1954.0643	1954.0586	-0.0057	-3	96	113	VAPEEHPVLLTEAPLNPK			
2215.0698	2215.074	0.0042	2	292	312	DLYANTVLSGGTTMYPGIADR			
2231.0649	2231.0657	0.0008	0	292	312	DLYANTVLSGGTTMYPGIADR	19	0	Oxidation (M)[14]
2231.0649	2231.0657	0.0008	0	292	312	DLYANTVLSGGTTMYPGIADR			Oxidation (M)[14]
2359.1599	2359.147	-0.0129	-5	291	312	KDLYANTVLSGGTTMYPGIADR			Oxidation (M)[15]
2746.4272	2746.322	-0.1052	-38	336	359	KYSVWIGGSILASLSTFQQMWISK			Oxidation (M)[20]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Heat shock protein 73	gi|13242237	10	385	100	314	100	81	100	18.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
858.4567	858.4989	0.0422	49	312	319	GTLDPVEK			
993.5251	993.5446	0.0195	20	129	137	EIAEAYLGK			
1074.4851	1074.4883	0.0032	3	590	597	EEFEHQQK			
1074.4851	1074.4883	0.0032	3	590	597	EEFEHQQK	17	0	
1074.4851	1074.4883	0.0032	3	590	597	EEFEHQQK			
1199.6742	1199.6796	0.0054	5	160	171	DAGTIAGLNVLR	1	0	
1199.6742	1199.6796	0.0054	5	160	171	DAGTIAGLNVLR			
1228.6281	1228.6344	0.0063	5	26	36	VEIIANDQGNR			
1228.6281	1228.6344	0.0063	5	26	36	VEIIANDQGNR	81	100	
1253.6161	1253.6226	0.0065	5	302	311	FEELNADLFR			
1253.6161	1253.6226	0.0065	5	302	311	FEELNADLFR	54	99.975	
1481.807	1481.8123	0.0053	4	329	342	SQIHDIVLVGGSTR	43	99.642	
1481.807	1481.8123	0.0053	4	329	342	SQIHDIVLVGGSTR			
1487.7013	1487.7056	0.0043	3	37	49	TTPSYVAFTDTER	22	55.959	
1487.7013	1487.7056	0.0043	3	37	49	TTPSYVAFTDTER	6	0	
1487.7013	1487.7056	0.0043	3	37	49	TTPSYVAFTDTER			
1691.7256	1691.7275	0.0019	1	221	236	STAGDTHLGGEDFDNR			
1691.7256	1691.7275	0.0019	1	221	236	STAGDTHLGGEDFDNR	60	99.992	
1691.7256	1691.7275	0.0019	1	221	236	STAGDTHLGGEDFDNR	6	0	
1981.9978	1982.0051	0.0073	4	138	155	TVTNAVVTVPAYFNDSQR			
1981.9978	1982.0051	0.0073	4	138	155	TVTNAVVTVPAYFNDSQR			
1981.9978	1982.0051	0.0073	4	138	155	TVTNAVVTVPAYFNDSQR	36	98.042	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Heat shock protein 73	gi|13242237	15	615	100	496	100	128	100	27.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
858.4567	858.4993	0.0426	50	312	319	GTLDPVEK			
861.4424	861.4445	0.0021	2	252	258	DISENKR	31	93.737	
861.4424	861.4445	0.0021	2	252	258	DISENKR			
930.5367	930.5312	-0.0055	-6	416	423	RNTTIPTK			

993.5251	993.5345	0.0094	9	129	137	EIAEAYLGK			
1074.4851	1074.4819	-0.0032	-3	590	597	EEFEHQQK	39	99.003	
1074.4851	1074.4819	-0.0032	-3	590	597	EEFEHQQK			
1081.5676	1081.5557	-0.0119	-11	349	357	LLQDFFNGK			
1197.6626	1197.6613	-0.0013	-1	459	469	FELTGIPPAPR			
1199.6742	1199.6758	0.0016	1	160	171	DAGTIAGLNVLR			
1199.6742	1199.6758	0.0016	1	160	171	DAGTIAGLNVLR	10	0	
1228.6281	1228.6284	0.0003	0	26	36	VEIIANDQGNR	81	100	
1228.6281	1228.6284	0.0003	0	26	36	VEIIANDQGNR			
1253.6161	1253.615	-0.0011	-1	302	311	FEELNADLFR	73	100	
1253.6161	1253.615	-0.0011	-1	302	311	FEELNADLFR			
1481.807	1481.807	0	0	329	342	SQIHDIVLVGGSTR			
1481.807	1481.807	0	0	329	342	SQIHDIVLVGGSTR	43	99.556	
1487.7013	1487.6978	-0.0035	-2	37	49	TTPSYVAFTDTER	5	0	
1487.7013	1487.6978	-0.0035	-2	37	49	TTPSYVAFTDTER	32	94.52	
1487.7013	1487.6978	-0.0035	-2	37	49	TTPSYVAFTDTER			
1691.7256	1691.7228	-0.0028	-2	221	236	STAGDTHLGGEDFDNR			
1691.7256	1691.7228	-0.0028	-2	221	236	STAGDTHLGGEDFDNR	60	99.991	
1691.7256	1691.7228	-0.0028	-2	221	236	STAGDTHLGGEDFDNR	8	0	
1981.9978	1982	0.0022	1	138	155	TVTNAVVTVPAYFNDSQR	17	0	
1981.9978	1982	0.0022	1	138	155	TVTNAVVTVPAYFNDSQR			
1981.9978	1982	0.0022	1	138	155	TVTNAVVTVPAYFNDSQR	128	100	
2774.3267	2774.3555	0.0288	10	424	447	QTQTFTTYSDNQPGVLIQVYEGER			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Dihydropyrimidinase related protein-2 (DRP	spt|P47942	4	84	99.993	54	99.984	41	99.675	11.0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1071.5906	1071.5784	-0.0122	-11	8	16	NIPRITSDR			
1682.8707	1682.8469	-0.0238	-14	452	467	IVLEDGTLHVTEGSGR			
1792.8348	1792.8136	-0.0212	-12	346	361	DNFTLIPEGTNGTEER			
1792.8348	1792.8136	-0.0212	-12	346	361	DNFTLIPEGTNGTEER	41	99.675	
2377.1741	2377.1936	0.0195	8	190	211	DIGAIAQVHAENGDIIAEEQQR			
2377.1741	2377.1936	0.0195	8	190	211	DIGAIAQVHAENGDIIAEEQQR	13	0	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Dihydropyrimidinase related protein-2 (DRP	spt|P47942	10	387	100	313	100	71	100	27.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
908.4988	908.4886	-0.0102	-11	391	397	VFNLYPR	38	99.14	
908.4988	908.4886	-0.0102	-11	391	397	VFNLYPR	29	92.511	
908.4988	908.4886	-0.0102	-11	391	397	VFNLYPR			
1015.553	1015.5515	-0.0015	-1	259	268	SAAEVIAQAR	26	84.814	
1015.553	1015.5515	-0.0015	-1	259	268	SAAEVIAQAR			
1140.6088	1140.6078	-0.001	-1	472	480	KPFPDFVYK			
1140.6088	1140.6078	-0.001	-1	472	480	KPFPDFVYK	18	16.547	
1294.6936	1294.7034	0.0098	8	64	75	MVIPGGIDVHTR	18	6.795	
1294.6936	1294.7034	0.0098	8	64	75	MVIPGGIDVHTR			
1682.8707	1682.8824	0.0117	7	452	467	IVLEDGTLHVTEGSGR			
1682.8707	1682.8824	0.0117	7	452	467	IVLEDGTLHVTEGSGR	45	99.809	
1682.8707	1682.8824	0.0117	7	452	467	IVLEDGTLHVTEGSGR	69	100	
1792.8348	1792.8494	0.0146	8	346	361	DNFTLIPEGTNGTEER	33	97.275	
1792.8348	1792.8494	0.0146	8	346	361	DNFTLIPEGTNGTEER			
1911.0222	1911.0306	0.0084	4	174	189	FQLTDSQIYEVLSVIR			
1911.0222	1911.0306	0.0084	4	174	189	FQLTDSQIYEVLSVIR	26	85.531	
1911.0222	1911.0306	0.0084	4	174	189	FQLTDSQIYEVLSVIR			

2169.0684	2169.0771	0.0087	4	533	552	NLHQSGFSLSGAQIDDNIPR			
2169.0684	2169.0771	0.0087	4	533	552	NLHQSGFSLSGAQIDDNIPR	13	0	
2377.1741	2377.179	0.0049	2	190	211	DIGAIAQVHAENGDIIAEEQQR			
2377.1741	2377.179	0.0049	2	190	211	DIGAIAQVHAENGDIIAEEQQR	10	0	
2377.1741	2377.179	0.0049	2	190	211	DIGAIAQVHAENGDIIAEEQQR	71	100	
2900.5112	2900.49	-0.0212	-7	212	238	ILDLGITGPEGHVLSRPEEVEAEAVNR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Dihydropyrimidinase related protein-2 (DRP	spt|P47942	12	336	100	254	100	90	100	24.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
844.4999	844.5272	0.0273	32	486	492	SRLAELR			
908.4988	908.504	0.0052	6	391	397	VFNLYPR	44	99.81	
908.4988	908.504	0.0052	6	391	397	VFNLYPR	32	96.841	
908.4988	908.504	0.0052	6	391	397	VFNLYPR			
1015.553	1015.56	0.007	7	259	268	SAAEVIAQAR	54	99.979	
1015.553	1015.56	0.007	7	259	268	SAAEVIAQAR			
1015.553	1015.56	0.007	7	259	268	SAAEVIAQAR	58	99.991	
1071.5906	1071.6365	0.0459	43	8	16	NIPRITSDR			
1084.6361	1084.6305	-0.0056	-5	441	451	GSPLVVISQGK			
1140.6088	1140.6045	-0.0043	-4	472	480	KPFPDFVYK			
1323.7631	1323.7603	-0.0028	-2	44	56	QIGENLIVPGGVK			
1563.7723	1563.7279	-0.0444	-28	497	511	GLYDGPVCEVSVTPK			
1682.8707	1682.8723	0.0016	1	452	467	IVLEDGTLHVTEGSGR	90	100	
1682.8707	1682.8723	0.0016	1	452	467	IVLEDGTLHVTEGSGR			
1682.8707	1682.8723	0.0016	1	452	467	IVLEDGTLHVTEGSGR			
1792.8348	1792.8348	0	0	346	361	DNFTLIPEGTNGTEER	32	96.552	
1792.8348	1792.8348	0	0	346	361	DNFTLIPEGTNGTEER			
2169.0684	2169.0657	-0.0027	-1	533	552	NLHQSGFSLSGAQIDDNIPR			
2377.1741	2377.1785	0.0044	2	190	211	DIGAIAQVHAENGDIIAEEQQR	29	93.883	
2377.1741	2377.1785	0.0044	2	190	211	DIGAIAQVHAENGDIIAEEQQR	13	0	
2377.1741	2377.1785	0.0044	2	190	211	DIGAIAQVHAENGDIIAEEQQR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Alpha-internexin	spt|P23565	15	399	100	270	100	60	99.99	29.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
800.4624	800.4758	0.0134	17	162	168	AQALLER			
800.4624	800.4758	0.0134	17	162	168	AQALLER	19	0	
848.4624	848.4718	0.0094	11	139	145	VGELFQR	3	0	
848.4624	848.4718	0.0094	11	139	145	VGELFQR			
848.4624	848.4718	0.0094	11	139	145	VGELFQR			
917.4686	917.4779	0.0093	10	202	210	DVDGATLAR			
930.5254	930.5294	0.004	4	323	330	TIEIEGLR			
930.5254	930.5294	0.004	4	323	330	TIEIEGLR	28	84.21	
975.4529	975.4608	0.0079	8	310	316	EEIHEYR	60	99.989	
975.4529	975.4608	0.0079	8	310	316	EEIHEYR	41	99.209	
975.4529	975.4608	0.0079	8	310	316	EEIHEYR			
1016.5007	1016.5162	0.0155	15	169	177	DGLAEEVQR			
1029.5575	1029.5594	0.0019	2	339	346	QILELEER	29	85.466	
1029.5575	1029.5594	0.0019	2	339	346	QILELEER			
1056.6047	1056.608	0.0033	3	121	130	ALEAELAALR			
1056.6047	1056.608	0.0033	3	121	130	ALEAELAALR	58	99.983	
1061.5222	1061.5334	0.0112	11	152	161	AQLEEASSAR			
1072.5382	1072.5511	0.0129	12	96	104	EQLQGLNDR			
1072.5382	1072.5511	0.0129	12	96	104	EQLQGLNDR			

1124.5807	1124.587	0.0063	6	112	120	VHQLETQNR			
1124.5807	1124.587	0.0063	6	112	120	VHQLETQNR	12	0	
1133.5698	1133.5756	0.0058	5	291	300	FANLNEQAAR	36	97.626	
1133.5698	1133.5756	0.0058	5	291	300	FANLNEQAAR			
1390.7576	1390.7599	0.0023	2	217	228	VESLLDELAFVR			
1484.7704	1484.7705	0.0001	0	69	83	LPASDGLDLSQAAAR	6	0	
1484.7704	1484.7705	0.0001	0	69	83	LPASDGLDLSQAAAR	27	79.136	
1484.7704	1484.7705	0.0001	0	69	83	LPASDGLDLSQAAAR			
2175.0312	2175.0369	0.0057	3	347	366	HSAEVAGYQDSIGQLESDLR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Alpha-internexin	spt|P23565	18	592	100	409	100	81	100	36.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
800.4624	800.4699	0.0075	9	162	168	AQALLER	42	99.245	
800.4624	800.4699	0.0075	9	162	168	AQALLER	24	51.839	
800.4624	800.4699	0.0075	9	162	168	AQALLER			
848.4624	848.4682	0.0058	7	139	145	VGELFQR	4	0	
848.4624	848.4682	0.0058	7	139	145	VGELFQR			
875.4216	875.4323	0.0107	12	331	338	GANESLER			
917.4686	917.4716	0.003	3	202	210	DVDGATLAR			
930.5254	930.5275	0.0021	2	323	330	TIEIEGLR			
930.5254	930.5275	0.0021	2	323	330	TIEIEGLR	44	99.498	
975.4529	975.4576	0.0047	5	310	316	EEIHEYR	60	99.987	
975.4529	975.4576	0.0047	5	310	316	EEIHEYR			
1016.5007	1016.5073	0.0066	6	169	177	DGLAEEVQR			
1029.5575	1029.5627	0.0052	5	339	346	QILELEER	43	99.471	
1029.5575	1029.5627	0.0052	5	339	346	QILELEER			
1056.6047	1056.6089	0.0042	4	121	130	ALEAELAALR			
1056.6047	1056.6089	0.0042	4	121	130	ALEAELAALR	81	100	
1061.5222	1061.5303	0.0081	8	152	161	AQLEEASSAR			
1072.5382	1072.5437	0.0055	5	96	104	EQLQGLNDR	43	99.426	
1072.5382	1072.5437	0.0055	5	96	104	EQLQGLNDR			
1121.5837	1121.5928	0.0091	8	378	386	EYQDLLNVK			
1124.5807	1124.5861	0.0054	5	112	120	VHQLETQNR	18	0	
1124.5807	1124.5861	0.0054	5	112	120	VHQLETQNR			
1133.5698	1133.5773	0.0075	7	291	300	FANLNEQAAR	15	0	
1133.5698	1133.5773	0.0075	7	291	300	FANLNEQAAR	41	99.012	
1133.5698	1133.5773	0.0075	7	291	300	FANLNEQAAR			
1390.7576	1390.7623	0.0047	3	217	228	VESLLDELAFVR			
1484.7704	1484.7736	0.0032	2	69	83	LPASDGLDLSQAAAR			
1484.7704	1484.7736	0.0032	2	69	83	LPASDGLDLSQAAAR	37	97.859	
1484.7704	1484.7736	0.0032	2	69	83	LPASDGLDLSQAAAR	23	34.13	
1883.912	1883.9011	-0.0109	-6	471	487	VGESFEETLEETVVSTK			
2175.0312	2175.0388	0.0076	3	347	366	HSAEVAGYQDSIGQLESDLR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Heat shock 105kDa/110kDa protein 1	gi|58865372	7	81	99.986	48	99.89	29	91.083	9.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
943.5206	943.5269	0.0063	7	716	723	VLEELGQR	29	91.083	
943.5206	943.5269	0.0063	7	716	723	VLEELGQR			
1050.5691	1050.5728	0.0037	4	774	782	SLHQDPVVR			
1050.5691	1050.5728	0.0037	4	774	782	SLHQDPVVR	6	0	
1161.5647	1161.5685	0.0038	3	707	715	FQEAEERPR			
1161.5647	1161.5685	0.0038	3	707	715	FQEAEERPR			

1161.5647	1161.5685	0.0038	3	707	715	FQEAEERPR			
1282.6387	1282.6436	0.0049	4	186	196	QDLPNADEKPR			
1282.6387	1282.6436	0.0049	4	186	196	QDLPNADEKPR	13	0	
1461.718	1461.7216	0.0036	2	361	374	DVSTTLNADEAVAR			
1479.7074	1479.7104	0.003	2	20	33	AGGIETIANEFSDR			
1479.7074	1479.7104	0.003	2	20	33	AGGIETIANEFSDR			
1531.7961	1531.8008	0.0047	3	332	346	TEEVSAIEIVGGATR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Guanine deaminase	trm|Q9JKB7	10	658	100	584	100	146	100	21.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
909.588	909.5818	-0.0062	-7	206	213	VKPIVTPR	40	99.324	
909.588	909.5818	-0.0062	-7	206	213	VKPIVTPR			
949.4988	949.4901	-0.0087	-9	446	454	QVVPFSSSV			
949.4988	949.4901	-0.0087	-9	446	454	QVVPFSSSV			
998.4941	998.4921	-0.002	-2	428	435	FLYLGDDR	74	100	
998.4941	998.4921	-0.002	-2	428	435	FLYLGDDR	74	100	
998.4941	998.4921	-0.002	-2	428	435	FLYLGDDR			
1058.6357	1058.6313	-0.0044	-4	6	14	TPQLALIFR			
1058.6357	1058.6313	-0.0044	-4	6	14	TPQLALIFR	60	99.994	
1107.568	1107.5548	-0.0132	-12	436	445	NIEEVYVGGK			
1173.6262	1173.623	-0.0032	-3	394	403	DFDALLINPR			
1173.6262	1173.623	-0.0032	-3	394	403	DFDALLINPR	38	99.056	
1173.6262	1173.623	-0.0032	-3	394	403	DFDALLINPR	69	100	
1371.759	1371.7596	0.0006	0	371	384	LATLGGSQALGLDR			
1371.759	1371.7596	0.0006	0	371	384	LATLGGSQALGLDR	94	100	
1371.759	1371.7596	0.0006	0	371	384	LATLGGSQALGLDR	137	100	
1436.7267	1436.7164	-0.0103	-7	42	53	IVFLEESSQQEK			
1436.7267	1436.7164	-0.0103	-7	42	53	IVFLEESSQQEK	59	99.991	
1544.7227	1544.7255	0.0028	2	114	126	FQSTDVAEEVYTR	89	100	
1544.7227	1544.7255	0.0028	2	114	126	FQSTDVAEEVYTR	146	100	
1544.7227	1544.7255	0.0028	2	114	126	FQSTDVAEEVYTR			
1712.8351	1712.8308	-0.0043	-3	232	245	THDLYIQSHISENR			
1712.8351	1712.8308	-0.0043	-3	232	245	THDLYIQSHISENR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Creatine kinase	gb|AAA40932.1	9	429	100	346	100	97	100	28.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
983.4693	983.431	-0.0383	-39	216	223	GIWHNDNK			
983.4693	983.431	-0.0383	-39	216	223	GIWHNDNK			
983.4693	983.431	-0.0383	-39	216	223	GIWHNDNK			
1058.6105	1058.6376	0.0271	26	299	307	LPHLGKHEK			
1159.5491	1159.5507	0.0016	1	2	11	PFSNSHNTQK			
1232.6157	1232.615	-0.0007	-1	87	96	DLFDPIIEDR			
1232.6157	1232.615	-0.0007	-1	87	96	DLFDPIIEDR	69	100	
1254.5498	1254.55	0.0002	0	97	107	HGGYQPSDEHK	34	97.492	
1254.5498	1254.55	0.0002	0	97	107	HGGYQPSDEHK			
1303.7256	1303.7306	0.005	4	33	43	VLTPELYAELR	22	65.853	
1303.7256	1303.7306	0.005	4	33	43	VLTPELYAELR	77	100	
1303.7256	1303.7306	0.005	4	33	43	VLTPELYAELR			
1602.8334	1602.8363	0.0029	2	157	172	LAVEALSSLDGDLSGR	97	100	
1602.8334	1602.8363	0.0029	2	157	172	LAVEALSSLDGDLSGR	10	0	
1602.8334	1602.8363	0.0029	2	157	172	LAVEALSSLDGDLSGR			
1964.9308	1964.9358	0.005	3	321	341	GTGGVDTAAVGGVFDVSNADR	25	82.886	

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1964.9308	1964.9358	0.005	3	321	341	GTGGVDTAAVGGVFDVSNADR			
1964.9308	1964.9358	0.005	3	321	341	GTGGVDTAAVGGVFDVSNADR	9	0	
2518.1692	2518.1831	0.0139	6	108	130	TDLNPDNLQGGDDLDPN			
2518.1692	2518.1831	0.0139	6	108	130	TDLNPDNLQGGDDLDPNYVLSSR	44	99.784	
2518.1692	2518.1831	0.0139	6	108	130	TDLNPDNLQGGDDLDPNYVLSSR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Enolase 2, gamma	gi|26023949	6	142	100	90	100	68	99.999	14.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
800.3824	800.3976	0.0152	19	257	262	YDLDFK			
848.4161	848.4239	0.0078	9	423	429	FAGHNFR			
848.4161	848.4239	0.0078	9	423	429	FAGHNFR			
848.4161	848.4239	0.0078	9	423	429	FAGHNFR			
1130.6204	1130.6077	-0.0127	-11	184	193	LGAEVYHTLK			
1174.5586	1174.5623	0.0037	3	413	422	IEEELGEEAR	64	99.997	
1174.5586	1174.5623	0.0037	3	413	422	IEEELGEEAR			
1174.5586	1174.5623	0.0037	3	413	422	IEEELGEEAR	68	99.999	
1380.7118	1380.705	-0.0068	-5	16	28	GNPTVEVDLHTAK			
1380.7118	1380.705	-0.0068	-5	16	28	GNPTVEVDLHTAK			
1804.9438	1804.9406	-0.0032	-2	33	50	AAVPSGASTGIYEALELR	23	56.682	
1804.9438	1804.9406	-0.0032	-2	33	50	AAVPSGASTGIYEALELR	17	0	
1804.9438	1804.9406	-0.0032	-2	33	50	AAVPSGASTGIYEALELR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Guanine deaminase	trm|Q9JKB7	9	360	100	293	100	115	100	20.0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
885.4352	885.437	0.0018	2	106	112	YTFPTEK			
909.588	909.5894	0.0014	2	206	213	VKPIVTPR			
909.588	909.5894	0.0014	2	206	213	VKPIVTPR	28	85.262	
992.5046	992.5482	0.0436	44	385	393	EIGNFEVGK			
998.4941	998.5018	0.0077	8	428	435	FLYLGDDR			
998.4941	998.5018	0.0077	8	428	435	FLYLGDDR	45	99.759	
1107.568	1107.5649	-0.0031	-3	436	445	NIEEVYVGGK			
1173.6262	1173.6289	0.0027	2	394	403	DFDALLINPR			
1173.6262	1173.6289	0.0027	2	394	403	DFDALLINPR	83	100	
1173.6262	1173.6289	0.0027	2	394	403	DFDALLINPR			
1371.759	1371.7617	0.0027	2	371	384	LATLGGSQALGLDR			
1371.759	1371.7617	0.0027	2	371	384	LATLGGSQALGLDR			
1371.759	1371.7617	0.0027	2	371	384	LATLGGSQALGLDR	22	50.404	
1436.7267	1436.7228	-0.0039	-3	42	53	IVFLEESSQQEK			
1544.7227	1544.7273	0.0046	3	114	126	FQSTDVAEEVYTR	18	0	
1544.7227	1544.7273	0.0046	3	114	126	FQSTDVAEEVYTR			
1544.7227	1544.7273	0.0046	3	114	126	FQSTDVAEEVYTR	115	100	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
COP9 signalosome subunit 4	gi|51948518	5	180	100	150	100	63	99.996	13.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
834.4468	834.4628	0.016	19	201	207	FIEAAQR	42	99.535	
834.4468	834.4628	0.016	19	201	207	FIEAAQR	38	98.73	
834.4468	834.4628	0.016	19	201	207	FIEAAQR			
970.4952	970.5009	0.0057	6	215	222	TIVHESER	39	99.028	
970.4952	970.5009	0.0057	6	215	222	TIVHESER			

970.4952	970.5009	0.0057	6	215	222	TIVHESER	18	0	
1206.5961	1206.6086	0.0125	10	291	302	ATTADGSSILDR			
1206.5961	1206.6086	0.0125	10	291	302	ATTADGSSILDR	7	0	
1377.7372	1377.7406	0.0034	2	96	107	VISFEEQVASIR	28	88.149	
1377.7372	1377.7406	0.0034	2	96	107	VISFEEQVASIR			
1377.7372	1377.7406	0.0034	2	96	107	VISFEEQVASIR	63	99.996	
2023.9607	2023.9629	0.0022	1	154	170	LYLEDDDPVQAEAYINR			
2023.9607	2023.9629	0.0022	1	154	170	LYLEDDDPVQAEAYINR			

Protein Name	**Accession No.**	**Peptide Count**	**Protein Score**	**Protein Score C.I.%**	**Total Ion Score**	**Total Ion C.I. %**	**Best Ion Score**	**Best Ion C.I.%**	**% Coverage**
Guanine nucleotide binding protein, alpha o	cra|rCP51914	6	137	100	84	100	48	99.886	17.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
836.4512	836.4588	0.0076	9	228	234	KDLFGEK			
891.4682	891.4689	0.0007	1	155	162	LFDVGGQR			
891.4682	891.4689	0.0007	1	155	162	LFDVGGQR	26	82.984	
891.4682	891.4689	0.0007	1	155	162	LFDVGGQR	11	0	
1044.4996	1044.5084	0.0088	8	111	118	YYLDSLDR	6	0	
1044.4996	1044.5084	0.0088	8	111	118	YYLDSLDR	10	0	
1298.5933	1298.6355	0.0422	32	43	54	AMDTLGVEYGDK			
1298.5933	1298.6355	0.0422	32	43	54	AMDTLGVEYGDK			
1298.5933	1298.6355	0.0422	32	43	54	AMDTLGVEYGDK			
1445.6907	1445.6952	0.0045	3	11	23	IIHEDGFSGEDVK			
1689.8442	1689.8507	0.0065	4	119	133	IGAADYQPTEQDILR			
1689.8442	1689.8507	0.0065	4	119	133	IGAADYQPTEQDILR	7	0	
1689.8442	1689.8507	0.0065	4	119	133	IGAADYQPTEQDILR	48	99.886	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Malate dehydrogenase 1	gb|AAH59124.1	6	241	100	196	100	79	100	16.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
811.442	811.4605	0.0185	23	249	255	AISDHIR	57	99.982	
811.442	811.4605	0.0185	23	249	255	AISDHIR	52	99.949	
811.442	811.4605	0.0185	23	249	255	AISDHIR			
858.5406	858.5117	-0.0289	-34	163	170	AKSQIALK			
917.4938	917.4992	0.0054	6	171	179	LGVTADDVK			
1007.5407	1007.547	0.0063	6	206	214	EVGVYEALK			
1178.6165	1178.6277	0.0112	10	221	230	GEFITTVQQR	79	100	
1178.6165	1178.6277	0.0112	10	221	230	GEFITTVQQR			
1178.6165	1178.6277	0.0112	10	221	230	GEFITTVQQR	74	100	
1393.7111	1393.7247	0.0136	10	299	310	FVEGLPINDFSR			
1393.7111	1393.7247	0.0136	10	299	310	FVEGLPINDFSR	60	99.992	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Serine/threonine specific protein phosphata	trm|Q9WUV7	8	79	99.973	20	76.74	20	76.74	13.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1007.5421	1007.5262	-0.0159	-16	20	28	AVPFPPSHR	20	76.74	
1007.5421	1007.5262	-0.0159	-16	20	28	AVPFPPSHR			
1072.6361	1072.6195	-0.0166	-15	64	73	IITEGASILR			
1176.5643	1176.551	-0.0133	-11	33	42	EVFDNDGKPR			
1185.5939	1185.5947	0.0008	1	155	163	HLTEYFTFK			
1247.6378	1247.6259	-0.0119	-10	101	112	LFEVGGSPANTR			
1247.6378	1247.6259	-0.0119	-10	101	112	LFEVGGSPANTR			
1260.6259	1260.6167	-0.0092	-7	113	122	YLFLGDYVDR			

1369.6608	1369.6516	-0.0092	-7	244	254	TQEHFTHNTVR			
2441.3433	2441.2908	-0.0525	-22	425	449	GLTPTGMLPSGVLSGGKQTLQSAIK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Glyoxylase domain-containing protein 4	spt|Q5I0D1	5	112	100	81	100	58	99.99	17.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
841.4202	841.4359	0.0157	19	125	130	FYLQDR			
861.498	861.501	0.003	3	6	12	ALHFVFK			
861.498	861.501	0.003	3	6	12	ALHFVFK	23	75.328	
1081.5577	1081.5635	0.0058	5	17	24	FQTVHFFR			
1081.5577	1081.5635	0.0058	5	17	24	FQTVHFFR	58	99.991	
1553.7482	1553.7476	-0.0006	0	110	124	VAEGVFETEAPGGYK			
1784.964	1784.9264	-0.0376	-21	221	237	ESQSILTPLVSLDTPGK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Tumor protein, translationally-controlled 1	rf|NP_446319.1	2	115	100	92	100	46	99.88	5.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1028.5371	1028.4962	-0.0409	-40	103	110	LEEQKPER	46	99.883	
1028.5371	1028.4962	-0.0409	-40	103	110	LEEQKPER			
1213.6534	1213.614	-0.0394	-32	101	110	GKLEEQKPER	46	99.86	
1213.6534	1213.614	-0.0394	-32	101	110	GKLEEQKPER			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Peroxiredoxin 2	gi|34849738	5	295	100	226	100	79	100	27.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
876.5189	876.5029	-0.016	-18	128	135	GLFIIDAK	29	89.035	
876.5189	876.5029	-0.016	-18	128	135	GLFIIDAK			
937.4373	937.4267	-0.0106	-11	120	127	NDEGIAYR	59	99.989	
937.4373	937.4267	-0.0106	-11	120	127	NDEGIAYR			
937.4373	937.4267	-0.0106	-11	120	127	NDEGIAYR	45	99.744	
1108.5997	1108.5862	-0.0135	-12	110	119	SLSQNYGVLK	60	99.992	
1108.5997	1108.5862	-0.0135	-12	110	119	SLSQNYGVLK			
1211.6742	1211.6682	-0.006	-5	140	150	QITVNDLPVGR			
1211.6742	1211.6682	-0.006	-5	140	150	QITVNDLPVGR	79	100	
1211.6742	1211.6682	-0.006	-5	140	150	QITVNDLPVGR	39	98.995	
1706.9686	1706.9591	-0.0095	-6	93	109	EGGLGPLNIPLLADVTK			
1706.9686	1706.9591	-0.0095	-6	93	109	EGGLGPLNIPLLADVTK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Ferritin, heavy polypeptide 1	gi|6978859	5	146	100	99	100	42	99.805	28.0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
876.5189	876.5171	-0.0018	-2	81	87	IFLQDIK			
1153.5959	1153.6022	0.0063	5	148	157	ELGDHVTNLR	42	99.805	
1153.5959	1153.6022	0.0063	5	148	157	ELGDHVTNLR			
1267.7004	1267.6975	-0.0029	-2	110	120	SVNQSLLELHK			
1345.6284	1345.6355	0.0071	5	55	64	YFLHQSHEER	34	98.823	
1345.6284	1345.6355	0.0071	5	55	64	YFLHQSHEER			
1545.7041	1545.7073	0.0032	2	11	23	QNYHQDSEAAINR	23	84.448	
1545.7041	1545.7073	0.0032	2	11	23	QNYHQDSEAAINR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Proteasome subunit R-DELTA	dbj|BAA01586.1	6	125	100	67	99.999	54	99.978	26.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
847.4268	847.434	0.0072	8	164	172	DGSSGGVIR			
847.4268	847.434	0.0072	8	164	172	DGSSGGVIR			
1083.543	1083.5366	-0.0064	-6	17	26	TTTGSYIANR			
1083.543	1083.5366	-0.0064	-6	17	26	TTTGSYIANR			
1110.6517	1110.6393	-0.0124	-11	184	193	QVLLGDQIPK			
1171.6429	1171.6461	0.0032	3	173	183	LAAIQQSGVER			
1171.6429	1171.6461	0.0032	3	173	183	LAAIQQSGVER	45	99.806	
1171.6429	1171.6461	0.0032	3	173	183	LAAIQQSGVER	54	99.978	
1490.7598	1490.7704	0.0106	7	2	16	AVQFDGGVVLGADSR			
2362.0986	2362.0947	-0.0039	-2	120	141	QSFAIGGSGSSYIYGYVDATYR			
2362.0986	2362.0947	-0.0039	-2	120	141	QSFAIGGSGSSYIYGYVDATYR	13	0	
2362.0986	2362.0947	-0.0039	-2	120	141	QSFAIGGSGSSYIYGYVDATYR	13	0	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Calcium binding protein P22	rf|NP_077053.1	5	97	100	35	98.153	35	98.153	33.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1262.6124	1262.5518	-0.0606	-48	20	30	ETGFSHSQITR			
1262.6124	1262.5518	-0.0606	-48	20	30	ETGFSHSQITR			
1262.6124	1262.5518	-0.0606	-48	20	30	ETGFSHSQITR			
1307.7318	1307.6749	-0.0569	-44	54	65	IPELAINPLGDR			
1307.7318	1307.6749	-0.0569	-44	54	65	IPELAINPLGDR	35	98.153	
1412.7128	1412.6581	-0.0547	-39	99	111	SKDVNGPEPLNSR			
1524.7653	1524.7168	-0.0485	-32	35	48	FTSLDKGENGTLSR			
1885.9078	1885.9009	-0.0069	-4	66	81	IINAFFSEGEDQVNFR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Gamma-actin	spt|P4501887	5	221	100	181	100	65	100	18.0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
976.4482	976.4561	0.0079	8	19	28	AGFAGDDAPR	49	99.907	
976.4482	976.4561	0.0079	8	19	28	AGFAGDDAPR			
1132.527	1132.5363	0.0093	8	197	206	GYSFTTTAER			
1132.527	1132.5363	0.0093	8	197	206	GYSFTTTAER	6	0	
1132.527	1132.5363	0.0093	8	197	206	GYSFTTTAER			
1516.7026	1516.7031	0.0005	0	360	372	QEYDESGPSIVHR	61	99.995	
1516.7026	1516.7031	0.0005	0	360	372	QEYDESGPSIVHR	27	87.25	
1516.7026	1516.7031	0.0005	0	360	372	QEYDESGPSIVHR			
1790.8918	1790.8929	0.0011	1	239	254	SYELPDGQVITIGNER	17	0	
1790.8918	1790.8929	0.0011	1	239	254	SYELPDGQVITIGNER			
1790.8918	1790.8929	0.0011	1	239	254	SYELPDGQVITIGNER	65	99.998	
1954.0643	1954.0625	-0.0018	-1	96	113	VAPEEHPVLLTEAPLNPK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Heat shock protein 4	gi|24025637	8	98	100	47	99.887	21	54.744	12.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1149.5535	1149.5765	0.023	20	689	697	FQESEERPK			
1149.5535	1149.5765	0.023	20	689	697	FQESEERPK	1	0	
1149.5535	1149.5765	0.023	20	689	697	FQESEERPK			

1295.6954	1295.707	0.0116	9	186	196	QDLPALEEKPR	21	54.744
1295.6954	1295.707	0.0116	9	186	196	QDLPALEEKPR		
1321.7111	1321.7242	0.0131	10	222	234	VLATAFDTTLGGR		
1321.7111	1321.7242	0.0131	10	222	234	VLATAFDTTLGGR	9	0
1321.7111	1321.7242	0.0131	10	222	234	VLATAFDTTLGGR	10	0
1492.7642	1492.7711	0.0069	5	333	346	EDIYAVEIVGGATR		
1495.7023	1495.7151	0.0128	9	20	33	AGGIETIANEYSDR	16	0
1495.7023	1495.7151	0.0128	9	20	33	AGGIETIANEYSDR		
1495.7023	1495.7151	0.0128	9	20	33	AGGIETIANEYSDR	11	0
1519.7599	1519.7638	0.0039	3	361	374	ELSTTLNADEAVTR		
1584.7653	1584.7693	0.004	3	639	651	FVSEDDRNNFTLK		
1584.7653	1584.7693	0.004	3	639	651	FVSEDDRNNFTLK		
1735.9265	1735.9169	-0.0096	-6	391	405	EFSITDVVPYPISLR		

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Heat shock protein 4	gi|24025637	8	129	100	74	100	36	98.364	12.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1149.5535	1149.5645	0.011	10	689	697	FQESEERPK			
1149.5535	1149.5645	0.011	10	689	697	FQESEERPK	11	0	
1149.5535	1149.5645	0.011	10	689	697	FQESEERPK	2	0	
1295.6954	1295.6942	-0.0012	-1	186	196	QDLPALEEKPR			
1295.6954	1295.6942	-0.0012	-1	186	196	QDLPALEEKPR	36	98.364	
1321.7111	1321.7123	0.0012	1	222	234	VLATAFDTTLGGR	11	0	
1321.7111	1321.7123	0.0012	1	222	234	VLATAFDTTLGGR			
1321.7111	1321.7123	0.0012	1	222	234	VLATAFDTTLGGR	10	0	
1492.7642	1492.7583	-0.0059	-4	333	346	EDIYAVEIVGGATR			
1492.7642	1492.7583	-0.0059	-4	333	346	EDIYAVEIVGGATR			
1495.7023	1495.702	-0.0003	0	20	33	AGGIETIANEYSDR	14	0	
1495.7023	1495.702	-0.0003	0	20	33	AGGIETIANEYSDR	15	0	
1495.7023	1495.702	-0.0003	0	20	33	AGGIETIANEYSDR			
1519.7599	1519.7552	-0.0047	-3	361	374	ELSTTLNADEAVTR			
1584.7653	1584.7573	-0.008	-5	639	651	FVSEDDRNNFTLK			
1735.9265	1735.9124	-0.0141	-8	391	405	EFSITDVVPYPISLR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Dynamin 1	gi|18093102	13	149	100	54	99.967	25	75.48	15.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
839.5097	839.5444	0.0347	41	459	465	IVTTHIR			
839.5097	839.5444	0.0347	41	459	465	IVTTHIR			
877.489	877.5189	0.0299	34	230	237	GYIGVVNR			
1065.6415	1065.6301	-0.0114	-11	114	123	GISPVPINLR			
1065.6415	1065.6301	-0.0114	-11	114	123	GISPVPINLR			
1087.528	1087.5223	-0.0057	-5	316	324	NFRPDDPAR	17	0	
1087.528	1087.5223	-0.0057	-5	316	324	NFRPDDPAR			
1107.5792	1107.5605	-0.0187	-17	45	54	SSVLENFVGR			
1213.6284	1213.6031	-0.0253	-21	774	784	SPTSSPTPQRR			
1213.6284	1213.6031	-0.0253	-21	773	783	RSPTSSPTPQR	12	0	
1281.6738	1281.6373	-0.0365	-28	257	266	KFFLSHPSYR			
1335.7491	1335.7	-0.0491	-37	280	290	VLNQQLTNHIR			
1335.7491	1335.7	-0.0491	-37	280	290	VLNQQLTNHIR			
1335.7491	1335.7	-0.0491	-37	280	290	VLNQQLTNHIR			
1344.7118	1344.661	-0.0508	-38	511	522	TSGNQDEILVIR			
1375.7117	1375.6608	-0.0509	-37	584	594	HIFALFNTEQR			
1709.8857	1709.824	-0.0617	-36	143	157	VPVGDQPPDIEFQIR	25	75.48	

1709.8857	1709.824	-0.0617	-36	143	157	VPVGDQPPDIEFQIR			
1867.8668	1867.8132	-0.0536	-29	344	361	IEGSGDQIDTYELSGGAR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Dynamin 1	gi|18093102	13	143	100	57	99.99	26	85.265	17.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
804.4362	804.4749	0.0387	48	446	451	LQQYPR	16	0	
804.4362	804.4749	0.0387	48	446	451	LQQYPR			
839.5097	839.5434	0.0337	40	459	465	IVTTHIR			
877.489	877.5247	0.0357	41	230	237	GYIGVVNR			
1065.6415	1065.6625	0.021	20	114	123	GISPVPINLR			
1065.6415	1065.6625	0.021	20	114	123	GISPVPINLR			
1087.528	1087.5548	0.0268	25	316	324	NFRPDDPAR			
1107.5792	1107.5878	0.0086	8	45	54	SSVLENFVGR			
1153.5789	1153.598	0.0191	17	258	266	FFLSHPSYR			
1213.6284	1213.6503	0.0219	18	774	784	SPTSSPTPQRR			
1335.7491	1335.7513	0.0022	2	280	290	VLNQQLTNHIR			
1335.7491	1335.7513	0.0022	2	280	290	VLNQQLTNHIR			
1335.7491	1335.7513	0.0022	2	280	290	VLNQQLTNHIR			
1344.7118	1344.7107	-0.0011	-1	511	522	TSGNQDEILVIR			
1709.8857	1709.8768	-0.0089	-5	143	157	VPVGDQPPDIEFQIR	26	85.265	
1709.8857	1709.8768	-0.0089	-5	143	157	VPVGDQPPDIEFQIR			
1867.8668	1867.8528	-0.014	-7	344	361	IEGSGDQIDTYELSGGAR	16	0	
1867.8668	1867.8528	-0.014	-7	344	361	IEGSGDQIDTYELSGGAR			
2300.2397	2300.1753	-0.0644	-28	394	414	NIHGIRTGLFTPDLAFEATVK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Transitional endoplasmic reticulum ATPase	spt|P00572	8	149	100	101	100	47	99.93	14.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
837.5305	837.571	0.0405	48	232	239	AIGVKPPR	17	27.02	
837.5305	837.571	0.0405	48	232	239	AIGVKPPR	17	22.695	
837.5305	837.571	0.0405	48	232	239	AIGVKPPR			
947.5672	947.5834	0.0162	17	148	155	KGDIFLVR			
947.5672	947.5834	0.0162	17	148	155	KGDIFLVR	20	61.434	
947.5672	947.5834	0.0162	17	148	155	KGDIFLVR	31	97.282	
1075.5378	1075.527	-0.0108	-10	278	287	LAGESESNLR			
1075.5378	1075.527	-0.0108	-10	278	287	LAGESESNLR	5	0	
1116.5028	1116.4882	-0.0146	-13	587	599	GGNIGDGGGAADR			
1242.6324	1242.5927	-0.0397	-32	366	377	EVDIGIPDATGR			
1242.6324	1242.5927	-0.0397	-32	366	377	EVDIGIPDATGR	47	99.93	
1408.6427	1408.6453	0.0026	2	734	744	DHFEEAMRFAR			
1823.9174	1823.8531	-0.0643	-35	488	502	ELQELVQYPVEHPDK			
2518.4253	2518.4868	0.0615	24	616	638	NVFIIGATNRPDIIDPAILRPGR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Transitional endoplasmic reticulum ATPase	spt|P00572	11	172	100	108	100	55	99.988	17.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
837.5305	837.5698	0.0393	47	232	239	AIGVKPPR	19	43.13	
837.5305	837.5698	0.0393	47	232	239	AIGVKPPR	17	10.487	
837.5305	837.5698	0.0393	47	232	239	AIGVKPPR			
947.5672	947.5832	0.016	17	148	155	KGDIFLVR			
947.5672	947.5832	0.016	17	148	155	KGDIFLVR	34	98.521	

947.5672	947.5832	0.016	17	148	155	KGDIFLVR	26	90.453	
1075.5378	1075.5292	-0.0086	-8	278	287	LAGESESNLR			
1116.5028	1116.4899	-0.0129	-12	587	599	GGNIGDGGGAADR			
1118.5801	1118.5591	-0.021	-19	701	709	ESIESEIRR			
1118.5801	1118.5591	-0.021	-19	701	709	ESIESEIRR			
1203.6328	1203.6012	-0.0316	-26	278	288	LAGESESNLRK			
1242.6324	1242.5959	-0.0365	-29	366	377	EVDIGIPDATGR	55	99.988	
1242.6324	1242.5959	-0.0365	-29	366	377	EVDIGIPDATGR			
1329.691	1329.6427	-0.0483	-36	454	465	WALSQSNPSALR			
1408.6427	1408.649	0.0063	4	734	744	DHFEEAMRFAR			
1823.9174	1823.865	-0.0524	-29	488	502	ELQELVQYPVEHPDK			
2518.4253	2518.498	0.0727	29	616	638	NVFIIGATNRPDIIDPAILRPGR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
NADH dehydrogenase (ubiquinone) Fe-S pr	gi|53850628	13	297	100	200	100	48	99.88	22.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
980.5887	980.6003	0.0116	12	608	617	VAVTPPGLAR			
980.5887	980.6003	0.0116	12	608	617	VAVTPPGLAR	20	29.728	
1064.5524	1064.5459	-0.0065	-6	409	417	FEAPLFNAR	48	99.88	
1064.5524	1064.5459	-0.0065	-6	409	417	FEAPLFNAR	42	99.534	
1064.5524	1064.5459	-0.0065	-6	409	417	FEAPLFNAR			
1066.5383	1066.536	-0.0023	-2	703	712	ASQTMAKCVK			
1083.6156	1083.6028	-0.0128	-12	646	655	LGEVSPNLVR	8	0	
1083.6156	1083.6028	-0.0128	-12	646	655	LGEVSPNLVR			
1097.5222	1097.5112	-0.011	-10	593	602	SATYVNTEGR			
1403.7893	1403.7379	-0.0514	-37	429	441	VALIGSPVDLTYR	25	77.313	
1403.7893	1403.7379	-0.0514	-37	429	441	VALIGSPVDLTYR			
1403.7893	1403.7379	-0.0514	-37	429	441	VALIGSPVDLTYR	33	96.478	
1558.786	1558.7281	-0.0579	-37	451	464	ILQDIASGNHEFSK			
1608.7864	1608.7225	-0.0639	-40	185	200	FASEIAGVDDLGTTGR			
1608.7864	1608.7225	-0.0639	-40	185	200	FASEIAGVDDLGTTGR	24	72.974	
1611.8013	1611.7347	-0.0666	-41	312	325	GLLTYTSWEDALSR			
1611.8013	1611.7347	-0.0666	-41	312	325	GLLTYTSWEDALSR	4	0	
2071.1545	2071.1133	-0.0412	-20	519	538	IASQVAALDLGYKPGVEAIR			
2071.1545	2071.1133	-0.0412	-20	519	538	IASQVAALDLGYKPGVEAIR	27	86.455	
2071.1545	2071.1133	-0.0412	-20	519	538	IASQVAALDLGYKPGVEAIR	22	54.209	
2075.1018	2075.0698	-0.032	-15	625	643	ALSEIAGITLPYDTLDQVR			
2075.1018	2075.0698	-0.032	-15	625	643	ALSEIAGITLPYDTLDQVR	34	97.177	
2199.2495	2199.2139	-0.0356	-16	519	539	IASQVAALDLGYKPGVEAIRK			
2758.4622	2758.571	0.1088	39	383	408	SNYLLNTTIAGVEEADVVLLVGTNPR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Heat shock 70kD protein 5	cra|rCP25304	12	179	100	75	100	24	71.237	22.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
986.5153	986.5384	0.0231	23	533	540	LTPEEIER			
997.5173	997.5626	0.0453	45	298	306	ALSSQHQAR			
1074.5538	1074.5909	0.0371	35	524	532	ITITNDQNR			
1191.6368	1191.6481	0.0113	9	465	474	VYEGERPLTK			
1191.6368	1191.6481	0.0113	9	465	474	VYEGERPLTK			
1191.6368	1191.6481	0.0113	9	465	474	VYEGERPLTK			
1228.6281	1228.6337	0.0056	5	50	60	VEIIANDQGNR	11	0	
1228.6281	1228.6337	0.0056	5	50	60	VEIIANDQGNR			
1460.759	1460.7573	-0.0017	-1	354	367	SDIDEIVLVGGSTR			
1460.759	1460.7573	-0.0017	-1	354	367	SDIDEIVLVGGSTR			

1566.7798	1566.7679	-0.0119	-8	61	74	ITPSYVAFTPEGER			
1566.7798	1566.7679	-0.0119	-8	61	74	ITPSYVAFTPEGER	14	0	
1566.7798	1566.7679	-0.0119	-8	61	74	ITPSYVAFTPEGER	14	0	
1588.854	1588.8423	-0.0117	-7	353	367	KSDIDEIVLVGGSTR			
1815.9963	1815.9755	-0.0208	-11	198	214	IINEPTAAAIAYGLDKR			
1887.9712	1887.9561	-0.0151	-8	165	181	VTHAVVTVPAYFNDAQR	16	0	
1887.9712	1887.9561	-0.0151	-8	165	181	VTHAVVTVPAYFNDAQR			
1934.0131	1933.9957	-0.0174	-9	475	492	DNHLLGTFDLTGIPPAPR	24	66.824	
1934.0131	1933.9957	-0.0174	-9	475	492	DNHLLGTFDLTGIPPAPR	24	71.237	
1934.0131	1933.9957	-0.0174	-9	475	492	DNHLLGTFDLTGIPPAPR			
2148.9971	2148.9854	-0.0117	-5	307	324	IEIESFFEGEDFSETLTR	10	0	
2148.9971	2148.9854	-0.0117	-5	307	324	IEIESFFEGEDFSETLTR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Heat shock protein 73	gi|13242237	6	64	99.167	24	87.028	24	87.028	12.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1199.6742	1199.642	-0.0322	-27	160	171	DAGTIAGLNVLR			
1253.6161	1253.5853	-0.0308	-25	302	311	FEELNADLFR			
1481.807	1481.7478	-0.0592	-40	329	342	SQIHDIVLVGGSTR			
1481.807	1481.7478	-0.0592	-40	329	342	SQIHDIVLVGGSTR			
1487.7013	1487.6543	-0.047	-32	37	49	TTPSYVAFTDTER			
1691.7256	1691.6763	-0.0493	-29	221	236	STAGDTHLGGEDFDNR	24	87.028	
1691.7256	1691.6763	-0.0493	-29	221	236	STAGDTHLGGEDFDNR			
1981.9978	1981.9558	-0.042	-21	138	155	TVTNAVVTVPAYFNDSQR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Succinate dehydrogenase complex, subunit	gi|18426858	8	84	99.993	29	93.87	16	0	16.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1122.5902	1122.5731	-0.0171	-15	243	253	NTIIATGGYGR			
1122.5902	1122.5731	-0.0171	-15	243	253	NTIIATGGYGR	11	0	
1122.5902	1122.5731	-0.0171	-15	243	253	NTIIATGGYGR			
1318.7366	1318.6904	-0.0462	-35	629	639	VTLDYRPVIDK			
1318.7366	1318.6904	-0.0462	-35	629	639	VTLDYRPVIDK			
1329.6757	1329.6276	-0.0481	-36	305	317	GEGGILINSQGER	2	0	
1329.6757	1329.6276	-0.0481	-36	305	317	GEGGILINSQGER			
1329.6757	1329.6276	-0.0481	-36	305	317	GEGGILINSQGER			
1354.7227	1354.673	-0.0497	-37	188	199	TGHSLLHTLYGR			
1354.7227	1354.673	-0.0497	-37	188	199	TGHSLLHTLYGR			
1400.7533	1400.7	-0.0533	-38	531	542	VSQLYGDLQHLK			
1473.8424	1473.785	-0.0574	-39	444	457	LGANSLLDLVVFGR	16	0	
1473.8424	1473.785	-0.0574	-39	444	457	LGANSLLDLVVFGR			
1812.865	1812.8054	-0.0596	-33	593	607	IDEYDYSKPIEGQQK			
2167.1406	2167.1191	-0.0215	-10	354	371	DHVYLQLHHLPPEQLATR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Serum Albumin Precursor	spt|P02770	10	200	100	133	100	46	99.815	14.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1248.6371	1248.601	-0.0361	-29	35	44	FKDLGEQHFK			
1266.6365	1266.6023	-0.0342	-27	247	257	FPNAEFAEITK			
1266.6365	1266.6023	-0.0342	-27	247	257	FPNAEFAEITK			
1299.7056	1299.6666	-0.039	-30	362	372	HPDYSVSLLLR	11	0	
1299.7056	1299.6666	-0.039	-30	362	372	HPDYSVSLLLR			

1299.7056	1299.6666	-0.039	-30	362	372	HPDYSVSLLLR	10	0	
1439.7853	1439.7335	-0.0518	-36	439	452	APQVSTPTLVEAAR			
1439.7853	1439.7335	-0.0518	-36	439	452	APQVSTPTLVEAAR	46	99.797	
1453.7355	1453.7324	-0.0031	-2	410	421	NLVKTNCELYEK			
1453.7355	1453.7324	-0.0031	-2	410	421	NLVKTNCELYEK			
1455.8066	1455.7371	-0.0695	-48	361	372	RHPDYSVSLLLR			
1465.7798	1465.7249	-0.0549	-37	422	434	LGEYGFQNAVLVR			
1465.7798	1465.7249	-0.0549	-37	422	434	LGEYGFQNAVLVR	36	97.949	
1465.7798	1465.7249	-0.0549	-37	422	434	LGEYGFQNAVLVR	46	99.815	
1609.7897	1609.7301	-0.0596	-37	348	360	DVFLGTFLYEYSR	31	93.96	
1609.7897	1609.7301	-0.0596	-37	348	360	DVFLGTFLYEYSR			
2060.0276	2059.9717	-0.0559	-27	169	184	RHPYFYAPELLYYAEK			
2230.1213	2230.2	0.0787	35	509	527	RPCFSALTVDETYVPKEFK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Heat shock protein 73	gi|13242237	13	437	100	339	100	79	100	24.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
861.4424	861.4788	0.0364	42	252	258	DISENKR			
861.4424	861.4788	0.0364	42	252	258	DISENKR	6	0	
1081.5676	1081.5577	-0.0099	-9	349	357	LLQDFFNGK			
1197.6626	1197.6338	-0.0288	-24	459	469	FELTGIPPAPR			
1197.6626	1197.6338	-0.0288	-24	459	469	FELTGIPPAPR	1	0	
1199.6742	1199.6482	-0.026	-22	160	171	DAGTIAGLNVLR			
1199.6742	1199.6482	-0.026	-22	160	171	DAGTIAGLNVLR	27	85.602	
1228.6281	1228.5988	-0.0293	-24	26	36	VEIIANDQGNR			
1228.6281	1228.5988	-0.0293	-24	26	36	VEIIANDQGNR	41	99.405	
1253.6161	1253.5824	-0.0337	-27	302	311	FEELNADLFR			
1253.6161	1253.5824	-0.0337	-27	302	311	FEELNADLFR	79	100	
1253.6161	1253.5824	-0.0337	-27	302	311	FEELNADLFR	73	100	
1480.7543	1480.7019	-0.0524	-35	300	311	ARFEELNADLFR			
1480.7543	1480.7019	-0.0524	-35	300	311	ARFEELNADLFR			
1481.807	1481.7521	-0.0549	-37	329	342	SQIHDIVLVGGSTR			
1481.807	1481.7521	-0.0549	-37	329	342	SQIHDIVLVGGSTR	45	99.754	
1487.7013	1487.6484	-0.0529	-36	37	49	TTPSYVAFTDTER	7	0	
1487.7013	1487.6484	-0.0529	-36	37	49	TTPSYVAFTDTER			
1691.7256	1691.6685	-0.0571	-34	221	236	STAGDTHLGGEDFDNR	67	99.999	
1691.7256	1691.6685	-0.0571	-34	221	236	STAGDTHLGGEDFDNR			
1691.7256	1691.6685	-0.0571	-34	221	236	STAGDTHLGGEDFDNR	74	100	
1745.809	1745.7594	-0.0496	-28	584	597	NQTAEKEEFEHQQK			
1745.809	1745.7594	-0.0496	-28	584	597	NQTAEKEEFEHQQK			
1981.9978	1981.9542	-0.0436	-22	138	155	TVTNAVVTVPAYFNDSQR	34	97.054	
1981.9978	1981.9542	-0.0436	-22	138	155	TVTNAVVTVPAYFNDSQR	31	94.809	
1981.9978	1981.9542	-0.0436	-22	138	155	TVTNAVVTVPAYFNDSQR			
2774.3267	2774.4568	0.1301	47	424	447	QTQTFTTYSDNQPGVLIQVYEGER	28	88.107	
2774.3267	2774.4568	0.1301	47	424	447	QTQTFTTYSDNQPGVLIQVYEGER			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Dihydropyrimidinase related protein-2 (DRP	spt|P47942	9	278	100	206	100	44	99.559	22.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
908.4988	908.5223	0.0235	26	391	397	VFNLYPR			
908.4988	908.5223	0.0235	26	391	397	VFNLYPR	43	99.467	
908.4988	908.5223	0.0235	26	391	397	VFNLYPR	36	97.454	
1015.553	1015.5703	0.0173	17	259	268	SAAEVIAQAR	23	41.01	
1015.553	1015.5703	0.0173	17	259	268	SAAEVIAQAR			

1015.553	1015.5703	0.0173	17	259	268	SAAEVIAQAR	22	31.329	
1140.6088	1140.6252	0.0164	14	472	480	KPFPDFVYK			
1140.6088	1140.6252	0.0164	14	472	480	KPFPDFVYK			
1246.6348	1246.6833	0.0485	39	147	157	GIQEEMEALVK			
1682.8707	1682.8523	-0.0184	-11	452	467	IVLEDGTLHVTEGSGR			
1682.8707	1682.8523	-0.0184	-11	452	467	IVLEDGTLHVTEGSGR	22	32.271	
1682.8707	1682.8523	-0.0184	-11	452	467	IVLEDGTLHVTEGSGR	22	31.17	
1792.8348	1792.8182	-0.0166	-9	346	361	DNFTLIPEGTNGTEER			
1792.8348	1792.8182	-0.0166	-9	346	361	DNFTLIPEGTNGTEER	44	99.559	
1911.0222	1910.9985	-0.0237	-12	174	189	FQLTDSQIYEVLSVIR	14	0	
1911.0222	1910.9985	-0.0237	-12	174	189	FQLTDSQIYEVLSVIR	24	61.205	
1911.0222	1910.9985	-0.0237	-12	174	189	FQLTDSQIYEVLSVIR			
2169.0684	2169.0444	-0.024	-11	533	552	NLHQSGFSLSGAQIDDNIPR	25	63.711	
2169.0684	2169.0444	-0.024	-11	533	552	NLHQSGFSLSGAQIDDNIPR			
2377.1741	2377.1543	-0.0198	-8	190	211	DIGAIAQVHAENGDIIAEEQQR	25	66.904	
2377.1741	2377.1543	-0.0198	-8	190	211	DIGAIAQVHAENGDIIAEEQQR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Tubulin, alpha 1C	gi|58865558	6	118	100	62	99.998	50	99.963	16.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1085.6201	1085.6077	-0.0124	-11	113	121	EIIDLVLDR	12	0	
1085.6201	1085.6077	-0.0124	-11	113	121	EIIDLVLDR			
1487.8792	1487.8196	-0.0596	-40	230	243	LISQIVSSITASLR			
1701.9058	1701.842	-0.0638	-37	65	79	AVFVDLEPTVIDEVR			
1701.9058	1701.842	-0.0638	-37	65	79	AVFVDLEPTVIDEVR	50	99.963	
1718.8821	1718.8239	-0.0582	-34	216	229	NLDIERPTYTNLNR			
2409.2085	2409.2214	0.0129	5	244	264	FDGALNVDLTEFQTNLVPYPR			
2707.2854	2707.3733	0.0879	32	281	304	AYHEQLTVAEITNACFEPANQMVK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Heat shock protein 73	gi|13242237	14	498	100	388	100	86	100	25.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
861.4424	861.4396	-0.0028	-3	252	258	DISENKR	23	53.094	
861.4424	861.4396	-0.0028	-3	252	258	DISENKR			
1081.5676	1081.5653	-0.0023	-2	349	357	LLQDFFNGK			
1081.5676	1081.5653	-0.0023	-2	349	357	LLQDFFNGK	4	0	
1197.6626	1197.6584	-0.0042	-4	459	469	FELTGIPPAPR	12	0	
1197.6626	1197.6584	-0.0042	-4	459	469	FELTGIPPAPR			
1199.6742	1199.6736	-0.0006	-1	160	171	DAGTIAGLNVLR			
1199.6742	1199.6736	-0.0006	-1	160	171	DAGTIAGLNVLR	18	0	
1228.6281	1228.6274	-0.0007	-1	26	36	VEIIANDQGNR	31	92.982	
1228.6281	1228.6274	-0.0007	-1	26	36	VEIIANDQGNR			
1253.6161	1253.6144	-0.0017	-1	302	311	FEELNADLFR	79	100	
1253.6161	1253.6144	-0.0017	-1	302	311	FEELNADLFR	77	100	
1253.6161	1253.6144	-0.0017	-1	302	311	FEELNADLFR			
1450.8053	1450.7566	-0.0487	-34	346	357	IQKLLQDFFNGK			
1480.7543	1480.7552	0.0009	1	300	311	ARFEELNADLFR			
1480.7543	1480.7552	0.0009	1	300	311	ARFEELNADLFR			
1481.807	1481.8018	-0.0052	-4	329	342	SQIHDIVLVGGSTR	51	99.928	
1481.807	1481.8018	-0.0052	-4	329	342	SQIHDIVLVGGSTR			
1487.7013	1487.6997	-0.0016	-1	37	49	TTPSYVAFTDTER	5	0	
1487.7013	1487.6997	-0.0016	-1	37	49	TTPSYVAFTDTER			
1691.7256	1691.7236	-0.002	-1	221	236	STAGDTHLGGEDFDNR			
1691.7256	1691.7236	-0.002	-1	221	236	STAGDTHLGGEDFDNR	61	99.993	

1691.7256	1691.7236	-0.002	-1	221	236	STAGDTHLGGEDFDNR	86	100	
1745.809	1745.8121	0.0031	2	584	597	NQTAEKEEFEHQQK			
1745.809	1745.8121	0.0031	2	584	597	NQTAEKEEFEHQQK			
1981.9978	1981.9913	-0.0065	-3	138	155	TVTNAVVTVPAYFNDSQR	33	94.749	
1981.9978	1981.9913	-0.0065	-3	138	155	TVTNAVVTVPAYFNDSQR			
1981.9978	1981.9913	-0.0065	-3	138	155	TVTNAVVTVPAYFNDSQR	34	96.17	
2774.3267	2774.3086	-0.0181	-7	424	447	QTQTFTTYSDNQPGVLIQVYEGER			
2774.3267	2774.3086	-0.0181	-7	424	447	QTQTFTTYSDNQPGVLIQVYEGER	44	99.582	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Dihydropyrimidinase related protein-2 (DRP	spt|P47942	8	217	100	135	100	35	97.699	20.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
908.4988	908.5234	0.0246	27	391	397	VFNLYPR			
908.4988	908.5234	0.0246	27	391	397	VFNLYPR	27	83.599	
908.4988	908.5234	0.0246	27	391	397	VFNLYPR	29	90.117	
1015.553	1015.5529	-0.0001	0	259	268	SAAEVIAQAR			
1682.8707	1682.806	-0.0647	-38	452	467	IVLEDGTLHVTEGSGR	25	76.564	
1682.8707	1682.806	-0.0647	-38	452	467	IVLEDGTLHVTEGSGR			
1682.8707	1682.806	-0.0647	-38	452	467	IVLEDGTLHVTEGSGR	24	68.531	
1792.8348	1792.7654	-0.0694	-39	346	361	DNFTLIPEGTNGTEER	35	97.699	
1792.8348	1792.7654	-0.0694	-39	346	361	DNFTLIPEGTNGTEER			
1911.0222	1910.9672	-0.055	-29	174	189	FQLTDSQIYEVLSVIR			
1911.0222	1910.9672	-0.055	-29	174	189	FQLTDSQIYEVLSVIR	20	23.814	
2169.0684	2169.0439	-0.0245	-11	533	552	NLHQSGFSLSGAQIDDNIPR	25	73.765	
2169.0684	2169.0439	-0.0245	-11	533	552	NLHQSGFSLSGAQIDDNIPR			
2377.1741	2377.1934	0.0193	8	190	211	DIGAIAQVHAENGDIIAEEQQR			
2377.1741	2377.1934	0.0193	8	190	211	DIGAIAQVHAENGDIIAEEQQR			
2748.489	2748.4299	-0.0591	-22	441	467	GSPLVVISQGKIVLEDGTLHVTEGSGR			
2748.489	2748.4299	-0.0591	-22	441	467	GSPLVVISQGKIVLEDGTLHVTEGSGR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
T-complex protein 1	gi|6981642	5	158	100	125	100	45	99.842	11.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1147.6106	1147.5947	-0.0159	-14	434	443	EQLAIAEFAR			
1147.6106	1147.5947	-0.0159	-14	434	443	EQLAIAEFAR	23	73.679	
1205.6888	1205.6606	-0.0282	-23	516	526	FATEAAITILR			
1411.6713	1411.6219	-0.0494	-35	469	480	AFHNEAQVNPER			
1411.6713	1411.6219	-0.0494	-35	469	480	AFHNEAQVNPER	32	96.747	
1411.6713	1411.6219	-0.0494	-35	469	480	AFHNEAQVNPER	45	99.842	
1776.9126	1776.8523	-0.0603	-34	131	145	YINENLIINTDELGR	32	96.717	
1776.9126	1776.8523	-0.0603	-34	131	145	YINENLIINTDELGR			
1923.0909	1923.043	-0.0479	-25	248	264	LGVQVVITDPEKLDQIR			
1923.0909	1923.043	-0.0479	-25	248	264	LGVQVVITDPEKLDQIR	26	87.019	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Heat Shock Protein 1	gi|11560024	5	101	100	62	99.992	25	61.877	14.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
960.5109	960.5261	0.0152	16	421	429	VTDALNATR			
961.4849	961.5071	0.0222	23	302	310	APGFGDNRK	3	0	
961.4849	961.5071	0.0222	23	302	310	APGFGDNRK			
961.4849	961.5071	0.0222	23	302	310	APGFGDNRK			
1905.0552	1904.9963	-0.0589	-31	251	268	ISSVQSIVPALEIANAHR			

1905.0552	1904.9963	-0.0589	-31	251	268	ISSVQSIVPALEIANAHR	23	48.574	
1905.0552	1904.9963	-0.0589	-31	251	268	ISSVQSIVPALEIANAHR	25	61.877	
2365.3337	2365.3594	0.0257	11	269	290	KPLVIIAEDVDGEALSTLVLNR			
2365.3337	2365.3594	0.0257	11	269	290	KPLVIIAEDVDGEALSTLVLNR	24	56.929	
2560.2485	2560.3247	0.0762	30	97	121	LVQDVANNTNEEAGDGTTTATVLAR	13	0	
2560.2485	2560.3247	0.0762	30	97	121	LVQDVANNTNEEAGDGTTTATVLAR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Actin, cytoplasmic 2 (Gamma-actin)	spt|P63259	7	172	100	124	100	60	99.991	22.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
800.5352	800.5128	-0.0224	-28	62	68	RGILTLK			
976.4482	976.4453	-0.0029	-3	19	28	AGFAGDDAPR	31	92.938	
976.4482	976.4453	-0.0029	-3	19	28	AGFAGDDAPR			
1132.527	1132.5364	0.0094	8	197	206	GYSFTTTAER			
1132.527	1132.5364	0.0094	8	197	206	GYSFTTTAER			
1198.7054	1198.6938	-0.0116	-10	29	39	AVFPSIVGRPR	8	0	
1198.7054	1198.6938	-0.0116	-10	29	39	AVFPSIVGRPR			
1516.7026	1516.7084	0.0058	4	360	372	QEYDESGPSIVHR	32	93.835	
1516.7026	1516.7084	0.0058	4	360	372	QEYDESGPSIVHR	60	99.991	
1516.7026	1516.7084	0.0058	4	360	372	QEYDESGPSIVHR			
1790.8918	1790.8939	0.0021	1	239	254	SYELPDGQVITIGNER	23	53.344	
1790.8918	1790.8939	0.0021	1	239	254	SYELPDGQVITIGNER			
1790.8918	1790.8939	0.0021	1	239	254	SYELPDGQVITIGNER	25	69.246	
1954.0643	1954.0709	0.0066	3	96	113	VAPEEHPVLLTEAPLNPK			
1954.0643	1954.0709	0.0066	3	96	113	VAPEEHPVLLTEAPLNPK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
CNDP dipeptidase 2 (metallopeptidase M20	gi|58219062	5	67	99.582	24	89.355	24	89.355	16.0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1126.6215	1126.6255	0.004	4	150	159	TGQEIPVNLR			
1126.6215	1126.6255	0.004	4	150	159	TGQEIPVNLR			
1233.6473	1233.6448	-0.0025	-2	403	413	TVFGVEPDLTR			
1497.6968	1497.6833	-0.0135	-9	6	17	AVFQYIDENQDR	24	89.355	
1497.6968	1497.6833	-0.0135	-9	6	17	AVFQYIDENQDR			
1877.9392	1877.9293	-0.0099	-5	311	329	YPSLSLHGIEGAFSGSGAK			
2723.4324	2723.314	-0.1184	-43	340	363	FSIRLVPDMIPEVVSEQVSSYLSK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Enolase 2, gamma	gi|26023949	4	72	99.862	38	98.547	31	91.183	10.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
848.4161	848.4565	0.0404	48	423	429	FAGHNFR			
848.4161	848.4565	0.0404	48	423	429	FAGHNFR			
848.4161	848.4565	0.0404	48	423	429	FAGHNFR			
1130.6204	1130.5824	-0.038	-34	184	193	LGAEVYHTLK			
1174.5586	1174.5294	-0.0292	-25	413	422	IEEELGEEAR			
1174.5586	1174.5294	-0.0292	-25	413	422	IEEELGEEAR	8	0	
1174.5586	1174.5294	-0.0292	-25	413	422	IEEELGEEAR	5	0	
1804.9438	1804.8735	-0.0703	-39	33	50	AAVPSGASTGIYEALELR			
1804.9438	1804.8735	-0.0703	-39	33	50	AAVPSGASTGIYEALELR	27	80.079	
1804.9438	1804.8735	-0.0703	-39	33	50	AAVPSGASTGIYEALELR	31	91.183	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Actin, cytoplasmic 2 (Gamma-actin)	spt|P63259	7	360	100	300	100	102	100	22.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
800.5352	800.52	-0.0152	-19	62	68	RGILTLK			
800.5352	800.52	-0.0152	-19	62	68	RGILTLK			
800.5352	800.52	-0.0152	-19	62	68	RGILTLK			
976.4482	976.4386	-0.0096	-10	19	28	AGFAGDDAPR			
976.4482	976.4386	-0.0096	-10	19	28	AGFAGDDAPR	50	99.938	
1132.527	1132.5182	-0.0088	-8	197	206	GYSFTTTAER	43	99.698	
1132.527	1132.5182	-0.0088	-8	197	206	GYSFTTTAER			
1132.527	1132.5182	-0.0088	-8	197	206	GYSFTTTAER	48	99.903	
1515.7491	1515.73	-0.0191	-13	85	95	IWHHTFYNELR			
1515.7491	1515.73	-0.0191	-13	85	95	IWHHTFYNELR			
1516.7026	1516.6971	-0.0055	-4	360	372	QEYDESGPSIVHR	89	100	
1516.7026	1516.6971	-0.0055	-4	360	372	QEYDESGPSIVHR	93	100	
1516.7026	1516.6971	-0.0055	-4	360	372	QEYDESGPSIVHR			
1790.8918	1790.8815	-0.0103	-6	239	254	SYELPDGQVITIGNER	80	100	
1790.8918	1790.8815	-0.0103	-6	239	254	SYELPDGQVITIGNER	102	100	
1790.8918	1790.8815	-0.0103	-6	239	254	SYELPDGQVITIGNER			
1954.0643	1954.0592	-0.0051	-3	96	113	VAPEEHPVLLTEAPLNPK	7	0	
1954.0643	1954.0592	-0.0051	-3	96	113	VAPEEHPVLLTEAPLNPK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Actin, cytoplasmic 2 (Gamma-actin)	spt|P63259	7	336	100	263	100	100	100	23.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
976.4482	976.4605	0.0123	13	19	28	AGFAGDDAPR	40	99.098	
976.4482	976.4605	0.0123	13	19	28	AGFAGDDAPR	39	98.945	
976.4482	976.4605	0.0123	13	19	28	AGFAGDDAPR			
1132.527	1132.5128	-0.0142	-13	197	206	GYSFTTTAER			
1132.527	1132.5128	-0.0142	-13	197	206	GYSFTTTAER	17	0	
1198.7054	1198.6809	-0.0245	-20	29	39	AVFPSIVGRPR	26	76.109	
1198.7054	1198.6809	-0.0245	-20	29	39	AVFPSIVGRPR	29	88.67	
1198.7054	1198.6809	-0.0245	-20	29	39	AVFPSIVGRPR			
1515.7491	1515.692	-0.0571	-38	85	95	IWHHTFYNELR			
1515.7491	1515.692	-0.0571	-38	85	95	IWHHTFYNELR			
1516.7026	1516.656	-0.0466	-31	360	372	QEYDESGPSIVHR	60	99.991	
1516.7026	1516.656	-0.0466	-31	360	372	QEYDESGPSIVHR	100	100	
1516.7026	1516.656	-0.0466	-31	360	372	QEYDESGPSIVHR			
1790.8918	1790.8427	-0.0491	-27	239	254	SYELPDGQVITIGNER			
1790.8918	1790.8427	-0.0491	-27	239	254	SYELPDGQVITIGNER	70	100	
1790.8918	1790.8427	-0.0491	-27	239	254	SYELPDGQVITIGNER	54	99.965	
1954.0643	1954.0317	-0.0326	-17	96	113	VAPEEHPVLLTEAPLNPK	8	0	
1954.0643	1954.0317	-0.0326	-17	96	113	VAPEEHPVLLTEAPLNPK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Heat shock protein 1 (chaperonin)	gi|11560024	9	254	100	190	100	58	99.983	21.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
833.39	833.3827	-0.0073	-9	302	309	APGFGDNR	15	0	
833.39	833.3827	-0.0073	-9	302	309	APGFGDNR	15	0	
833.39	833.3827	-0.0073	-9	302	309	APGFGDNR			
855.4682	855.4647	-0.0035	-4	134	141	GANPVEIR			
855.4682	855.4647	-0.0035	-4	134	141	GANPVEIR	20	2.968	

960.5109	960.5073	-0.0036	-4	421	429	VTDALNATR			
960.5109	960.5073	-0.0036	-4	421	429	VTDALNATR	13	0	
961.4849	961.4968	0.0119	12	302	310	APGFGDNRK			
961.4849	961.4968	0.0119	12	302	310	APGFGDNRK			
1905.0552	1905.0482	-0.007	-4	251	268	ISSVQSIVPALEIANAHR	58	99.983	
1905.0552	1905.0482	-0.007	-4	251	268	ISSVQSIVPALEIANAHR			
1905.0552	1905.0482	-0.007	-4	251	268	ISSVQSIVPALEIANAHR	53	99.95	
1922.9528	1922.9435	-0.0093	-5	206	221	TLNDELEIIEGMKFDR			
2040.002	2040.0193	0.0173	8	371	387	IQEITEQLDITTSEYEK			
2365.3337	2365.3228	-0.0109	-5	269	290	KPLVIIAEDVDGEALSTLVLNR			
2365.3337	2365.3228	-0.0109	-5	269	290	KPLVIIAEDVDGEALSTLVLNR	30	89.287	
2560.2485	2560.2317	-0.0168	-7	97	121	LVQDVANNTNEEAGDGTTTATVLAR	39	98.617	
2560.2485	2560.2317	-0.0168	-7	97	121	LVQDVANNTNEEAGDGTTTATVLAR			
2560.2485	2560.2317	-0.0168	-7	97	121	LVQDVANNTNEEAGDGTTTATVLAR	54	99.96	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Annexin A3 (Annexin-3)	gi|122065130	10	201	100	66	99.998	35	97.59	33.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
943.4519	943.4833	0.0314	33	212	218	LTFDEYR	19	6.653	
943.4519	943.4833	0.0314	33	212	218	LTFDEYR	22	48.82	
943.4519	943.4833	0.0314	33	212	218	LTFDEYR			
986.5629	986.5803	0.0174	18	156	165	ALLTLADGGR			
1073.5837	1073.6167	0.033	31	281	289	SEIDLLDIR			
1180.5593	1180.5782	0.0189	16	265	275	GAGTDEFTLNR			
1180.5593	1180.5782	0.0189	16	265	275	GAGTDEFTLNR	10	0	
1180.5593	1180.5782	0.0189	16	265	275	GAGTDEFTLNR			
1558.8435	1558.8423	-0.0012	-1	156	170	ALLTLADGGRDESLK			
1636.9281	1636.9302	0.0021	1	250	264	NTPAFLAGRLHQALK			
1636.9281	1636.9302	0.0021	1	250	264	NTPAFLAGRLHQALK			
1636.9281	1636.9302	0.0021	1	250	264	NTPAFLAGRLHQALK			
1711.7882	1711.7799	-0.0083	-5	140	154	NLRDDISSETSGDFR			
1754.9435	1754.9231	-0.0204	-12	231	246	GELSGHFEDLLLAVVR			
2034.9879	2034.9795	-0.0084	-4	11	29	GTINNYPGFNPSVDAEAIR			
2034.9879	2034.9795	-0.0084	-4	11	29	GTINNYPGFNPSVDAEAIR	35	97.59	
2034.9879	2034.9795	-0.0084	-4	11	29	GTINNYPGFNPSVDAEAIR	25	77.762	
2163.0828	2163.061	-0.0218	-10	11	30	GTINNYPGFNPSVDAEAIRK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
F-actin capping protein subunit alpha-2	spt|P28497	4	110	100	63	99.997	33	97.284	22.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1197.6949	1197.6615	-0.0334	-28	38	47	LLLNNDNLLR			
1197.6949	1197.6615	-0.0334	-28	38	47	LLLNNDNLLR	33	97.284	
2029.0138	2028.9746	-0.0392	-19	194	210	IQVHYYEDGNVQLVSHK			
2029.0138	2028.9746	-0.0392	-19	194	210	IQVHYYEDGNVQLVSHK			
2101.05	2101.02	-0.03	-14	20	37	FIIHAPPGEFNEVFNDVR	30	94.63	
2101.05	2101.02	-0.03	-14	20	37	FIIHAPPGEFNEVFNDVR	23	72.205	
2101.05	2101.02	-0.03	-14	20	37	FIIHAPPGEFNEVFNDVR			
2107.0244	2107.0078	-0.0166	-8	48	66	EGAAHAFAQYNLDQFTPVK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Tyrosine 3-monooxgenase/tryptophan 5-mo	rf|NP_062250.1	3	64	99.147	40	98.767	40	98.767	26.0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification

1359.7267	1359.6882	-0.0385	-28	106	117	YLILNATHAESK			
1598.7405	1598.6853	-0.0552	-35	30	43	AVTEQGHELSNEER			
1598.7405	1598.6853	-0.0552	-35	30	43	AVTEQGHELSNEER	20	0	
1598.7405	1598.6853	-0.0552	-35	30	43	AVTEQGHELSNEER	40	98.767	
2159.0251	2159.021	-0.0041	-2	141	159	QTTVSNSQQAYQEAFEISK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Dimethylarginine dimethylaminohydrolase 2	gi|47087079	3	80	99.983	55	99.969	23	57.719	9.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
885.5152	885.5345	0.0193	22	106	113	ALQDLGLR			
885.5152	885.5345	0.0193	22	106	113	ALQDLGLR	14	0	
885.5152	885.5345	0.0193	22	106	113	ALQDLGLR	14	0	
927.5006	927.5251	0.0245	26	97	104	RPEVDGVR	23	57.719	
927.5006	927.5251	0.0245	26	97	104	RPEVDGVR			
1078.5527	1078.5383	-0.0144	-13	148	157	GAEIVADTFR	17	0	
1078.5527	1078.5383	-0.0144	-13	148	157	GAEIVADTFR			
1078.5527	1078.5383	-0.0144	-13	148	157	GAEIVADTFR	15	0	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Tubulin beta-2A chain	spt|Q13885	4	111	100	90	100	60	99.989	8.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1053.6091	1053.6299	0.0208	20	310	318	YLTVAAIFR			
1053.6091	1053.6299	0.0208	20	310	318	YLTVAAIFR			
1077.5323	1077.5485	0.0162	15	155	162	IREEYPDR	30	86.841	
1077.5323	1077.5485	0.0162	15	155	162	IREEYPDR			
1130.5953	1130.611	0.0157	14	242	251	FPGQLNADLR	58	99.981	
1130.5953	1130.611	0.0157	14	242	251	FPGQLNADLR	60	99.989	
1130.5953	1130.611	0.0157	14	242	251	FPGQLNADLR			
1355.6589	1355.6584	-0.0005	0	47	58	INVYYNEAAGNK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Protein phosphatase 2, catalytic subunit, be	gi|4758952	6	104	100	58	99.986	25	75.731	14.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
911.4621	911.4962	0.0341	37	303	309	RTPDYFL	10	0	
911.4621	911.4962	0.0341	37	303	309	RTPDYFL			
951.5118	951.5408	0.029	30	295	302	RGEPHVTR	20	21.105	
951.5118	951.5408	0.029	30	295	302	RGEPHVTR	23	65.002	
951.5118	951.5408	0.029	30	296	303	GEPHVTRR			
960.4744	960.5056	0.0312	32	42	49	ESNVQEVR			
1000.517	1000.548	0.031	31	22	29	QLNENQVR	0	0	
1000.517	1000.548	0.031	31	22	29	QLNENQVR			
1340.6633	1340.6693	0.006	4	284	294	YSFLQFDPAPR	25	75.731	
1340.6633	1340.6693	0.006	4	284	294	YSFLQFDPAPR	23	61.977	
1340.6633	1340.6693	0.006	4	284	294	YSFLQFDPAPR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
NSFL1 (p97) cofactor (p47)	gi|14010837	9	150	100	41	99.443	26	82.141	32.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
886.4053	886.4368	0.0315	36	94	101	FYAGGSER			
886.4053	886.4368	0.0315	36	94	101	FYAGGSER			

1026.5691	1026.5791	0.01	10	216	224	GEVPAELRR			
1038.5691	1038.5696	0.0005	0	102	111	SGQQIVGPPR			
1038.5691	1038.5696	0.0005	0	102	111	SGQQIVGPPR			
1038.5691	1038.5696	0.0005	0	102	111	SGQQIVGPPR			
1322.6222	1322.6255	0.0033	2	11	22	EFVAVTGAEEDR			
1339.7692	1339.7192	-0.05	-37	357	368	EANLLNAVIVQR			
1339.7692	1339.7192	-0.05	-37	357	368	EANLLNAVIVQR			
1339.7692	1339.7192	-0.05	-37	357	368	EANLLNAVIVQR			
1648.7812	1648.7145	-0.0667	-40	157	172	LGAAPEEESAYVAGER			
1648.7812	1648.7145	-0.0667	-40	157	172	LGAAPEEESAYVAGER			
1648.7812	1648.7145	-0.0667	-40	157	172	LGAAPEEESAYVAGER			
1754.8344	1754.7698	-0.0646	-37	200	214	SYQDPSNAQFLESIR	26	82.141	
1754.8344	1754.7698	-0.0646	-37	200	214	SYQDPSNAQFLESIR			
2057.0874	2057.0469	-0.0405	-20	283	301	ASSSILINEAEPTTNIQIR			
2057.0874	2057.0469	-0.0405	-20	283	301	ASSSILINEAEPTTNIQIR	15	0	
2099.8635	2099.8328	-0.0307	-15	77	93	DLIHDQDEEEEEEEGQR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Heat shock protein 1 (chaperonin)	gi|11560024	12	319	100	239	100	49	99.86	17.0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
815.5137	815.551	0.0373	46	340	346	ALLFVPR	46	99.731	
815.5137	815.551	0.0373	46	340	346	ALLFVPR	39	98.558	
815.5137	815.551	0.0373	46	340	346	ALLFVPR			
858.5406	858.5474	0.0068	8	459	465	KLSELLR			
1108.5421	1108.5658	0.0237	21	348	356	APFDLFENR			
1168.5706	1168.5862	0.0156	13	448	457	LGIHEDSQNR	21	4.037	
1168.5706	1168.5862	0.0156	13	448	457	LGIHEDSQNR	30	89.502	
1168.5706	1168.5862	0.0156	13	448	457	LGIHEDSQNR			
1235.6014	1235.6147	0.0133	11	501	511	DQVANSAFVER	20	0	
1235.6014	1235.6147	0.0133	11	501	511	DQVANSAFVER			
1249.5841	1249.6287	0.0446	36	174	185	TDTGEPMGRGTK			
1249.5841	1249.6287	0.0446	36	174	185	TDTGEPMGRGTK			
1264.6433	1264.6559	0.0126	10	347	356	RAPFDLFENR			
1264.6433	1264.6559	0.0126	10	347	356	RAPFDLFENR	20	0	
1311.5699	1311.5807	0.0108	8	192	201	EDQTEYLEER			
1311.5699	1311.5807	0.0108	8	192	201	EDQTEYLEER	32	92.395	
1348.6644	1348.6703	0.0059	4	329	339	HFSVEGQLEFR			
1348.6644	1348.6703	0.0059	4	329	339	HFSVEGQLEFR	26	73.448	
1513.7856	1513.7823	-0.0033	-2	388	401	GVVDSEDLPLNISR	32	92.771	
1513.7856	1513.7823	-0.0033	-2	388	401	GVVDSEDLPLNISR			
1513.7856	1513.7823	-0.0033	-2	388	401	GVVDSEDLPLNISR	49	99.86	
1786.9446	1786.9315	-0.0131	-7	634	648	HLEINPDHSIIETLR			
1786.9446	1786.9315	-0.0131	-7	634	648	HLEINPDHSIIETLR	16	0	
1786.9446	1786.9315	-0.0131	-7	634	648	HLEINPDHSIIETLR	14	0	
1833.7814	1833.7814	0	0	301	315	NPDDITNEEYGEFYK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Actin, cytoplasmic 2 (Gamma-actin)	spt|P63259	6	187	100	129	100	48	99.845	21.0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
976.4482	976.4778	0.0296	30	19	28	AGFAGDDAPR			
976.4482	976.4778	0.0296	30	19	28	AGFAGDDAPR	35	96.654	
1132.527	1132.5446	0.0176	16	197	206	GYSFTTTAER			
1132.527	1132.5446	0.0176	16	197	206	GYSFTTTAER			
1132.527	1132.5446	0.0176	16	197	206	GYSFTTTAER			

1198.7054	1198.7142	0.0088	7	29	39	AVFPSIVGRPR			
1198.7054	1198.7142	0.0088	7	29	39	AVFPSIVGRPR	10	0	
1516.7026	1516.696	-0.0066	-4	360	372	QEYDESGPSIVHR	48	99.845	
1516.7026	1516.696	-0.0066	-4	360	372	QEYDESGPSIVHR	19	0	
1516.7026	1516.696	-0.0066	-4	360	372	QEYDESGPSIVHR			
1790.8918	1790.8795	-0.0123	-7	239	254	SYELPDGQVITIGNER			
1790.8918	1790.8795	-0.0123	-7	239	254	SYELPDGQVITIGNER	36	97.133	
1790.8918	1790.8795	-0.0123	-7	239	254	SYELPDGQVITIGNER	26	75.027	
1954.0643	1954.0497	-0.0146	-7	96	113	VAPEEHPVLLTEAPLNPK			
1954.0643	1954.0497	-0.0146	-7	96	113	VAPEEHPVLLTEAPLNPK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Tubulin alpha	gi|223556	7	127	100	68	99.998	51	99.9	23.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1023.449	1023.4636	0.0146	14	97	105	EDAANNYAR			
1023.449	1023.4636	0.0146	14	97	105	EDAANNYAR	4	0	
1085.6201	1085.624	0.0039	4	113	121	EIIDLVLDR			
1085.6201	1085.624	0.0039	4	113	121	EIIDLVLDR	5	0	
1410.7739	1410.7594	-0.0145	-10	85	96	QLFHPEQLITGK			
1410.7739	1410.7594	-0.0145	-10	85	96	QLFHPEQLITGK			
1410.7739	1410.7594	-0.0145	-10	85	96	QLFHPEQLITGK			
1701.9058	1701.8801	-0.0257	-15	65	79	AVFVDLEPTVIDEVR	27	71.582	
1701.9058	1701.8801	-0.0257	-15	65	79	AVFVDLEPTVIDEVR			
1701.9058	1701.8801	-0.0257	-15	65	79	AVFVDLEPTVIDEVR	51	99.9	
1718.8821	1718.8632	-0.0189	-11	216	229	NLDIERPTYTNLNR	8	0	
1718.8821	1718.8632	-0.0189	-11	216	229	NLDIERPTYTNLNR			
1824.9854	1824.9506	-0.0348	-19	353	370	VGINYQPPTVVPGGDLAK			
2409.2085	2409.2148	0.0063	3	244	264	FDGALNVDLTEFQTNLVPYPR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
H+ transporting ATPase	rf|NP_476561.1	19	646	100	484	100	116	100	50.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
848.4593	848.4594	0.0001	0	1	7	MALRAMR			
873.4788	873.4739	-0.0049	-6	30	37	EQALAVSR			
877.4526	877.4526	0	0	38	44	NYLSQPR			
877.4526	877.4526	0	0	38	44	NYLSQPR	31	93.206	
877.4526	877.4526	0	0	38	44	NYLSQPR	41	99.248	
921.4458	921.4412	-0.0046	-5	404	412	SAIGEGMTR			
937.4407	937.4297	-0.011	-12	404	412	SAIGEGMTR			Oxidation (M)[7]
1104.5354	1104.53	-0.0054	-5	121	130	TPVSEDMLGR			
1120.5303	1120.5217	-0.0086	-8	121	130	TPVSEDMLGR			Oxidation (M)[7]
1298.6045	1298.6053	0.0008	1	110	120	TSCEFTGDILR	101	100	Carbamidomethyl (C)[3]
1298.6045	1298.6053	0.0008	1	110	120	TSCEFTGDILR			Carbamidomethyl (C)[3]
1338.6437	1338.6447	0.001	1	461	471	NFITQGPYENR			
1338.6437	1338.6447	0.001	1	461	471	NFITQGPYENR	96	100	
1437.7373	1437.7405	0.0032	2	495	506	IPQSTLSEFYPR	72	100	
1437.7373	1437.7405	0.0032	2	495	506	IPQSTLSEFYPR			
1437.7373	1437.7405	0.0032	2	495	506	IPQSTLSEFYPR	116	100	
1520.7954	1520.7828	-0.0126	-8	94	108	AVVQVFEGTSGIDAK			
1556.8319	1556.8228	-0.0091	-6	68	81	YAEIVHLTLPDGTK			
1596.9108	1596.9116	0.0008	1	387	400	QIYPPINVLPSLSR			
1596.9108	1596.9116	0.0008	1	387	400	QIYPPINVLPSLSR	85	100	
1647.9427	1647.9269	-0.0158	-10	49	64	TVSGVNGPLVILDHVK			
1896.8837	1896.8845	0.0008	0	322	337	GFPGYMYTDLATIYER			

1912.8785	1912.877	-0.0015	-1	322	337	GFPGYMYTDLATIYER			Oxidation (M)[6]
1934.0051	1934.0004	-0.0047	-2	292	308	HVLVILTDMSSYAEALR			Oxidation (M)[9]
2048.0593	2048.0579	-0.0014	-1	8	29	GIVNGAAPELPVPTGGPMAGAR			Oxidation (M)[18]
2178.1487	2178.155	0.0063	3	189	208	IPIFSAAGLPHNEIAAQICR	45	99.715	Carbamidomethyl (C)[19]
2178.1487	2178.155	0.0063	3	189	208	IPIFSAAGLPHNEIAAQICR			Carbamidomethyl (C)[19]
2197.0383	2197.1338	0.0955	43	322	340	GFPGYMYTDLATIYERAGR			Oxidation (M)[6]
2441.1687	2441.1953	0.0266	11	164	185	IYPEEMIQTGISAIDGMNSIAR			Oxidation (M)[6,17]
2485.2214	2485.2373	0.0159	6	142	163	GPVVLAEDFLDIMGQPINPQCR			Carbamidomethyl (C)[21]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
SNAP-25B	dbj|BAA20152.1	9	153	100	85	100	75	100	7.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
831.4431	831.4696	0.0265	32	136	142	RVTNDAR			
1064.4677	1064.4695	0.0018	2	9	16	NELEEMQR			Oxidation (M)[6]
1064.4677	1064.4695	0.0018	2	9	16	NELEEMQR			Oxidation (M)[6]
1224.6041	1224.6045	0.0004	0	125	135	EQMAISGGFIR			Oxidation (M)[3]
1224.6041	1224.6045	0.0004	0	125	135	EQMAISGGFIR			Oxidation (M)[3]
1248.6616	1248.6284	-0.0332	-27	31	40	RMLQLVEESK			Oxidation (M)[2]
1434.6707	1434.6779	0.0072	5	18	30	ADQLADESLESTR	75	100	
1434.6707	1434.6779	0.0072	5	18	30	ADQLADESLESTR			
1434.6707	1434.6779	0.0072	5	18	30	ADQLADESLESTR	44	99.517	
1676.8159	1676.8105	-0.0054	-3	46	59	TLVMLDEQGEQLER			Oxidation (M)[4]
1676.8159	1676.8105	-0.0054	-3	46	59	TLVMLDEQGEQLER			Oxidation (M)[4]
1676.8159	1676.8105	-0.0054	-3	46	59	TLVMLDEQGEQLER	4	0	Oxidation (M)[4]
1776.7639	1776.7579	-0.006	-3	162	176	HMALDMGNEIDTQNR			Oxidation (M)[2,6]
1776.7639	1776.7579	-0.006	-3	162	176	HMALDMGNEIDTQNR	5	0	Oxidation (M)[2,6]
1983.8204	1983.8989	0.0785	40	1	16	MAEDADMRNELEEMQR			Oxidation (M)[1]
2176.0186	2176.022	0.0034	2	143	161	ENEMDENLEQVSGIIGNLR			Oxidation (M)[4]
2176.0186	2176.022	0.0034	2	143	161	ENEMDENLEQVSGIIGNLR			Oxidation (M)[4]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
SNAP-25B	dbj|BAA20152.1	12	290	100	148	100	52	99.869	44.0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
817.4315	817.4338	0.0023	3	23	29	ASHSFLR			
817.4315	817.4338	0.0023	3	23	29	ASHSFLR	32	88.654	
821.4263	821.4359	0.0096	12	30	37	GLFGGNTR	23	0	
821.4263	821.4359	0.0096	12	30	37	GLFGGNTR	18	0	
821.4263	821.4359	0.0096	12	30	37	GLFGGNTR			
853.405	853.4102	0.0052	6	314	320	EFDSISR			
853.405	853.4102	0.0052	6	314	320	EFDSISR	52	99.869	
1000.5244	1000.5168	-0.0076	-8	71	78	LHMQLQSK			Oxidation (M)[3]
1317.5449	1317.5438	-0.0011	-1	38	47	IEEACEMYTR			Carbamidomethyl (C)[5]
1317.5449	1317.5438	-0.0011	-1	38	47	IEEACEMYTR			Carbamidomethyl (C)[5]
1405.7509	1405.7484	-0.0025	-2	321	331	LDQWLTTMLLR			Oxidation (M)[8]
1482.7587	1482.7572	-0.0015	-1	217	229	VAAYAAQLEQYQK			
1508.6362	1508.6344	-0.0018	-1	277	288	YEEMFPAFTDSR			Oxidation (M)[4]
1508.6362	1508.6344	-0.0018	-1	277	288	YEEMFPAFTDSR	41	98.364	Oxidation (M)[4]
1508.6362	1508.6344	-0.0018	-1	277	288	YEEMFPAFTDSR	8	0	Oxidation (M)[4]
1582.7133	1582.7101	-0.0032	-2	79	93	HDSATSFVDAGNAYK			
2060.9771	2060.9761	-0.001	0	296	313	LLEAHEEQNSEAYTEAVK			
2060.9771	2060.9761	-0.001	0	296	313	LLEAHEEQNSEAYTEAVK			
2135.0688	2135.0654	-0.0034	-2	230	248	AIEIYEQVGANTMDNPLLK			Oxidation (M)[13]
2467.1228	2467.1248	0.002	1	95	116	ADPQEAINCLNAAIDIYTDMGR			Oxidation (M)[20]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
alpha-soluble NSF attachment protein	pir|S58285	11	398	100	259	100	104	100	46.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
869.3999	869.4064	0.0065	7	265	271	EYDSISR			
869.3999	869.4064	0.0065	7	265	271	EYDSISR	27	57.725	
1175.5538	1175.5592	0.0054	5	286	295	TIQGDEEDLR	47	99.52	
1175.5538	1175.5592	0.0054	5	286	295	TIQGDEEDLR			
1184.5616	1184.5587	-0.0029	-2	107	116	AIEIYTDMGR	6	0	Oxidation (M)[8]
1184.5616	1184.5587	-0.0029	-2	107	116	AIEIYTDMGR			Oxidation (M)[8]
1253.583	1253.5865	0.0035	3	38	47	IEEACEIYAR			Carbamidomethyl (C)[5]
1253.583	1253.5865	0.0035	3	38	47	IEEACEIYAR	81	100	Carbamidomethyl (C)[5]
1418.6943	1418.6959	0.0016	1	7	19	QAEAMALLAEAER			Oxidation (M)[5]
1433.6511	1433.6479	-0.0032	-2	95	106	ADPQEAINCLMR			Carbamidomethyl (C)[9]
1460.6692	1460.6735	0.0043	3	228	239	YEELFPAFSDSR	104	100	
1460.6692	1460.6735	0.0043	3	228	239	YEELFPAFSDSR			
1460.6692	1460.6735	0.0043	3	228	239	YEELFPAFSDSR	30	78.118	
1468.743	1468.7383	-0.0047	-3	168	180	VAGYAAQLEQYQK			
1558.7173	1558.712	-0.0053	-3	141	153	AIAHYEQSADYYK			
2067.0315	2067.0212	-0.0103	-5	181	199	AIDIYEQVGTSAMDSPLL			Oxidation (M)[13]
2090.9875	2090.9797	-0.0078	-4	247	264	LLEAHEEQNVDSYTESVK			
2090.9875	2090.9797	-0.0078	-4	247	264	LLEAHEEQNVDSYTESVK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
RAB GDP dissociation inhibitor alpha	spt|P50398	7	150	100	93	100	47	99.673	17.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
938.4941	938.4993	0.0052	6	131	138	LYSESLAR			
938.4941	938.4993	0.0052	6	131	138	LYSESLAR	25	44.157	
938.4941	938.4993	0.0052	6	131	138	LYSESLAR	14	0	
1141.5922	1141.5934	0.0012	1	10	18	MLLYTEVTR			Oxidation (M)[1]
1141.5922	1141.5934	0.0012	1	10	18	MLLYTEVTR			Oxidation (M)[1]
1476.7152	1476.7177	0.0025	2	199	210	QLICDPSYIPDR	16	0	Carbamidomethyl (C)[4]
1476.7152	1476.7177	0.0025	2	199	210	QLICDPSYIPDR	8	0	Carbamidomethyl (C)[4]
1476.7152	1476.7177	0.0025	2	199	210	QLICDPSYIPDR			Carbamidomethyl (C)[4]
1484.6686	1484.6689	0.0003	0	77	89	TFEGVDPQTTSMR	4	0	Oxidation (M)[12]
1484.6686	1484.6689	0.0003	0	77	89	TFEGVDPQTTSMR			Oxidation (M)[12]
1722.8796	1722.8923	0.0127	7	269	284	YIAIASTTVETAEPEK			
1852.8383	1852.8461	0.0078	4	114	128	TDDYLDQPCLETINR			Carbamidomethyl (C)[9]
1852.8383	1852.8461	0.0078	4	114	128	TDDYLDQPCLETINR			Carbamidomethyl (C)[9]
1852.8383	1852.8461	0.0078	4	114	128	TDDYLDQPCLETINR	47	99.673	Carbamidomethyl (C)[9]
2199.0571	2199.0671	0.01	5	230	248	NTNDANSCQIIIPQNQVNR			Carbamidomethyl (C)[8]
2199.0571	2199.0671	0.01	5	230	248	NTNDANSCQIIIPQNQVNR			Carbamidomethyl (C)[8]
2199.0571	2199.0671	0.01	5	230	248	NTNDANSCQIIIPQNQVNR			Carbamidomethyl (C)[8]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Protein disulfide isomerase A3 precursor	spt|P11598	12	173	100	80	100	28	58.011	24.0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
877.489	877.4939	0.0049	6	297	304	LNFAVASR			
877.489	877.4939	0.0049	6	297	304	LNFAVASR	20	0	
995.5632	995.5688	0.0056	6	131	140	QAGPASVPLR			
995.5632	995.5688	0.0056	6	131	140	QAGPASVPLR	0	0	
997.5101	997.5241	0.014	14	153	161	DASVVGFFR			
997.5101	997.5241	0.014	14	153	161	DASVVGFFR	16	0	

1188.5354	1188.5348	-0.0006	-1	336	344	FVMQEEFSR			Oxidation (M)[3]
1188.5354	1188.5348	-0.0006	-1	336	344	FVMQEEFSR			Oxidation (M)[3]
1191.6005	1191.6041	0.0036	3	63	73	LAPEYEAAATR	28	58.011	
1191.6005	1191.6041	0.0036	3	63	73	LAPEYEAAATR			
1191.6005	1191.6041	0.0036	3	63	73	LAPEYEAAATR			
1236.5127	1236.5243	0.0116	9	108	119	DGEEAGAYDGPR			
1244.6633	1244.6599	-0.0034	-3	184	194	FAHTNVESLVK			
1397.7059	1397.7083	0.0024	2	472	482	ELNDFISYLQR			
1397.7059	1397.7083	0.0024	2	472	482	ELNDFISYLQR	17	0	
1593.8483	1593.8467	-0.0016	-1	483	496	EATNPPIIQEEKPK			
1744.8864	1744.9275	0.0411	24	131	146	QAGPASVPLRTEDEFK			
1749.8541	1749.8126	-0.0415	-24	380	395	VVVAESFDDIVNAEDK			
1749.8541	1749.8126	-0.0415	-24	380	395	VVVAESFDDIVNAEDK			
1792.8977	1792.839	-0.0587	-33	180	194	DNYRFAHTNVESLVK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Unnamed protein product	emb|CAA37654.1	9	227	100	130	100	35	92.025	21.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
833.39	833.4079	0.0179	21	276	283	APGFGDNR	31	77.986	
833.39	833.4079	0.0179	21	276	283	APGFGDNR			
833.39	833.4079	0.0179	21	276	283	APGFGDNR	30	71.64	
855.4682	855.4739	0.0057	7	108	115	GANPVEIR	35	92.025	
855.4682	855.4739	0.0057	7	108	115	GANPVEIR			
912.5876	912.5808	-0.0068	-7	267	275	VGLQVVAVK			
960.5109	960.517	0.0061	6	395	403	VTDALNATR	27	46.086	
960.5109	960.517	0.0061	6	395	403	VTDALNATR	19	0	
960.5109	960.517	0.0061	6	395	403	VTDALNATR			
1520.7512	1520.7471	-0.0041	-3	180	192	TLNDELEIIEGMK			Oxidation (M)[12]
1684.905	1684.9052	0.0002	0	404	420	AAVEEGIVLGGGCALLR	17	0	Carbamidomethyl (C)[13]
1684.905	1684.9052	0.0002	0	404	420	AAVEEGIVLGGGCALLR			Carbamidomethyl (C)[13]
1905.0552	1905.0566	0.0014	1	225	242	ISSVQSIVPALEIANAHR			
2040.002	2040.0024	0.0004	0	345	361	IQEITEQLDITTSEYEK			
2560.2485	2560.251	0.0025	1	71	95	LVQDVANNTNEEAGDGTTTATVLAR			
2560.2485	2560.251	0.0025	1	71	95	LVQDVANNTNEEAGDGTTTATVLAR			
2560.2485	2560.251	0.0025	1	71	95	LVQDVANNTNEEAGDGTTTATVLAR	20	0	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Enolase 2, gamma	gi|26023949	8	184	100	90	100	68	99.995	21.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
800.3824	800.3976	0.0152	19	257	262	YDLDFK			
848.4161	848.4239	0.0078	9	423	429	FAGHNFR			
848.4161	848.4239	0.0078	9	423	429	FAGHNFR			
848.4161	848.4239	0.0078	9	423	429	FAGHNFR			
1130.6204	1130.6077	-0.0127	-11	184	193	LGAEVYHTLK			
1174.5586	1174.5623	0.0037	3	413	422	IEEELGEEAR	68	99.995	
1174.5586	1174.5623	0.0037	3	413	422	IEEELGEEAR			
1174.5586	1174.5623	0.0037	3	413	422	IEEELGEEAR	64	99.988	
1380.7118	1380.705	-0.0068	-5	16	28	GNPTVEVDLHTAK			
1380.7118	1380.705	-0.0068	-5	16	28	GNPTVEVDLHTAK			
1620.7396	1620.7461	0.0065	4	240	253	MVIGMDVAASEFYR			Oxidation (M)[1,5]
1620.7786	1620.7461	-0.0325	-20	90	103	LDNLMLELDGTENK			Oxidation (M)[5]
1620.7786	1620.7461	-0.0325	-20	90	103	LDNLMLELDGTENK			Oxidation (M)[5]
1804.9438	1804.9406	-0.0032	-2	33	50	AAVPSGASTGIYEALELR			
1804.9438	1804.9406	-0.0032	-2	33	50	AAVPSGASTGIYEALELR	23	0	

1804.9438	1804.9406	-0.0032	-2	33	50	AAVPSGASTGIYEALELR	17	0	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Guanine nucleotide binding protein, alpha o	cra|rCP51914	6	144	100	84	100	48	99.6	17.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
836.4512	836.4588	0.0076	9	228	234	KDLFGEK			
891.4682	891.4689	0.0007	1	155	162	LFDVGGQR			
891.4682	891.4689	0.0007	1	155	162	LFDVGGQR	11	0	
891.4682	891.4689	0.0007	1	155	162	LFDVGGQR	26	40.441	
1044.4996	1044.5084	0.0088	8	111	118	YYLDSLDR	10	0	
1044.4996	1044.5084	0.0088	8	111	118	YYLDSLDR	6	0	
1044.4996	1044.5084	0.0088	8	111	118	YYLDSLDR			
1298.5933	1298.6355	0.0422	32	43	54	AMDTLGVEYGDK			
1298.5933	1298.6355	0.0422	32	43	54	AMDTLGVEYGDK			
1298.5933	1298.6355	0.0422	32	43	54	AMDTLGVEYGDK			
1445.6907	1445.6952	0.0045	3	11	23	IIHEDGFSGEDVK			
1689.8442	1689.8507	0.0065	4	119	133	IGAADYQPTEQDILR	48	99.6	
1689.8442	1689.8507	0.0065	4	119	133	IGAADYQPTEQDILR			
1689.8442	1689.8507	0.0065	4	119	133	IGAADYQPTEQDILR	7	0	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Translationally controlled tumor protein (TC	rf|XP_344132.1	3	129	100	92	100	46	99.57	5.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
851.3815	851.3894	0.0079	9	157	163	DSLEMEK			
1028.5371	1028.4962	-0.0409	-40	95	102	IEEQKPER	46	99.57	
1028.5371	1028.4962	-0.0409	-40	95	102	IEEQKPER			Carbamidomethyl (C)[7]
1213.6534	1213.614	-0.0394	-32	93	102	GKIEEQKPER			
1213.6534	1213.614	-0.0394	-32	93	102	GKIEEQKPER	46	99.483	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Peroxiredoxin 2	spt|P35704	5	293	100	226	100	79	100	27.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
876.5189	876.5029	-0.016	-18	128	135	GLFIIDAK	29	69.146	
876.5189	876.5029	-0.016	-18	128	135	GLFIIDAK			
937.4373	937.4267	-0.0106	-11	120	127	NDEGIAYR	45	99.278	
937.4373	937.4267	-0.0106	-11	120	127	NDEGIAYR			
937.4373	937.4267	-0.0106	-11	120	127	NDEGIAYR	59	99.969	
1108.5997	1108.5862	-0.0135	-12	110	119	SLSQNYGVLK	60	99.978	
1108.5997	1108.5862	-0.0135	-12	110	119	SLSQNYGVLK			
1211.6742	1211.6682	-0.006	-5	140	150	QITVNDLPVGR			
1211.6742	1211.6682	-0.006	-5	140	150	QITVNDLPVGR	39	97.173	
1211.6742	1211.6682	-0.006	-5	140	150	QITVNDLPVGR	79	100	
1706.9686	1706.9591	-0.0095	-6	93	109	EGGLGPLNIPLLADVTK			
1706.9686	1706.9591	-0.0095	-6	93	109	EGGLGPLNIPLLADVTK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Proteasome subunit, beta type 6 precursor	spt|P28073	8	198	100	121	100	54	99.946	38.2

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
847.4268	847.434	0.0072	8	164	172	DGSSGGVIR			
847.4268	847.434	0.0072	8	164	172	DGSSGGVIR			

1083.543	1083.5366	-0.0064	-6	17	26	TTTGSYIANR			
1083.543	1083.5366	-0.0064	-6	17	26	TTTGSYIANR			
1110.6517	1110.6393	-0.0124	-11	184	193	QVLLGDQIPK			
1171.6429	1171.6461	0.0032	3	173	183	LAAIQQSGVER	45	99.529	
1171.6429	1171.6461	0.0032	3	173	183	LAAIQQSGVER			
1171.6429	1171.6461	0.0032	3	173	183	LAAIQQSGVER	54	99.946	
1490.7598	1490.7704	0.0106	7	2	16	AVQFDGGVVLGADSR			
1568.7461	1568.7571	0.011	7	31	42	LTPIHDHIFCCR	54	99.943	Carbamidomethyl (C)[10,11]
1568.7461	1568.7571	0.011	7	31	42	LTPIHDHIFCCR	8	0	Carbamidomethyl (C)[10,11]
1568.7461	1568.7571	0.011	7	31	42	LTPIHDHIFCCR			Carbamidomethyl (C)[10,11]
1952.9204	1952.9756	0.0552	28	147	163	DECLQFTANALALAMER			Carbamidomethyl (C)[3]
1952.9204	1952.9756	0.0552	28	147	163	DECLQFTANALALAMER			Carbamidomethyl (C)[3]
2362.0986	2362.0947	-0.0039	-2	120	141	QSFAIGGSGSSYIYGYVDATYR			
2362.0986	2362.0947	-0.0039	-2	120	141	QSFAIGGSGSSYIYGYVDATYR	13	0	
2362.0986	2362.0947	-0.0039	-2	120	141	QSFAIGGSGSSYIYGYVDATYR	13	0	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Isocitrate dehydrogenase 3 (NAD+) alpha	gi|16758446	14	522	100	375	100	127	100	38.5

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
818.4617	818.4658	0.0041	5	170	177	LITEGASK			
855.4682	855.4697	0.0015	2	193	200	SNVTAVHK	42	99.008	
855.4682	855.4697	0.0015	2	193	200	SNVTAVHK	43	99.035	
855.4682	855.4697	0.0015	2	193	200	SNVTAVHK			
987.4968	987.499	0.0022	2	78	85	WMIPPEAK			Oxidation (M)[2]
1028.516	1028.5328	0.0168	16	59	66	APIQWEER	43	99.179	
1028.516	1028.5328	0.0168	16	59	66	APIQWEER			
1041.5687	1041.5758	0.0071	7	67	77	NVTAIQGPGGK			
1054.5238	1054.5271	0.0033	3	206	214	MSDGLFLQK			Oxidation (M)[1]
1123.5817	1123.5925	0.0108	10	327	336	IEAACFATIK			Carbamidomethyl (C)[5]
1142.5411	1142.5515	0.0104	9	317	326	HMGLFDHAAK			Oxidation (M)[2]
1216.5996	1216.6183	0.0187	15	179	188	IAEFAFEYAR	86	100	
1216.5996	1216.6183	0.0187	15	179	188	IAEFAFEYAR	88	100	
1216.5996	1216.6183	0.0187	15	179	188	IAEFAFEYAR			
1316.5245	1316.5454	0.0209	16	351	360	CSDFTEEICR			Carbamidomethyl (C)[1,9]
1316.5245	1316.5454	0.0209	16	351	360	CSDFTEEICR	75	100	Carbamidomethyl (C)[1,9]
1391.7529	1391.7712	0.0183	13	135	146	TPYTDVNIVTIR	127	100	
1391.7529	1391.7712	0.0183	13	135	146	TPYTDVNIVTIR			
1391.7529	1391.7712	0.0183	13	135	146	TPYTDVNIVTIR	99	100	
1606.8734	1606.8842	0.0108	7	101	115	TPIAAGHPSMNLLLR			Oxidation (M)[10]
1606.8734	1606.8842	0.0108	7	101	115	TPIAAGHPSMNLLLR			Oxidation (M)[10]
1894.9435	1894.948	0.0045	2	300	316	DMANPTALLLSAVMMLR			Oxidation (M)[2,14,15]
2502.2358	2502.2295	-0.0063	-3	147	169	ENTEGEYSGIEHVIVDGVVQSIK			
2502.2358	2502.2295	-0.0063	-3	147	169	ENTEGEYSGIEHVIVDGVVQSIK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Isocitrate dehydrogenase 3 (NAD+) alpha	gi|16758446	12	490	100	367	100	123	100	35.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
855.4682	855.4721	0.0039	5	193	200	SNVTAVHK			
855.4682	855.4721	0.0039	5	193	200	SNVTAVHK	42	98.953	
855.4682	855.4721	0.0039	5	193	200	SNVTAVHK	28	73.4	
987.4968	987.4988	0.002	2	78	85	WMIPPEAK			Oxidation (M)[2]
1028.516	1028.5276	0.0116	11	59	66	APIQWEER	27	65.969	
1028.516	1028.5276	0.0116	11	59	66	APIQWEER			
1041.5687	1041.5729	0.0042	4	67	77	NVTAIQGPGGK			

1054.5238	1054.5273	0.0035	3	206	214	MSDGLFLQK			Oxidation (M)[1]
1142.5411	1142.5481	0.007	6	317	326	HMGLFDHAAK			Oxidation (M)[2]
1216.5996	1216.6154	0.0158	13	179	188	IAEFAFEYAR	52	99.907	
1216.5996	1216.6154	0.0158	13	179	188	IAEFAFEYAR	101	100	
1216.5996	1216.6154	0.0158	13	179	188	IAEFAFEYAR			
1316.5245	1316.5406	0.0161	12	351	360	CSDFTEEICR			Carbamidomethyl (C)[1,9]
1316.5245	1316.5406	0.0161	12	351	360	CSDFTEEICR	74	100	Carbamidomethyl (C)[1,9]
1391.7529	1391.7651	0.0122	9	135	146	TPYTDVNIVTIR	123	100	
1391.7529	1391.7651	0.0122	9	135	146	TPYTDVNIVTIR	92	100	
1391.7529	1391.7651	0.0122	9	135	146	TPYTDVNIVTIR			
1606.8734	1606.8762	0.0028	2	101	115	TPIAAGHPSMNLLLR			Oxidation (M)[10]
1606.8734	1606.8762	0.0028	2	101	115	TPIAAGHPSMNLLLR			Oxidation (M)[10]
1894.9435	1894.9338	-0.0097	-5	300	316	DMANPTALLLSAVMMLR			Oxidation (M)[2,14,15]
2502.2358	2502.2271	-0.0087	-3	147	169	ENTEGEYSGIEHVIVDGVVQSIK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Platelet-activating factor acetylhydrolase IB	gi|11693154	3	75	99.904	55	99.981	55	99.981	15.7

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
910.5104	910.4982	-0.0122	-13	143	150	GEKPNPLR			
993.6818	993.6725	-0.0093	-9	134	142	IIVLGLLPR	55	99.981	
993.6818	993.6725	-0.0093	-9	134	142	IIVLGLLPR			
2045.045	2045.0396	-0.0054	-3	61	79	ELFSPLHALNFGIGGDTTR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Growth factor receptor bound protein 2	cra|rCP46282	6	226	100	155	100	63	99.987	25.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
918.5155	918.5193	0.0038	4	143	149	NQQIFLR	49	99.666	
918.5155	918.5193	0.0038	4	143	149	NQQIFLR			
918.5155	918.5193	0.0038	4	143	149	NQQIFLR	63	99.987	
928.4999	928.5024	0.0025	3	79	86	HDGAFLIR			
962.5053	962.5117	0.0064	7	194	201	NYVTPVNR			
962.5053	962.5117	0.0064	7	194	201	NYVTPVNR	40	97.19	
1091.5269	1091.5247	-0.0022	-2	101	109	FGNDVQHFK	14	0	
1091.5269	1091.5247	-0.0022	-2	101	109	FGNDVQHFK	35	91.256	
1091.5269	1091.5247	-0.0022	-2	101	109	FGNDVQHFK			
1334.5729	1334.5679	-0.005	-4	182	193	GACHGQTGMFPR			Oxidation (M)[9]
1334.5729	1334.5679	-0.005	-4	182	193	GACHGQTGMFPR			Oxidation (M)[9]
1334.5729	1334.5679	-0.005	-4	182	193	GACHGQTGMFPR			Carbamidomethyl (C)[3]
1506.7335	1506.7389	0.0054	4	125	136	FNSLNELVDYHR			
1506.7335	1506.7389	0.0054	4	125	136	FNSLNELVDYHR	18	0	
1506.7335	1506.7389	0.0054	4	125	136	FNSLNELVDYHR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Stathmin (Phosphoprotein p19)	spt|P13668	8	448	100	341	100	106	100	52.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
817.405	817.4184	0.0134	16	53	59	LEAAEER			
817.405	817.4184	0.0134	16	53	59	LEAAEER	19	0	
912.4785	912.4784	-0.0001	0	62	69	SHEAEVLK			
912.4785	912.4784	-0.0001	0	62	69	SHEAEVLK	50	99.599	
945.4999	945.5049	0.005	5	52	59	KLEAAEER	71	99.997	
945.4999	945.5049	0.005	5	52	59	KLEAAEER			
945.4999	945.5049	0.005	5	52	59	KLEAAEER	37	91.508	

1011.5217	1011.525	0.0033	3	126	133	DKHVEEVR	75	99.999	
1011.5217	1011.525	0.0033	3	126	133	DKHVEEVR			
1074.5677	1074.5638	-0.0039	-4	43	51	DLSLEEIQK	20	0	
1074.5677	1074.5638	-0.0039	-4	43	51	DLSLEEIQK			
1139.6055	1139.6189	0.0134	12	76	84	EHEKEVLQK			
1165.5483	1165.5483	0	0	85	94	AIEENNNFSK			
1165.5483	1165.5483	0	0	85	94	AIEENNNFSK			
1388.7532	1388.756	0.0028	2	14	26	ASGQAFELILSPR	70	99.996	
1388.7532	1388.756	0.0028	2	14	26	ASGQAFELILSPR			
1388.7532	1388.756	0.0028	2	14	26	ASGQAFELILSPR	106	100	

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Beta-synuclein (Phosphoneuroprotein 14)	gi|2501106	4	199	100	135	100	90	100	41.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
873.4675	873.4404	-0.0271	-31	13	21	EGVVAAAEK			
951.5145	951.4857	-0.0288	-30	35	43	EGVLYVGSK	40	96.793	
951.5145	951.4857	-0.0288	-30	35	43	EGVLYVGSK			
951.5145	951.4857	-0.0288	-30	35	43	EGVLYVGSK	41	97.333	
1272.6793	1272.6532	-0.0261	-21	46	58	EGVVQGVASVAEK	90	100	
1272.6793	1272.6532	-0.0261	-21	46	58	EGVVQGVASVAEK			
1272.6793	1272.6532	-0.0261	-21	46	58	EGVVQGVASVAEK	45	99.071	
2326.2148	2326.2219	0.0071	3	61	85	EQASHLGGAVFSGAGNIAAATGLVK	4	0	
2326.2148	2326.2219	0.0071	3	61	85	EQASHLGGAVFSGAGNIAAATGLVK			
2326.2148	2326.2219	0.0071	3	61	85	EQASHLGGAVFSGAGNIAAATGLVK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Low M(r) phosphotyrosine protein phosphat	gi|257209	4	166	100	114	100	55	99.919	31.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
989.5414	989.5461	0.0047	5	21	29	SPIAEAVFR	55	99.904	
989.5414	989.5461	0.0047	5	21	29	SPIAEAVFR			
989.5414	989.5461	0.0047	5	21	29	SPIAEAVFR	55	99.919	
1262.6627	1262.6582	-0.0045	-4	115	125	IELLGSYDPQK			
1262.6627	1262.6582	-0.0045	-4	115	125	IELLGSYDPQK	28	59.275	
1447.6812	1447.6949	0.0137	9	31	42	LVTDENVSDNWR			
1955.8981	1955.9064	0.0083	4	43	60	IDSAATSTYEVGNPPDYR	31	76.511	
1955.8981	1955.9064	0.0083	4	43	60	IDSAATSTYEVGNPPDYR	31	76.727	
1955.8981	1955.9064	0.0083	4	43	60	IDSAATSTYEVGNPPDYR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Synuclein, alpha	gi|9507125	4	240	100	185	100	79	100	41.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
951.5145	951.5161	0.0016	2	35	43	EGVLYVGSK	36	93.199	
951.5145	951.5161	0.0016	2	35	43	EGVLYVGSK			
1325.7059	1325.7047	-0.0012	-1	46	58	EGVVHGVTTVAEK	79	100	
1325.7059	1325.7047	-0.0012	-1	46	58	EGVVHGVTTVAEK	24	0	
1325.7059	1325.7047	-0.0012	-1	46	58	EGVVHGVTTVAEK			
1505.7958	1505.795	-0.0008	-1	81	96	TVEGAGNIAAATGFVK	50	99.752	
1505.7958	1505.795	-0.0008	-1	81	96	TVEGAGNIAAATGFVK	22	0	
1505.7958	1505.795	-0.0008	-1	81	96	TVEGAGNIAAATGFVK			
1928.0447	1928.0422	-0.0025	-1	61	80	EQVTNVGGAVVTGVTAVAQK			
1928.0447	1928.0422	-0.0025	-1	61	80	EQVTNVGGAVVTGVTAVAQK	20	0	
1928.0447	1928.0422	-0.0025	-1	61	80	EQVTNVGGAVVTGVTAVAQK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Synuclein, alpha	gi|9507125	5	394	100	314	100	93	100	47.9

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
873.4675	873.4681	0.0006	1	13	21	EGVVAAAEK			
951.5145	951.5106	-0.0039	-4	35	43	EGVLYVGSK	39	96.469	
951.5145	951.5106	-0.0039	-4	35	43	EGVLYVGSK	45	98.979	
951.5145	951.5106	-0.0039	-4	35	43	EGVLYVGSK			
1325.7059	1325.7023	-0.0036	-3	46	58	EGVVHGVTTVAEK			
1325.7059	1325.7023	-0.0036	-3	46	58	EGVVHGVTTVAEK	34	86.135	
1325.7059	1325.7023	-0.0036	-3	46	58	EGVVHGVTTVAEK	90	100	
1505.7958	1505.7883	-0.0075	-5	81	96	TVEGAGNIAAATGFVK			
1505.7958	1505.7883	-0.0075	-5	81	96	TVEGAGNIAAATGFVK	39	95.616	
1505.7958	1505.7883	-0.0075	-5	81	96	TVEGAGNIAAATGFVK	86	100	
1928.0447	1928.0354	-0.0093	-5	61	80	EQVTNVGGAVVTGVTAVAQK	93	100	
1928.0447	1928.0354	-0.0093	-5	61	80	EQVTNVGGAVVTGVTAVAQK	30	68.165	
1928.0447	1928.0354	-0.0093	-5	61	80	EQVTNVGGAVVTGVTAVAQK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Cu-Zn superoxide dismutase	gi|203658	5	362	100	304	100	75	100	39.0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1095.5177	1095.4684	-0.0493	-45	72	81	KHGGPADEER			
1095.5177	1095.4684	-0.0493	-45	72	81	KHGGPADEER	35	95.408	
1137.6011	1137.5525	-0.0486	-43	82	93	HVGDLGNVAAGK			
1137.6011	1137.5525	-0.0486	-43	82	93	HVGDLGNVAAGK	70	99.998	
1174.5698	1174.5244	-0.0454	-39	94	104	DGVANVSIEDR			
1174.5698	1174.5244	-0.0454	-39	94	104	DGVANVSIEDR	68	99.998	
1174.5698	1174.5244	-0.0454	-39	94	104	DGVANVSIEDR	58	99.977	
1367.7642	1367.7257	-0.0385	-28	105	117	VISLSGEHSIIGR	75	100	
1367.7642	1367.7257	-0.0385	-28	105	117	VISLSGEHSIIGR	34	93.72	
1367.7642	1367.7257	-0.0385	-28	105	117	VISLSGEHSIIGR			
1510.7648	1510.7275	-0.0373	-25	12	25	GDGPVQGVIHFEQK	56	99.963	
1510.7648	1510.7275	-0.0373	-25	12	25	GDGPVQGVIHFEQK	14	0	
1510.7648	1510.7275	-0.0373	-25	12	25	GDGPVQGVIHFEQK			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Protein phosphatase 3, regulatory subunit B	gi|4506025	6	248	100	177	100	61	99.984	54.1

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1187.6267	1187.6246	-0.0021	-2	126	135	DTQLQQIVDK			
1187.6267	1187.6246	-0.0021	-2	126	135	DTQLQQIVDK	17	0	
1187.6267	1187.6246	-0.0021	-2	126	135	DTQLQQIVDK	15	0	
1274.6335	1274.6373	0.0038	3	136	147	TIINADKDGDGR			
1369.6998	1369.696	-0.0038	-3	74	85	EFIEGVSQFSVK	28	66.431	
1369.6998	1369.696	-0.0038	-3	74	85	EFIEGVSQFSVK			
1369.6998	1369.696	-0.0038	-3	74	85	EFIEGVSQFSVK	55	99.93	
1582.8112	1582.807	-0.0042	-3	104	117	DGYISNGELFQVLK	61	99.984	
1582.8112	1582.807	-0.0042	-3	104	117	DGYISNGELFQVLK	18	0	
1582.8112	1582.807	-0.0042	-3	104	117	DGYISNGELFQVLK			
1783.8385	1783.8372	-0.0013	-1	58	73	VIDIFDTDGNGEVDFK	8	0	
1783.8385	1783.8372	-0.0013	-1	58	73	VIDIFDTDGNGEVDFK			
1783.8385	1783.8372	-0.0013	-1	58	73	VIDIFDTDGNGEVDFK	45	99.284	
3174.5623	3174.5669	0.0046	1	30	57	LDLDNSGSLSVEEFMSLPELQQNPLVQR			Oxidation (M)[15]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Fatty acid binding protein 3	gi|13162363	4	181	100	124	100	67	99.996	39.8

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
907.4995	907.5041	0.0046	5	22	30	SLGVGFATR	57	99.962	
907.4995	907.5041	0.0046	5	22	30	SLGVGFATR	52	99.884	
907.4995	907.5041	0.0046	5	22	30	SLGVGFATR			
1206.575	1206.5822	0.0072	6	97	106	WDGQETTLTR			
1206.575	1206.5822	0.0072	6	97	106	WDGQETTLTR	37	96.443	
1206.575	1206.5822	0.0072	6	97	106	WDGQETTLTR	67	99.996	
1523.8904	1523.8967	0.0063	4	113	126	LILTLTHGNVVSTR			
2285.0569	2285.062	0.0051	2	59	78	NTEISFQLGVEFDEVTADDR			

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Profilin-2 (Profilin II)	gi|20178018	6	340	100	249	100	79	100	43.6

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
908.5273	908.52	-0.0073	-8	108	115	VLVFVMGK	37	95.875	Oxidation (M)[6]
908.5273	908.52	-0.0073	-8	108	115	VLVFVMGK			Oxidation (M)[6]
967.4955	967.4948	-0.0007	-1	116	125	EGVHGGGLNK	52	99.876	
967.4955	967.4948	-0.0007	-1	116	125	EGVHGGGLNK	77	100	
967.4955	967.4948	-0.0007	-1	116	125	EGVHGGGLNK			
1340.6844	1340.6814	-0.003	-2	56	68	EGFFTNGLTLGGK			
1340.6844	1340.6814	-0.003	-2	56	68	EGFFTNGLTLGGK	33	88.186	
1434.6971	1434.7017	0.0046	3	91	104	SQGGEPTYNVAVGR	79	100	
1434.6971	1434.7017	0.0046	3	91	104	SQGGEPTYNVAVGR	45	99.397	
1434.6971	1434.7017	0.0046	3	91	104	SQGGEPTYNVAVGR			
1611.8125	1611.8138	0.0013	1	54	68	DREGFFTNGLTLGGK			
1611.8125	1611.8138	0.0013	1	54	68	DREGFFTNGLTLGGK			
1705.7045	1705.6942	-0.0103	-6	75	88	DSLYVDSDCTMDIR			Oxidation (M)[11]
1705.7045	1705.6942	-0.0103	-6	75	88	DSLYVDSDCTMDIR	19	0	Carbamidomethyl (C)[9]
1705.7045	1705.6942	-0.0103	-6	75	88	DSLYVDSDCTMDIR	23	0	Carbamidomethyl (C)[9]

Protein Name	Accession No.	Peptide Count	Protein Score	Protein Score C.I.%	Total Ion Score	Total Ion C.I. %	Best Ion Score	Best Ion C.I.%	% Coverage
Endoplasmic reticulum protein 29	gi|16758848	7	203	100	121	100	42	98.165	30.4

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
802.4417	802.4583	0.0166	21	237	242	KEELQR	24	0	
802.4417	802.4583	0.0166	21	237	242	KEELQR	27	46.219	
802.4417	802.4583	0.0166	21	237	242	KEELQR			
822.4104	822.4362	0.0258	31	70	75	QDEFKR	13	0	
822.4104	822.4362	0.0258	31	70	75	QDEFKR			
1034.5994	1034.6095	0.0101	10	243	251	SLNILTAFR	39	96.528	
1034.5994	1034.6095	0.0101	10	243	251	SLNILTAFR			
1034.5994	1034.6095	0.0101	10	243	251	SLNILTAFR	19	0	
1247.5579	1247.5643	0.0064	5	60	69	FDTQYPYGEK			
1320.6622	1320.6678	0.0056	4	113	122	ESYPVFYLFR			
1320.6622	1320.6678	0.0056	4	113	122	ESYPVFYLFR			
1324.7147	1324.7227	0.008	6	37	48	GALPLDTVTFYK			
1660.8176	1660.8188	0.0012	1	209	223	ILDQGEDFPASELAR			
1660.8176	1660.8188	0.0012	1	209	223	ILDQGEDFPASELAR	42	98.165	
1660.8176	1660.8188	0.0012	1	209	223	ILDQGEDFPASELAR	42	98.144	