Spot Idx/Pos	181/H17	1	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	CTCL tumor antigen se20-7 [Homo sapiens]	gi|11385652	73769.5	56	98.434		

Peptide Information

Calc. Mass		Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1302.7449	1302.7048		-0.0401	-31	125	135	VKQEVVDVMKK			
1332.7191	1332.7322		0.0131	10	95	105	KLKAEMDEQIK			
1635.8588	1635.8796		0.0208	13	74	88	AAFEELEKALSTAQK			
1638.9788	1638.9512		-0.0276	-17	416	429	ALKDQINQLELLLK			
1722.8591	1722.9172		0.0581	34	163	175	LQTREREFQEQMK			
1764.8948	1764.9423		0.0475	27	167	180	EREFQEQMKVALEK			
1765.9153	1765.9631		0.0478	27	294	307	LQVLKQQYQTEMEK			
1767.9598	1767.9252		-0.0346	-20	136	150	SSEEQIAKLQKLHEK			
1980.0647	1980.1284		0.0637	32	176	192	VALEKSQSEYLKISQEK			
1980.0647	1980.1284		0.0637	32	176	192	VALEKSQSEYLKISQEK			
2008.0344	2008.0818		0.0474	24	71	88	SERAAFEELEKALSTAQK			
2011.0355	2011.0939		0.0584	29	434	450	HLKEHQAHVENLEADIK			
2202.1111	2202.1943		0.0832	38	324	341	EIIFQAHIEEMNEKTLEK			
2215.175	2215.208		0.033	15	16	34	NLIEQLEQDKGMVIAETKR			
2229.2271	2229.2144		-0.0127	-6	116	134	ISLQQELSRVKQEVVDVMK			
2373.2329	2373.291		0.0581	24	13	33	DAKNLIEQLEQDKGMVIAETK			
2651.3523	2651.4546		0.1023	39	220	241	DLQQEAETYRTRILELESSLEK			
2783.4182	2783.4326		0.0144	5	393	415	NHHQQQVDSIIKEHEVSIQRTEK			
2783.4182	2783.4326		0.0144	5	393	415	NHHQQQVDSIIKEHEVSIQRTEK			

20	putative protein product of HMFN0672 [Homo sapiens]	gi|51555	92622.3	40	28.403		

Peptide Information

Calc. Mass		Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1108.6108	1108.6534		0.0426	38	59	67	RVLSNTYQK			
1221.6698	1221.7092		0.0394	32	556	566	NGIYASRTLAR			
1221.6698	1221.7092		0.0394	32	556	566	NGIYASRTLAR			
1253.696	1253.7197		0.0237	19	172	181	LLHRTEELSR			
1264.726	1264.7104		-0.0156	-12	444	453	EYIRKSLLDK			
1288.7153	1288.7308		0.0155	12	386	395	NEMIKLQRTR			
1298.6997	1298.7285		0.0288	22	756	765	EMEKLHRSLR			
1334.7201	1334.7512		0.0311	23	494	504	FAEEKVELLEK			
1735.9635	1735.9049		-0.0586	-34	551	566	AVCLKNGIYASRTLAR			
1765.9199	1765.9631		0.0432	24	340	355	ACQRGFCRDVALVVTK			
1875.9745	1875.9874		0.0129	7	312	328	CSVIWVISDIERVSGGR			
2033.996	2034.0406		0.0446	22	746	762	ELADVGSEYKEMEKLHR			
2227.2544	2227.2356		-0.0188	-8	225	244	IPTSRVITLKAEEAEELSIK			
2240.2471	2240.2817		0.0346	15	348	366	DVALVVTKMDKLHLPEYLR			
2261.177	2261.1936		0.0166	7	235	253	AEEAEELSIKLDPYIRTQR			
2299.1975	2299.1907		-0.0068	-3	706	724	AQERMQHQFQQLKTGIVEK			
2379.3394	2379.2786		-0.0608	-26	630	650	KNFLIQEISAILGGLEDHILR			
2800.3423	2800.4329		0.0906	32	2	25	AETKDVFGQEPHPVEDDLYKEPTR			

28	dynamin 2 isoform 3 [Homo sapiens]	gi|56549	97590.9	38	1.168		

Peptide Information

Calc. Mass		Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
991.5683	991.6061		0.0378	38	446	453	LSSYPRLR			
1106.5914	1106.6289		0.0375	34	559	567	YMLPLDNLK			
1158.6729	1158.6517		-0.0212	-18	300	309	LQSQLLSLEK			
1348.7471	1348.7173		-0.0298	-22	654	665	NLVDSYVAIINK			
1474.776	1474.8234		0.0474	32	316	327	NFRPDDPTRKTK			
1621.8835	1621.936		0.0525	32	400	414	TGLFTPDLAFEAIVK			
1635.8448	1635.8796		0.0348	21	446	458	LSSYPRLREETER			
1735.9125	1735.9049		-0.0076	-4	45	59	SSVLENFVGRDFLPR			
1762.9445	1762.884		-0.0605	-34	230	245	GYIGVVNRSQKDIEGK			
1875.9435	1875.9874		0.0439	23	257	271	KFFLSHPAYRHMADR			
1899.9854	1899.9282		-0.0572	-30	669	684	DLMPKTIMHLMINNTK			
2254.2666	2254.2515		-0.0151	-7	846	866	RPPAAPSRPTIIRPAEPSLLD			
2273.1692	2273.1973		0.0281	12	167	188	ESSLILAVTPANMDLANSDALK			
2289.2634	2289.1868		-0.0766	-33	654	673	NLVDSYVAIINKSIRDLMPK			
2341.1685	2341.2292		0.0607	26	365	382	IFHERFPFELVKMEFDEK			
2497.2292	2497.2791		0.0499	20	570	590	DVEKGFMSNKHVFAIFNTEQR			
3139.824	3139.7295		-0.0945	-30	114	142	GISPVPINLRVYSPHVLNLTLIDLPGITK			

32	golgin-165	gi|55330	66309.7	38	0		

Peptide Information

Calc. Mass		Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1074.6152	1074.6427		0.0275	26	415	423	EKEKVNSLK			
1074.6152	1074.6427		0.0275	26	415	423	EKEKVNSLK			
1081.5887	1081.6182		0.0295	27	341	349	LALELEHEK			
1266.7052	1266.7295		0.0243	19	341	351	LALELEHEKGK			
1266.7052	1266.7295		0.0243	19	341	351	LALELEHEKGK			
1282.6862	1282.7196		0.0334	26	127	137	TAEAELSRLHR			
1332.7117	1332.7322		0.0205	15	7	20	TGDSAALQAVKSGK			
1348.733	1348.7173		-0.0157	-12	229	240	AYENAVGILSRR			
1596.8162	1596.829		0.0128	8	113	125	ELRQELMQVHGEK			
1635.8812	1635.8796		-0.0016	-1	5	20	FRTGDSAALQAVKSGK			
1716.865	1716.8021		-0.0629	-37	312	325	EKVLELEDELQESR			
1965.0624	1965.0811		0.0187	10	127	143	TAEAELSRLHREVAQVR			
2014.0563	2014.1117		0.0554	28	530	546	EIQSLKQQLDLTEQQGR			
2208.2234	2208.2935		0.0701	32	275	294	IQALEAELQAVSHSKTLLEK			
2208.2234	2208.2935		0.0701	32	275	294	IQALEAELQAVSHSKTLLEK			
2221.2773	2221.239		-0.0383	-17	376	394	READLVQLNLQVQAVLQRK			
2299.2	2299.1907		-0.0093	-4	528	546	EREIQSLKQQLDLTEQQGR			

Spot Idx/Pos	182/H19	2	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	Splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated) [Homo sapi	gi|29881667	76140.7	57	98.636		

Peptide Information

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

				Seq.	Seq.		Score		
1120.5204	1120.5302	0.0098	9	682	693	GMGPGTPAGYGR			
1143.6268	1143.6382	0.0114	10	366	376	FATHAAALSVR			
1143.6268	1143.6382	0.0114	10	366	376	FATHAAALSVR			
1153.6364	1153.6501	0.0137	12	333	342	GFGFIKLESR			
1267.6211	1267.6398	0.0187	15	33	44	SPPPGMGLNQNR			
1341.6656	1341.6849	0.0193	14	667	681	FGQGGAGPVGGQGPR			
1341.6656	1341.6849	0.0193	14	667	681	FGQGGAGPVGGQGPR			
1347.6776	1347.6803	0.0027	2	6	18	FRSRGGGGGGFHR			
1398.7964	1398.801	0.0046	3	364	376	VRFATHAAALSVR			
1649.8856	1649.9034	0.0178	11	272	286	ISDSEGFKANLSLLR			
1743.8945	1743.8977	0.0032	2	343	358	ALAEIAKAELDDTPMR			
1762.7819	1762.7941	0.0122	7	480	493	FAQHGTFEYEYSQR			
1762.7819	1762.7941	0.0122	7	480	493	FAQHGTFEYEYSQR			
1964.0123	1964.0171	0.0048	2	299	315	LFVGNLPADITEDEFKR			
1964.0123	1964.0171	0.0048	2	299	315	LFVGNLPADITEDEFKR			
2428.1196	2428.1335	0.0139	6	517	536	DKLESEMEDAYHEHQANLLR			
2639.2986	2639.3003	0.0017	1	377	399	NLSPYVSNELLEEAFSQFGPIER			
2639.2986	2639.3003	0.0017	1	377	399	NLSPYVSNELLEEAFSQFGPIER			
2673.2791	2673.2612	-0.0179	-7	243	267	GGRQHHPPYHQQHHQGPPPGGPGGR			

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
4	tumor rejection antigen (gp96) 1 [Homo sapiens]	gi|4507677	92411.3	44	73.399		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1015.473	1015.4883	0.0153	15	396	404	GLFDEYGSK			
1485.7543	1485.766	0.0117	8	435	448	GVVDSDDLPLNVSR			
1544.8278	1544.8228	-0.005	-3	103	116	ELISNASDALDKIR			
1751.8243	1751.8429	0.0186	11	415	428	RVFITDDFHDMMPK			
1751.8243	1751.8429	0.0186	11	415	428	RVFITDDFHDMMPK			
2112.1116	2112.1108	-0.0008	0	143	161	NLLHVTDTGVGMTREELVK			
2260.0627	2260.0723	0.0096	4	512	530	FQSSHHPTDITSLDQYVER			
2260.0627	2260.0723	0.0096	4	512	530	FQSSHHPTDITSLDQYVER			
2265.1145	2265.1028	-0.0117	-5	664	683	AQAYQTGKDISTNYYASQKK			
2283.1414	2283.1443	0.0029	1	411	428	LYVRRVFITDDFHDMMPK			
2299.0481	2299.0669	0.0188	8	640	660	LTESPCALVASQYGWSGNMER			
2728.3384	2728.3604	0.022	8	44	67	TDDEVVQREEEAIQLDGLNASQIR			
2733.4556	2733.4648	0.0092	3	701	724	IKEDEDDKTVLDLAVVLFETATLR			
3157.5354	3157.5505	0.0151	5	40	67	EGSRTDDEVVQREEEAIQLDGLNASQIR			

Spot Idx/Pos	183/H21	3	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	premembrane [Dengue virus type 2]	gi|18308050	13563.5	45	0	4	0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1139.5625	1139.5715	0.009	8	7	16	NGEPHMIVSR	4	0	
1139.5625	1139.5715	0.009	8	7	16	NGEPHMIVSR			
1412.6151	1412.6093	-0.0058	-4	107	118	TETWMSSEGAWK			
1524.7587	1524.7587	0	0	7	19	NGEPHMIVSRQEK			
1565.8468	1565.8579	0.0111	7	92	106	SVALVPHVGMGLETR			
1565.8468	1565.8579	0.0111	7	92	106	SVALVPHVGMGLETR			

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
2	prM (M) protein [Dengue virus type 2]	gi|25059129	18859.3	40	0	4	0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1139.5625	1139.5715	0.009	8	7	16	NGEPHMIVSR	4	0	
1139.5625	1139.5715	0.009	8	7	16	NGEPHMIVSR			
1412.6151	1412.6093	-0.0058	-4	107	118	TETWMSSEGAWK			
1524.7587	1524.7587	0	0	7	19	NGEPHMIVSRQEK			
1565.8468	1565.8579	0.0111	7	92	106	SVALVPHVGMGLETR			
1565.8468	1565.8579	0.0111	7	92	106	SVALVPHVGMGLETR			

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
15	polyprotein [Dengue virus type 2]	gi|58234 17119.3	33	0	4	0	

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1139.5625	1139.5715	0.009	8	99	108	NGEPHMIVSR	4	0	
1139.5625	1139.5715	0.009	8	99	108	NGEPHMIVSR			
1524.7587	1524.7587	0	0	99	111	NGEPHMIVSRQEK			
3337.7402	3337.7163	-0.0239	-7	79	108	TAGMIIMLIPTVMAFHLTTRNGEPHMIVSR			

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
16	polyprotein [Dengue virus type 2]	gi|52219 17111.2	33	0	4	0	

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1139.5625	1139.5715	0.009	8	99	108	NGEPHMIVSR	4	0	
1139.5625	1139.5715	0.009	8	99	108	NGEPHMIVSR			
1524.7587	1524.7587	0	0	99	111	NGEPHMIVSRQEK			
3337.7402	3337.7163	-0.0239	-7	79	108	TVGMIIMLIPTAMAFHLTTRNGEPHMIVSR			

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
2	NME1-NME2 protein [Homo sapiens]	gi|66392203	30117.6	29	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1344.7633	1344.7715	0.0082	6	7	18	TFIAIKPDGVQR			
1344.7633	1344.7715	0.0082	6	122	133	TFIAIKPDGVQR			
1785.9163	1785.9147	-0.0016	-1	204	220	VMLGETNPADSKPGTIR			
1785.9163	1785.9147	-0.0016	-1	89	105	VMLGETNPADSKPGTIR			

Spot Idx/Pos	184/H23	4	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
4	NME1-NME2 protein [Homo sapiens]	gi|66392203	30117.6	23	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1344.7633	1344.7639	0.0006	0	122	133	TFIAIKPDGVQR			
1344.7633	1344.7639	0.0006	0	7	18	TFIAIKPDGVQR			
1785.9163	1785.9246	0.0083	5	89	105	VMLGETNPADSKPGTIR			
1785.9163	1785.9246	0.0083	5	204	220	VMLGETNPADSKPGTIR			

Spot Idx/Pos	193/H14	5	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	splicing factor homolog - human	gi|543010	54233.3	65	99.794		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1147.6179	1147.6321	0.0142	12	271	279	WKALIEMEK			
1195.6581	1195.6519	-0.0062	-5	110	119	GFGFIRLETR			
1231.6792	1231.6819	0.0027	2	191	202	GIVEFSGKPAAR			
1248.6735	1248.6707	-0.0028	-2	97	107	YGKAGEVFIHK			
1457.7706	1457.7668	-0.0038	-3	338	348	KQLELRQEEER			
1538.6694	1538.6843	0.0149	10	384	398	MGQMAMGGAMGINNR			
1695.7471	1695.7589	0.0118	7	257	270	FAQPGSFEYEYAMR			
1695.7471	1695.7589	0.0118	7	257	270	FAQPGSFEYEYAMR			
1812.9888	1812.989	0.0002	0	120	135	TLAEIAKVELDNMPLR			
1814.0031	1813.995	-0.0081	-4	185	202	GRPSGKGIVEFSGKPAAR			
1859.9207	1859.9332	0.0125	7	76	91	LFVGNLPPDITEEEMR			
1859.9207	1859.9332	0.0125	7	76	91	LFVGNLPPDITEEEMR			
1880.0183	1879.993	-0.0253	-13	138	153	QLRVRFACHSASLHVR			
1988.0156	1988.0286	0.013	7	76	92	LFVGNLPPDITEEEMRK			
2163.0649	2163.074	0.0091	4	435	456	FGQAATMEGIGAIGGTPPAFNR			
2163.0649	2163.074	0.0091	4	435	456	FGQAATMEGIGAIGGTPPAFNR			
2231.1487	2231.1167	-0.032	-14	74	92	SRLFVGNLPPDITEEEMRK			
2498.177	2498.1924	0.0154	6	294	313	EKLEMEMEAARHEHQVMLMR			
2668.3252	2668.3274	0.0022	1	154	176	NLPQYVSNELLEEAFSVFGQVER			
2668.3252	2668.3274	0.0022	1	154	176	NLPQYVSNELLEEAFSVFGQVER			
3451.7058	3451.7124	0.0066	2	399	434	GAMPPAPVPAGTPAPPGPATMMPDGTLGLTPPTTER			

12	polypyrimidine tract-binding protein 1 isoform c [Homo sapiens]	gi|14165466	57185.6	24	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1184.6521	1184.6644	0.0123	10	2	13	DGIVPDIAVGTK			
1431.7379	1431.7369	-0.001	-1	123	134	GQPIYIQFSNHK			
2039.0959	2039.0962	0.0003	0	349	366	VTPQSLFILFGVYGDVQR			
2039.0959	2039.0962	0.0003	0	349	366	VTPQSLFILFGVYGDVQR			
2144.0002	2144.0244	0.0242	11	419	437	EGQEDQGLTKDYGNSPLHR			
2275.2766	2275.2791	0.0025	1	326	348	IAIPGLAGAGNSVLLVSNLNPER			
2275.2766	2275.2791	0.0025	1	326	348	IAIPGLAGAGNSVLLVSNLNPER			
3206.5132	3206.5435	0.0303	9	95	122	NQAFIEMNTEEAANTMVNYYTSVTPVLR			
3391.6296	3391.6753	0.0457	13	93	122	GKNQAFIEMNTEEAANTMVNYYTSVTPVLR			
3680.8845	3680.8735	-0.011	-3	147	185	AQAALQAVNSVQSGNLALAASAAAVDAGMAMAGQSPVLR			

Spot Idx/Pos	138/F4	6	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	non-POU domain containing, octamer-binding [Homo sapiens]	gi|34932414	54197.3	87	99.999		

Protein Group

splicing factor homolog - human	gi|543010	54233.3

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1147.6179	1147.5594	-0.0585	-51	271	279	WKALIEMEK			
1180.5714	1180.5752	0.0038	3	305	313	HEHQVMLMR			
1195.6581	1195.5901	-0.068	-57	110	119	GFGFIRLETR			
1336.6235	1336.6051	-0.0184	-14	294	304	EKLEMEMEAAR			
1480.7179	1480.6635	-0.0544	-37	366	378	QQEGFKGTFPDAR			
1538.6694	1538.6031	-0.0663	-43	384	398	MGQMAMGGAMGINNR			
1538.6694	1538.6031	-0.0663	-43	384	398	MGQMAMGGAMGINNR			
1636.819	1636.7764	-0.0426	-26	365	378	RQQEGFKGTFPDAR			
1695.7471	1695.6763	-0.0708	-42	257	270	FAQPGSFEYEYAMR			
1695.7471	1695.6763	-0.0708	-42	257	270	FAQPGSFEYEYAMR			
1812.9888	1812.8975	-0.0913	-50	120	135	TLAEIAKVELDNMPLR			
1824.8479	1824.8483	0.0004	0	358	371	QQEEMMRRQQEGFK			
1859.9207	1859.8271	-0.0936	-50	76	91	LFVGNLPPDITEEEMR			
1859.9207	1859.8271	-0.0936	-50	76	91	LFVGNLPPDITEEEMR			
2163.0649	2162.9634	-0.1015	-47	435	456	FGQAATMEGIGAIGGTPPAFNR			
2163.0649	2162.9634	-0.1015	-47	435	456	FGQAATMEGIGAIGGTPPAFNR			
2231.1487	2231.0532	-0.0955	-43	74	92	SRLFVGNLPPDITEEEMRK			
2303.0549	2303.0408	-0.0141	-6	252	270	EQPPRFAQPGSFEYEYAMR			
2498.177	2498.0669	-0.1101	-44	294	313	EKLEMEMEAARHEHQVMLMR			
2668.3252	2668.187	-0.1382	-52	154	176	NLPQYVSNELLEEAFSVFGQVER			
2668.3252	2668.187	-0.1382	-52	154	176	NLPQYVSNELLEEAFSVFGQVER			
3451.7058	3451.4951	-0.2107	-61	399	434	GAMPPAPVPAGTPAPPGPATMMPDGTLGLTPPTTER			

3	heterogeneous nuclear ribonucleoprotein M isoform b [Homo sapiens]	gi|14141154	73512.3	65	99.774		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1167.5833	1167.5872	0.0039	3	620	628	NLPFDFTWK			
1214.5759	1214.6051	0.0292	24	38	48	GEGERPAQNEK			
1336.671	1336.6051	-0.0659	-49	647	659	MENGKSKGCGVVK			
1383.6143	1383.5405	-0.0738	-53	568	582	MGLAMGGGGGASFDR			
1480.7069	1480.6635	-0.0434	-29	398	410	MGLVMDRMGSVER			
1550.7413	1550.8208	0.0795	51	433	446	MGQTMERIGSGVER			
1550.7413	1550.8208	0.0795	51	433	446	MGQTMERIGSGVER			
1715.8164	1715.8145	-0.0019	-1	113	127	GCAVVEFKMEESMKK			
1739.9591	1739.87	-0.0891	-51	70	83	RYRAFITNIPFDVK			
1821.9163	1821.8356	-0.0807	-44	652	668	SKGCGVVKFESPEVAER			
2163.0476	2162.9634	-0.0842	-39	589	612	GNFGGSFAGSFGGAGGHAPGVARK			
2163.0476	2162.9634	-0.0842	-39	589	612	GNFGGSFAGSFGGAGGHAPGVARK			
2211.05	2210.9856	-0.0644	-29	398	417	MGLVMDRMGSVERMGS			

						GIER			
2249.0947	2248.9844	-0.1103	-49	512	531	MATGLERMGANNLERMGLER			
2273.1487	2273.0679	-0.0808	-36	465	485	VGQTIERMGSGVERMGPAIER			
2283.0896	2283.0515	-0.0381	-17	634	653	FNECGHVLYADIKMENGKSK			
2599.2107	2599.2087	-0.002	-1	365	390	MGPGIDRLGGAGMERMGAGLGHGMDR			
2733.3125	2733.1404	-0.1721	-63	493	518	MVPAGMGAGLERMGPVMDRMATGLER			
2829.416	2829.2468	-0.1692	-60	95	120	VGEVTYVELLMDAEGKSRGCAVVEFK			

12	ZNF225 [amino acids 79-706] [Homo sapiens]	gi|9502402	73081.2	56	98.283		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1044.5221	1044.4824	-0.0397	-38	343	351	AHSGEKPYR			
1380.6654	1380.621	-0.0444	-32	443	453	FTQNSQLYSHR			
1403.6558	1403.5857	-0.0701	-50	268	278	CEECGKRFIYR			
1550.7822	1550.8208	0.0386	25	415	426	FTQNSQLYTHRR			
1550.7822	1550.8208	0.0386	25	414	425	RFTQNSQLYTHR			
1566.7805	1566.735	-0.0455	-29	251	264	SALNSHRMVHTGEK			
1695.765	1695.6763	-0.0887	-52	119	133	VHMGEKLYNCDVCGK			
1695.765	1695.6763	-0.0887	-52	119	133	VHMGEKLYNCDVCGK			
1715.8361	1715.8145	-0.0216	-13	338	351	YSHQRAHSGEKPYR			
1729.8993	1729.8163	-0.083	-48	557	570	WASTHLTHQRLHSR			
1815.8879	1815.8359	-0.052	-29	235	250	EKPFRCDTCGKSFGLK			
1875.8839	1875.8468	-0.0371	-20	511	526	LHGDEKPFKCEECGKR			
1923.9163	1923.8796	-0.0367	-19	240	257	CDTCGKSFGLKSALNSHR			
2077.1301	2077.051	-0.0791	-38	502	519	ASSILNHKRLHGDEKPFK			
2211.0684	2210.9856	-0.0828	-37	455	474	VHTGVKPYKCEECGKGFNSK			
2242.979	2243.0322	0.0532	24	464	482	CEECGKGFNSKFNLDMHQR			
2249.1064	2248.9844	-0.122	-54	106	124	SFCYSSALRIHQRVHMGEK			

Spot Idx/Pos	194/H16	7	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded	
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13	

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
5	hypothetical protein [Homo sapiens]	gi|34365255	56551.9	32	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
975.5105	975.512	0.0015	2	319	326	SEVKDEIR			
1360.7001	1360.6941	-0.006	-4	295	305	KQMANQKDLER			
1491.7537	1491.7567	0.003	2	140	152	ESEESKLDQVLSK			
1647.837	1647.8448	0.0078	5	195	209	SGELLALQKEADSMR			
1678.8767	1678.8824	0.0057	3	125	137	LVQQEMMFQRLQK			
1708.8687	1708.8544	-0.0143	-8	169	182	WCESLEKTLSQTKR			
1837.9918	1838.0012	0.0094	5	210	224	ADFSLLRNQFLTERK			
1840.9398	1840.9482	0.0084	5	108	122	QQQLQVLQNEIEENK			
2034.9912	2034.9933	0.0021	1	160	175	VRTLQEEERWCESLEK			
2217.1042	2217.1138	0.0096	4	278	294	RLMKELNQMQYEYTELK			
2226.1182	2226.1306	0.0124	6	26	44	DKLSLHNDISAMQQQLQEK			
2262.1836	2262.1836	0	0	67	85	QDLLHTTKHQDVLLSEQTR			
2338.1509	2338.1682	0.0173	7	377	395	LNFSQVHIMDEHWRGEALR			

14	HSPA8 protein [Homo sapiens]	gi|48257068	64633.1	27	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1199.6742	1199.6604	-0.0138	-12	101	112	DAGTIAGLNVLR			
1235.624	1235.632	0.008	6	178	187	MVNHFIAEFK			
1252.6605	1252.6497	-0.0108	-9	68	78	MKEIAEAYLGK			
1253.616	1253.6311	0.0151	12	243	252	FEELNADLFR			
1391.7252	1391.7244	-0.0008	-1	178	188	MVNHFIAEFKR			
1480.7543	1480.7609	0.0066	4	241	252	ARFEELNADLFR			
1480.7543	1480.7609	0.0066	4	241	252	ARFEELNADLFR			
1653.8318	1653.8531	0.0213	13	30	43	HWPFMVVNDAGRPK			
1745.8088	1745.7985	-0.0103	-6	525	538	NQTAEKEEFEHQQK			
1838.0129	1838.0012	-0.0117	-6	267	283	LDKSQIHDIVLVGGSTR			
1952.0599	1952.035	-0.0249	-13	393	410	DNNLLGKFELTGIPPAPR			
1981.9977	1981.9973	-0.0004	0	79	96	TVTNAVVTVPAYFNDSQR			
1981.9977	1981.9973	-0.0004	0	79	96	TVTNAVVTVPAYFNDSQR			
2774.3267	2774.3303	0.0036	1	365	388	QTQTFTTYSDNQPGVLIQVYEGER			
2997.4575	2997.4656	0.0081	3	214	240	TLSSSTQASIEIDSLYEGIDFYTSITR			

29	centriole associated protein CEP110 [Homo sapiens]	gi|3435244	116741.2	24	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
975.5105	975.512	0.0015	2	831	838	SEVKDEIR			
1187.6378	1187.6272	-0.0106	-9	477	487	RVLAAAEENSK			
1360.7001	1360.6941	-0.006	-4	807	817	KQMANQKDLER			
1443.755	1443.7632	0.0082	6	163	175	ADQQLRSLQADAK			
1524.7726	1524.7831	0.0105	7	194	207	IVAAKDSDFQCLSK			
1524.7726	1524.7831	0.0105	7	194	207	IVAAKDSDFQCLSK			
1551.7496	1551.7626	0.013	8	625	637	ERESEESKLETSK			
1647.837	1647.8448	0.0078	5	707	721	SGELLALQKEADSMR			
1678.8767	1678.8824	0.0057	3	612	624	LVQQEMMFQRLQK			
1708.8687	1708.8544	-0.0143	-8	681	694	WCESLEKTLSQTKR			
1799.8955	1799.9078	0.0123	7	41	55	SLECEVEELHRTVQK			
1837.9918	1838.0012	0.0094	5	722	736	ADFSLLRNQFLTERK			
1840.9398	1840.9482	0.0084	5	595	609	QQQLQVLQNEIEENK			
2034.9912	2034.9933	0.0021	1	672	687	VRTLQEEERWCESLEK			
2217.1042	2217.1138	0.0096	4	790	806	RLMKELNQMQYEYTELK			
2226.1182	2226.1306	0.0124	6	513	531	DKLSLHNDISAMQQQLQEK			
2262.1836	2262.1836	0	0	554	572	QDLLHTTKHQDVLLSEQTR			
2283.1509	2283.1655	0.0146	6	256	275	SQVTSQQQEMAVLDRQLGHK			
2338.1521	2338.1682	0.0161	7	132	151	FTDAKRSLLQTESDAEELER			

33	heat shock 70kDa protein 8 isoform 2 variant [Homo sapiens]	gi|62896815	53466.4	24	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1199.6742	1199.6604	-0.0138	-12	160	171	DAGTIAGLNVLR			

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1235.624	1235.632	0.008	6	237	246	MVNHFIAEFK			
1252.6605	1252.6497	-0.0108	-9	127	137	MKEIAEAYLGK			
1253.616	1253.6311	0.0151	12	302	311	FEELNADLFR			
1391.7252	1391.7244	-0.0008	-1	237	247	MVNHFIAEFKR			
1480.7543	1480.7609	0.0066	4	300	311	ARFEELNADLFR			
1480.7543	1480.7609	0.0066	4	300	311	ARFEELNADLFR			
1653.8318	1653.8531	0.0213	13	89	102	HWPFMVVNDAGRPK			
1838.0129	1838.0012	-0.0117	-6	326	342	LDKSQIHDIVLVGGSTR			
1981.9977	1981.9973	-0.0004	0	138	155	TVTNAVVTVPAYFNDSQR			
1981.9977	1981.9973	-0.0004	0	138	155	TVTNAVVTVPAYFNDSQR			
2774.3267	2774.3303	0.0036	1	424	447	QTQTFTTYSDNQPGVLIQVYEGER			
2997.4575	2997.4656	0.0081	3	273	299	TLSSSTQASIEIDSLYEGIDFYTSITR			

Spot Idx/Pos	140/F8	8	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
2	dead box, X isoform [Homo sapiens]	gi|25805	73226	44	74.005		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
895.5148	895.5149	0.0001	0	38	44	YIPPHLR			
1182.5497	1182.5872	0.0375	32	100	110	GRSDYDGIGSR			
1182.5497	1182.5872	0.0375	32	100	110	GRSDYDGIGSR			
1300.6392	1300.6202	-0.019	-15	479	488	DREEALHQFR			
1300.6392	1300.6202	-0.019	-15	479	488	DREEALHQFR			
1320.6793	1320.6575	-0.0218	-17	277	287	ELAVQIYEEAR			
1320.6793	1320.6575	-0.0218	-17	277	287	ELAVQIYEEAR			
1336.6388	1336.625	-0.0138	-10	352	362	MLDMGFEPQIR			
1336.6388	1336.625	-0.0138	-10	352	362	MLDMGFEPQIR			
1485.8787	1485.8275	-0.0512	-34	264	276	KQYPISLVLAPTR			
1502.7094	1502.7466	0.0372	25	82	95	SSFFSDRGSGSRGR			
1524.7804	1524.756	-0.0244	-16	535	548	VGNLGLATSFFNER			
1524.7804	1524.756	-0.0244	-16	535	548	VGNLGLATSFFNER			
1557.7947	1557.7716	-0.0231	-15	395	407	DFLDEYIFLAVGR			
1557.7947	1557.7716	-0.0231	-15	395	407	DFLDEYIFLAVGR			
2083.0242	2082.9902	-0.034	-16	512	528	HVINFDLPSDIEEYVHR			
2332.2546	2332.1785	-0.0761	-33	231	252	TAAFLLPILSQIYSDGPGEALR			

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
8	heterogeneous nuclear ribonucleoprotein M isoform a variant [Homo sapiens]	gi|62089046	65211.2	21	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1427.7133	1427.7297	0.0164	11	477	491	MGPAMGPALGAGIER			
1613.7773	1613.7665	-0.0108	-7	342	356	MGPLGLDHMASSIER			
2034.9528	2034.9397	-0.0131	-6	513	535	GNFGGSFAGSFGGAGGHAPGVAR			
2034.9528	2034.9397	-0.0131	-6	513	535	GNFGGSFAGSFGGAGGHAPGVAR			
2211.05	2211.05	0	0	322	341	MGLVMDRMGSVERMGSGIER			
2283.0896	2283.1208	0.0312	14	558	577	FNECGHVLYADIKMENGKSK			
2286.115	2286.1216	0.0066	3	469	491	MGANSLERMGPAMGPALGAGIER			

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
9	golgin-245 [Homo sapiens]	gi|1173565	244378.2	48	88.388		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
895.5359	895.5149	-0.021	-23	336	342	LQKLHEK			
1104.5782	1104.569	-0.0092	-8	1166	1175	ADIESLVTEK			
1104.5782	1104.569	-0.0092	-8	1166	1175	ADIESLVTEK			
1182.6224	1182.5872	-0.0352	-30	2	11	ERSLSSYRGK			
1182.6224	1182.5872	-0.0352	-30	2	11	ERSLSSYRGK			
1233.6508	1233.6006	-0.0502	-41	1508	1517	KQLLSQMEEK			
1233.6508	1233.6006	-0.0502	-41	1508	1517	KQLLSQMEEK			
1439.7375	1439.7792	0.0417	29	373	384	SQSEYLKISQEK			
1439.7375	1439.7792	0.0417	29	373	384	SQSEYLKISQEK			
1502.806	1502.7466	-0.0594	-40	838	850	KELENTALELSQK			
1524.7903	1524.756	-0.0343	-22	1050	1062	SNKSLEDKSLEFK			
1524.7903	1524.756	-0.0343	-22	1050	1062	SNKSLEDKSLEFK			
1592.8577	1592.905	0.0473	30	456	468	HNKEITVMVEKHK			
1635.8588	1635.8716	0.0128	8	266	280	AAFEELEKALSTAQK			
1778.9143	1778.8341	-0.0802	-45	410	423	LRDLQQEAETYRTR			
1833.9812	1833.9382	-0.043	-23	1063	1078	KLSEELAIQLDICCKK			
1910.9528	1910.9139	-0.0389	-20	1509	1523	QLLSQMEEKEEQYKK			
1930.0062	1929.9452	-0.061	-32	44	59	IAELREELQMDQQAKK			
1951.0494	1950.9677	-0.0817	-42	1588	1603	TYEEKISVLQRNLTEK			
1971.0028	1970.9785	-0.0243	-12	172	187	EALQEQLDERLQELEK			
1982.9487	1982.9662	0.0175	9	1913	1928	RYEEILDAREEEMTAK			
2078.0083	2077.9739	-0.0344	-17	580	596	MDEQKNHHQQQVDSIIK			
2082.0171	2082.0344	0.0173	8	1914	1930	YEEILDAREEEMTAKVR			
2084.0518	2083.9934	-0.0584	-28	1981	1996	EQEFREQIHNLEDRLK			
2233.1445	2233.0481	-0.0964	-43	534	553	LDVNQTELESLSSELSEVLK			
2256.1177	2256.0205	-0.0972	-43	728	746	QNSEMEQKVKSLTQVYESK			

Spot Idx/Pos	141/F10	9	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	PRO2446 [Homo sapiens]	gi|7959903	27175.8	77	99.988		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1343.7065	1343.7135	0.007	5	183	193	DNTINLIHTFR			
1354.726	1354.7419	0.0159	12	52	63	DSIVHQAGMLKR			
1450.7549	1450.7675	0.0126	9	136	148	ASHTAPQVLFSHR			
1450.7549	1450.7675	0.0126	9	136	148	ASHTAPQVLFSHR			
1606.8561	1606.8541	-0.002	-1	135	148	RASHTAPQVLFSHR			
1760.7874	1760.7946	0.0072	4	73	86	YFQFQEEGKEGENR			
1760.7874	1760.7946	0.0072	4	73	86	YFQFQEEGKEGENR			
1918.0181	1918.0171	-0.001	-1	8	23	FYKELQAHGADELLKR			
1955.9167	1955.9307	0.014	7	87	102	AVIHYRDDETMYVESK			
2083.0957	2083.0916	-0.0041	-2	106	124	VTVVFSTVFKDDDDVVIGK			
2257.2087	2257.2166	0.0079	3	136	155	ASHTAPQVLFSHREPPLELK			
2257.2087	2257.2166	0.0079	3	136	155	ASHTAPQVLFSHREPPLELK			
2413.241	2413.2661	0.0251	10	183	201	DNTINLIHTFRDYLHYHIK			
2992.5376	2992.5549	0.0173	6	106	131	VTVVFSTVFKDDDDVVIGKVFMQEFK			
3088.5513	3088.5608	0.0095	3	24	51	VYGSFLVNPESGYNVSLLYDLENLPASK			

2	Chain A, Three-Dimensional Structure Of Human Electron Transfer Flavoprotein To 2.1 A Resolution	gi|2781202	33075.4	77	99.987	13	85.488

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1714.8005	1714.8143	0.0138	8	84	99	QFNYTHICAGASAFGK			
1736.0204	1736.0052	-0.0152	-9	68	83	GLLPEELTPLILATQK			
1736.0204	1736.0052	-0.0152	-9	68	83	GLLPEELTPLILATQK			
1751.0676	1751.066	-0.0016	-1	105	121	VAAKLEVAPISDIIAIK			
1812.9602	1812.9628	0.0026	1	215	231	LLYDLADQLHAAVGASR			
1812.9602	1812.9628	0.0026	1	215	231	LLYDLADQLHAAVGASR	13	85.488	
1904.917	1904.9191	0.0021	1	232	250	AAVDAGFVPNDMQVGQTGK			
2351.3154	2351.3098	-0.0056	-2	251	273	IVAPELYIAVGISGAIQHLAGMK			
2475.2625	2475.2732	0.0107	4	209	231	SGENFKLLYDLADQLHAAVGASR			
2475.2625	2475.2732	0.0107	4	209	231	SGENFKLLYDLADQLHAAVGASR			
2553.4648	2553.4614	-0.0034	-1	105	128	VAAKLEVAPISDIIAIKSPDTFVR			
2553.4648	2553.4614	-0.0034	-1	105	128	VAAKLEVAPISDIIAIKSPDTFVR			
2821.5054	2821.5051	-0.0003	0	2	28	QSTLVIAEHANDSLAPITLNTITAATR			
2821.5054	2821.5051	-0.0003	0	2	28	QSTLVIAEHANDSLAPITLNTITAATR			
2888.6494	2888.6521	0.0027	1	58	83	VLVAQHDVYKGLLPEELTPLILATQK			
2947.5813	2947.5933	0.012	4	277	303	TIVAINKDPEAPIFQVADYGIVADLFK			

3	actin related protein 2/3 complex subunit 2 [Homo sapiens]	gi|5031599	34311.5	74	99.975		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1101.6084	1101.6196	0.0112	10	1	9	MILLEVNNR			
1101.6084	1101.6196	0.0112	10	1	9	MILLEVNNR			
1343.7065	1343.7135	0.007	5	238	248	DNTINLIHTFR			
1354.726	1354.7419	0.0159	12	107	118	DSIVHQAGMLKR			
1450.7549	1450.7675	0.0126	9	191	203	ASHTAPQVLFSHR			
1450.7549	1450.7675	0.0126	9	191	203	ASHTAPQVLFSHR			
1606.8561	1606.8541	-0.002	-1	190	203	RASHTAPQVLFSHR			
1760.7874	1760.7946	0.0072	4	128	141	YFQFQEEGKEGENR			
1760.7874	1760.7946	0.0072	4	128	141	YFQFQEEGKEGENR			
1918.0181	1918.0171	-0.001	-1	63	78	FYKELQAHGADELLKR			
1955.9167	1955.9307	0.014	7	142	157	AVIHYRDDETMYVESK			
2083.0957	2083.0916	-0.0041	-2	161	179	VTVVFSTVFKDDDDVVIGK			
2257.2087	2257.2166	0.0079	3	191	210	ASHTAPQVLFSHREPPLELK			
2257.2087	2257.2166	0.0079	3	191	210	ASHTAPQVLFSHREPPLELK			
2413.241	2413.2661	0.0251	10	238	256	DNTINLIHTFRDYLHYHIK			
2992.5376	2992.5549	0.0173	6	161	186	VTVVFSTVFKDDDDVVIGKVFMQEFK			
3088.5513	3088.5608	0.0095	3	79	106	VYGSFLVNPESGYNVSLLYDLENLPASK			

Spot Idx/Pos	142/F12	10	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	actin related protein 2/3 complex subunit 2 [Homo sapiens]	gi|5031599	34311.5	113	100	10	72.814

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1101.6084	1101.605	-0.0034	-3	1	9	MILLEVNNR			
1101.6084	1101.605	-0.0034	-3	1	9	MILLEVNNR	8	50.643	
1270.6248	1270.6273	0.0025	2	180	189	VFMQEFKEGR			
1314.7489	1314.7307	-0.0182	-14	55	65	VMVSISLKFYK			
1343.7065	1343.7064	-0.0001	0	238	248	DNTINLIHTFR			
1354.726	1354.7288	0.0028	2	107	118	DSIVHQAGMLKR			
1450.7549	1450.7538	-0.0011	-1	191	203	ASHTAPQVLFSHR			
1450.7549	1450.7538	-0.0011	-1	191	203	ASHTAPQVLFSHR			
1479.7914	1479.8063	0.0149	10	66	78	ELQAHGADELLKR			
1606.8561	1606.8483	-0.0078	-5	190	203	RASHTAPQVLFSHR			
1760.7874	1760.7944	0.007	4	128	141	YFQFQEEGKEGENR			
1760.7874	1760.7944	0.007	4	128	141	YFQFQEEGKEGENR	3	0	
1918.0181	1918.0205	0.0024	1	63	78	FYKELQAHGADELLKR			
1955.9167	1955.9294	0.0127	6	142	157	AVIHYRDDETMYVESK			
1955.9167	1955.9294	0.0127	6	142	157	AVIHYRDDETMYVESK			
2083.0957	2083.0823	-0.0134	-6	161	179	VTVVFSTVFKDDDDVVIGK			
2257.2087	2257.2156	0.0069	3	191	210	ASHTAPQVLFSHREPPLELK			
2257.2087	2257.2156	0.0069	3	191	210	ASHTAPQVLFSHREPPLELK			
2413.241	2413.2507	0.0097	4	238	256	DNTINLIHTFRDYLHYHIK			
2990.5508	2990.5901	0.0393	13	204	230	EPPLELKDTDAAVGDNIGYITFVLFPR			
3088.5513	3088.5667	0.0154	5	79	106	VYGSFLVNPESGYNVSLLYDLENLPASK			

3	Chain A, Three-Dimensional Structure Of Human Electron Transfer Flavoprotein To 2.1 A Resolution	gi|2781202	33075.4	92	100	2	0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1171.647	1171.6427	-0.0043	-4	58	67	VLVAQHDVYK			
1714.8005	1714.8076	0.0071	4	84	99	QFNYTHICAGASAFGK			
1736.0204	1736.0026	-0.0178	-10	68	83	GLLPEELTPLILATQK			
1751.0676	1751.057	-0.0106	-6	105	121	VAAKLEVAPISDIIAIK			
1776.865	1776.8628	-0.0022	-1	170	185	ASSTSPVEISEWLDQK			
1776.865	1776.8628	-0.0022	-1	170	185	ASSTSPVEISEWLDQK	2	0	
1812.9602	1812.9636	0.0034	2	215	231	LLYDLADQLHAAVGASR			
1812.9602	1812.9636	0.0034	2	215	231	LLYDLADQLHAAVGASR			
1904.917	1904.9043	-0.0127	-7	232	250	AAVDAGFVPNDMQVGQTGK			
1904.917	1904.9043	-0.0127	-7	232	250	AAVDAGFVPNDMQVGQTGK			
2119.0918	2119.093	0.0012	1	170	188	ASSTSPVEISEWLDQKLTK			
2351.3154	2351.2976	-0.0178	-8	251	273	IVAPELYIAVGISGAIQHLAGMK			
2475.2625	2475.272	0.0095	4	209	231	SGENFKLLYDLADQLHAAVGASR			
2553.4648	2553.4648	0	0	105	128	VAAKLEVAPISDIIAIKSPD			

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
						TFVR			
2553.4648	2553.4648	0	0	105	128	VAAKLEVAPISDIIAIKSPDTFVR			
2821.5054	2821.5046	-0.0008	0	2	28	QSTLVIAEHANDSLAPITLNTITAATR			
2821.5054	2821.5046	-0.0008	0	2	28	QSTLVIAEHANDSLAPITLNTITAATR			
2888.6494	2888.6392	-0.0102	-4	58	83	VLVAQHDVYKGLLPEELTPLILATQK			
2947.5813	2947.5796	-0.0017	-1	277	303	TIVAINKDPEAPIFQVADYGIVADLFK			

Spot Idx/Pos	143/F14	11	**Instr./Spot Origin**	ab4700/042810		**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**			**Spectra**	3

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
17	Single-stranded DNA binding protein 1 [Homo sapiens]	gi|62205329	17348.1	15	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
883.4995	883.493	-0.0065	-7	39	46	VGQDPVLR			
1044.6312	1044.6343	0.0031	3	87	95	ISVFRPGLR			

Spot Idx/Pos	144/F16	12	**Instr./Spot Origin**	ab4700/042810		**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**			**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	Chain A, Human Mitochondrial Single-Stranded Dna Binding Protein	gi|2624694	15185.8	99	100		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
883.4995	883.4959	-0.0036	-4	23	30	VGQDPVLR			
1044.6312	1044.6274	-0.0038	-4	71	79	ISVFRPGLR			
1164.6959	1164.6891	-0.0068	-6	13	22	SLNRVHLLGR			
1616.7373	1616.7599	0.0226	14	98	110	IDYGEYMDKNNVR			
1778.8894	1778.9095	0.0201	11	36	50	NPVTIFSLATNEMWR			
1992.0647	1992.066	0.0013	1	112	129	QATTIIADNIIFLSDQTK			
2148.1658	2148.1343	-0.0315	-15	111	129	RQATTIIADNIIFLSDQTK			
2293.0842	2293.0598	-0.0244	-11	51	70	SGDSEVYQLGDVSQKTTWHR			
2320.1753	2320.1577	-0.0176	-8	31	50	QVEGKNPVTIFSLATNEMWR			
2378.2449	2378.2454	0.0005	0	112	132	QATTIIADNIIFLSDQTKEKE			

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
4	EP2E [Homo sapiens]	gi|10799277	9085.3	29	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1422.6763	1422.6794	0.0031	2	27	38	NTICRMQQGICR			
1422.6763	1422.6794	0.0031	2	27	38	NTICRMQQGICR			
2384.0161	2384.0339	0.0178	7	59	80	CCVSNTDEEGKEKPEMDGRSGI			
3354.7852	3354.7366	-0.0486	-14	2	31	KVFFLFAVLFCLVQTNSGDVPPGIRNTICR			

Spot Idx/Pos	195/H18	13	**Instr./Spot Origin**	ab4700/042810		**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**			**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	PREDICTED: similar to 60S ribosomal protein L35 [Homo sapiens]	gi|51459132	14555.4	48	88.388		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
817.5076	817.5087	0.0011	1	1	7	MAKIKAR			
823.5009	823.4944	-0.0065	-8	93	98	HRLNKR			
825.4941	825.4947	0.0006	1	8	14	DLHGKKK			
902.524	902.5374	0.0134	15	111	117	ERLCLLR			
924.5373	924.5402	0.0029	3	6	13	ARDLHGKK			
946.5468	946.5562	0.0094	10	104	110	TKKQQWK			
988.5785	988.5778	-0.0007	-1	33	43	VAKVTGGAASK			
995.5857	995.5863	0.0006	1	90	97	ATRHRLNK			
1012.5785	1012.5893	0.0108	11	99	106	EEHLKTKK			
1018.5891	1018.5967	0.0076	7	36	46	VTGGAASKLSK			
1030.6189	1030.6138	-0.0051	-5	111	118	ERLCLLRK			
1037.6213	1037.6206	-0.0007	-1	4	12	IKARDLHGK			

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
2	RPL13A protein [Homo sapiens]	gi|111494155	16706.4	39	19.667		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
828.5011	828.4939	-0.0072	-9	57	64	MVVPAALK			
844.5151	844.514	-0.0011	-1	105	110	IHYRKK			
872.5312	872.5234	-0.0078	-9	116	122	LRKQAEK			
915.5522	915.5591	0.0069	8	103	109	AKIHYRK			
915.5522	915.5591	0.0069	8	103	109	AKIHYRK			
971.5632	971.5668	0.0036	4	34	42	GQAALDRLK			
973.5676	973.571	0.0034	3	123	130	NVEKKIDK			
977.5679	977.5819	0.014	14	18	24	IFWRTVR			
977.5679	977.5819	0.014	14	18	24	IFWRTVR			
1044.5948	1044.6017	0.0069	7	101	108	EKAKIHYR			
1108.6248	1108.631	0.0062	6	128	136	IDKYTEVLK			
1267.7303	1267.7238	-0.0065	-5	22	32	TVRGMLPHKTK			
2866.4885	2866.5105	0.022	8	74	98	FAYLGRLAHEVGWKYQAVTATLEDK			

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
3	CCDC71 protein [Homo sapiens]	gi|48735006	24879.5	35	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
827.4846	827.4941	0.0095	11	120	126	VARTQPR			
845.5025	845.5119	0.0094	11	1	7	PKCLTRK			
853.5254	853.513	-0.0124	-15	163	169	DLPPKKR			
895.522	895.5322	0.0102	11	7	15	KGPGAGPRR			
944.5635	944.5654	0.0019	2	67	75	TQAKAAKAR			
945.5662	945.564	-0.0022	-2	100	108	VMAARAKAK			
1013.5962	1013.6022	0.006	6	127	136	GRGRPKGSAK			
1026.6166	1026.608	-0.0086	-8	118	126	AKVARTQPR			
1040.6072	1040.6086	0.0014	1	120	128	VARTQPRGR			
1041.6276	1041.613	-0.0146	-14	57	66	AARAQAKVAR			
1100.635	1100.6407	0.0057	5	223	232	LQPLLPYSAV			
1105.6146	1105.6022	-0.0124	-11	34	44	RMKGGSALGTK			
1171.6906	1171.678	-0.0126	-11	60	70	AQAKVARTQAK			
1184.6494	1184.6377	-0.0117	-10	146	155	NRPETVGQKR			

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
6	PREDICTED: similar to H3 histone, family 3B [Homo sapiens]	gi|88976633	15216.4	32	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
832.4999	832.4979	-0.002	-2	4	10	TKQTARK			
844.5073	844.514	0.0067	8	117	123	RVTIMPK			

858.5155	858.5172	0.0017	2	20	27	QLATKAAR			
931.5432	931.5523	0.0091	10	2	9	ARTKQTAR			
945.5727	945.564	-0.0087	-9	58	65	STELLVRK			
992.5635	992.5674	0.0039	4	51	57	EIRRYQK			
1032.5948	1032.6097	0.0149	14	42	50	YRPGTVALR			
1052.5847	1052.5978	0.0131	12	124	132	DIQLAHSIR			
1218.6841	1218.6906	0.0065	5	71	80	LVREIAQDFK			
1229.6959	1229.6937	-0.0022	-2	25	37	AARKSAPSTGGVK			

25	PREDICTED: similar to ribosomal protein L13a isoform 1 [Homo sapiens]	gi|89037070	23428.2	26	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
813.5305	813.533	0.0025	3	26	32	QVLLGRK			
844.5151	844.514	-0.0011	-1	166	171	IHYRKK			
872.5312	872.5234	-0.0078	-9	177	183	LRKQAEK			
915.5522	915.5591	0.0069	8	164	170	AKIHYRK			
915.5522	915.5591	0.0069	8	164	170	AKIHYRK			
971.5632	971.5668	0.0036	4	95	103	GQAALDRLK			
973.5676	973.571	0.0034	3	184	191	NVEKKIDK			
1018.5865	1018.5967	0.0102	10	117	125	RMVVPAAFK			
1044.5948	1044.6017	0.0069	7	162	169	EKAKIHYR			
1108.6248	1108.631	0.0062	6	189	197	IDKYTEVLK			
1267.7303	1267.7238	-0.0065	-5	83	93	TVRGMLPHKTK			
2000.009	2000.002	-0.007	-3	32	49	KVVVVCCEGINISGNFYR			

Spot Idx/Pos	146/F20	14	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
11	H1 histone family, member 0 [Homo sapiens]	gi|20810 20872.2 21	0				

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
870.577	870.5884	0.0114	13	162	169	TVKAKPVK			
895.6087	895.6135	0.0048	5	175	182	KAKPVKPK			
899.6036	899.61	0.0064	7	157	164	AKKPKTVK			
966.6458	966.6421	-0.0037	-4	176	184	AKPVKPKAK			
986.6356	986.6431	0.0075	8	74	82	RLVTTGVLK			
996.6564	996.6554	-0.001	-1	137	145	KPKATPVKK			
1053.6779	1053.6901	0.0122	12	165	174	AKPVKASKPK			

Spot Idx/Pos	147/F22	15	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
2	ARP3 actin-related protein 3 homolog [Homo sapiens]	gi|5031573	47341	38	0	2	0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
958.5792	958.5829	0.0037	4	341	348	RTVDARLK			
1214.5687	1214.5781	0.0094	8	266	275	EFSIDVGYER			
1409.7787	1409.7894	0.0107	8	199	209	DITYFIQQLLR			
1409.7787	1409.7894	0.0107	8	199	209	DITYFIQQLLR	2	0	
1499.6947	1499.7078	0.0131	9	80	91	HGIVEDWDLMER			
1499.6947	1499.7078	0.0131	9	80	91	HGIVEDWDLMER			
1768.9075	1768.9175	0.01	6	210	225	DREVGIPPEQSLETAK			
1769.9254	1769.9199	-0.0055	-3	226	240	AVKERYSYVCPDLVK			
1795.9799	1795.9689	-0.011	-6	212	228	EVGIPPEQSLETAKAVK			
1912.981	1912.9827	0.0017	1	318	334	NIVLSGGSTMFRDFGRR			
2154.2183	2154.1975	-0.0208	-10	192	209	HIPIAGRDITYFIQQLLR			
2482.1885	2482.1809	-0.0076	-3	103	123	AEPEDHYFLLTEPPLNTPENR			
2482.1885	2482.1809	-0.0076	-3	103	123	AEPEDHYFLLTEPPLNTPENR			

4	translation initiation factor [Homo sapiens]	gi|496902	46803.1	38	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1159.647	1159.6617	0.0147	13	330	339	VLISTDVWAR			
1212.6946	1212.7087	0.0141	12	106	116	ETQALILAPTR			
1417.7109	1417.7208	0.0099	7	196	206	GFKEQIYDVYR			
1469.7495	1469.7535	0.004	3	153	166	LDYGQHVVAGTPGR			
1588.8805	1588.8656	-0.0149	-9	374	387	KGVAINFVKNDDIR			
1827.9387	1827.9484	0.0097	5	52	67	GIYAYGFEKPSAIQQR			
1827.9387	1827.9484	0.0097	5	52	67	GIYAYGFEKPSAIQQR			
1994.0592	1994.0331	-0.0261	-13	244	260	DELTLEGIKQFFVAVER			
2140.1396	2140.1401	0.0005	0	340	358	GLDVPQVSLIINYDLPNNR			
2140.1548	2140.1401	-0.0147	-7	52	70	GIYAYGFEKPSAIQQRAIK			
2870.395	2870.373	-0.022	-8	388	411	ILRDIEQYYSTQIDEMPMNVADLI			

5	Growth-arrest-specific protein 7 (GAS-7)	gi|12643625	47236.7	36	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
873.4901	873.4961	0.006	7	278	284	ALTERQR			
1393.7321	1393.7365	0.0044	3	179	189	ERIKIEEDYAK			
1478.8074	1478.7898	-0.0176	-12	264	276	QLASRYASVEKAR			
1644.8591	1644.8368	-0.0223	-14	217	231	SLADEAEVHLKFSAK			
1707.8507	1707.8685	0.0178	10	87	103	KSTGDSQNLGSSSPSKK			
1759.937	1759.913	-0.024	-14	283	296	QRDLEMKTQQLEIK			
1762.9128	1762.9265	0.0137	8	254	268	CDHHIADLRKQLASR			
1772.954	1772.9673	0.0133	8	216	231	KSLADEAEVHLKFSAK			
1786.9333	1786.9213	-0.012	-7	146	162	DPQGNGTVAGFELLLQK			
2460.2363	2460.2466	0.0103	4	194	216	LSQNSLASQEEGSLGEAWAQVKK			

15	translation elongation factor 1 alpha 1-like 14 [Homo sapiens]	gi|15277711	42997.3	28	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1025.6101	1025.6255	0.0154	15	192	202	IGGIGTVPVGR			
1314.7416	1314.7347	-0.0069	-5	71	82	EHALLAYTLGVK			
1316.7355	1316.7366	0.0011	1	364	375	DMRQTVAVGVIK			
1404.7269	1404.7406	0.0137	10	21	32	YYVTIIDAPGHR			
1776.9313	1776.9458	0.0145	8	1	15	MQSERGITIDISLWK			
1908.0013	1908.0121	0.0108	6	21	36	YYVTIIDAPGHRDFIK			
1908.0013	1908.0121	0.0108	6	21	36	YYVTIIDAPGHRDFIK			
2515.3838	2515.3674	-0.0164	-7	203	226	VETGVLKPGMVVTFAPVNVTTEVK			
2515.3838	2515.3674	-0.0164	-7	203	226	VETGVLKPGMVVTFAPVNVTTEVK			
2938.3782	2938.3569	-0.0213	-7	332	359	SGDAAIVDMVPGKPMCVESFSDYPPLGR			
2938.3782	2938.3569	-0.0213	-7	332	359	SGDAAIVDMVPGKPMCVESFSDYPPLGR			

Spot Idx/Pos	148/F24	16	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein	Protein	Total Ion	Total Ion

				Score	C. I. %	Score	C. I. %
3	ARP3 actin-related protein 3 homolog [Homo sapiens]	gi|5031573	47341	37	0	4	0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1214.5687	1214.5735	0.0048	4	266	275	EFSIDVGYER			
1281.6619	1281.6547	-0.0072	-6	318	329	NIVLSGGSTMFR			
1409.7787	1409.7798	0.0011	1	199	209	DITYFIQQLLR			
1409.7787	1409.7798	0.0011	1	199	209	DITYFIQQLLR	4	0	
1499.6947	1499.6978	0.0031	2	80	91	HGIVEDWDLMER			
1499.6947	1499.6978	0.0031	2	80	91	HGIVEDWDLMER			
1768.9075	1768.9159	0.0084	5	210	225	DREVGIPPEQSLETAK			
1795.9799	1795.9746	-0.0053	-3	212	228	EVGIPPEQSLETAKAVK			
2040.1534	2040.1238	-0.0296	-15	358	374	LKPKPIDVQVITHHMQR			
2154.2183	2154.1868	-0.0315	-15	192	209	HIPIAGRDITYFIQQLLR			
2482.1885	2482.1848	-0.0037	-1	103	123	AEPEDHYFLLTEPPLNTPENR			
2482.1885	2482.1848	-0.0037	-1	103	123	AEPEDHYFLLTEPPLNTPENR			
2954.469	2954.4314	-0.0376	-13	80	102	HGIVEDWDLMERFMEQVIFKYLR			

4	translation initiation factor [Homo sapiens]	gi|496902	46803.1	36	0	2	0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1159.647	1159.6421	-0.0049	-4	330	339	VLISTDVWAR			
1262.6772	1262.6842	0.007	6	16	25	RLLKEEDMTK			
1417.7109	1417.7123	0.0014	1	196	206	GFKEQIYDVYR			
1469.7495	1469.7374	-0.0121	-8	153	166	LDYGQHVVAGTPGR			
1567.7903	1567.7986	0.0083	5	253	264	QFFVAVEREEWK			
1597.8445	1597.84	-0.0045	-3	152	166	KLDYGQHVVAGTPGR			
1640.8207	1640.8435	0.0228	14	1	16	MATTATMATSGSARKR			
1827.9387	1827.9415	0.0028	2	52	67	GIYAYGFEKPSAIQQR			
1827.9387	1827.9415	0.0028	2	52	67	GIYAYGFEKPSAIQQR			
2140.1396	2140.1318	-0.0078	-4	340	358	GLDVPQVSLIINYDLPNNR			
2140.1396	2140.1318	-0.0078	-4	340	358	GLDVPQVSLIINYDLPNNR	3	0	
3489.665	3489.6687	0.0037	1	17	46	LLKEEDMTKVEFETSEEVDVTPTFDTMGLR			

6	translation elongation factor 1 alpha 1-like 14 [Homo sapiens]	gi|15277711	42997.3	34	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1025.6101	1025.6062	-0.0039	-4	192	202	IGGIGTVPVGR			
1314.7416	1314.7267	-0.0149	-11	71	82	EHALLAYTLGVK			
1314.7416	1314.7267	-0.0149	-11	71	82	EHALLAYTLGVK			
1404.7269	1404.729	0.0021	1	21	32	YYVTIIDAPGHR			
1776.9313	1776.9452	0.0139	8	1	15	MQSERGITIDISLWK			
1908.0013	1907.9967	-0.0046	-2	21	36	YYVTIIDAPGHRDFIK			
1997.0126	1997.0341	0.0215	11	16	32	FETSKYYVTIIDAPGHR			
2515.3838	2515.387	0.0032	1	203	226	VETGVLKPGMVVTFAPVNVTTEVK			
2515.3838	2515.387	0.0032	1	203	226	VETGVLKPGMVVTFAPVNVTTEVK			
2852.4167	2852.4299	0.0132	5	37	65	NMITGTSQADCAVLIVAAGVGEFEAGISK			
2938.3782	2938.3789	0.0007	0	332	359	SGDAAIVDMVPGKPMCVESFSDYPPLGR			
2938.3782	2938.3789	0.0007	0	332	359	SGDAAIVDMVPGKPMCVESFSDYPPLGR			

11	phosphogluconate dehydrogenase [Homo sapiens]	gi|40068518	53105.9	27	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1411.7766	1411.7815	0.0049	3	332	343	IISYAQGFMLLR			
1493.7893	1493.7993	0.01	7	435	447	HEMLPASLIQAQR			
1591.8074	1591.8191	0.0117	7	120	136	GILFVGSGVSGGEEGAR			
1790.9393	1790.9468	0.0075	4	118	136	AKGILFVGSGVSGGEEGAR			
2160.1182	2160.1196	0.0014	1	88	107	LVPLLDTGDIIIDGGNSEYR			
2310.1399	2310.1406	0.0007	0	378	396	DAFDRNPELQNLLLDDFFK			
2463.3281	2463.311	-0.0171	-7	266	288	WTAISALEYGVPVTLIGEAVFAR			
2551.3191	2551.3152	-0.0039	-2	376	396	IKDAFDRNPELQNLLLDDFFK			
2595.1863	2595.2024	0.0161	6	185	206	MVHNGIEYGDMQLICEAYHLMK			

13	glucocorticoid receptor AF-1 specific elongation factor [Homo sapiens]	gi|7108915	46240	27	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1025.6101	1025.6062	-0.0039	-4	220	230	IGGIGTVPVGR			
1314.7416	1314.7267	-0.0149	-11	99	110	EHALLAYTLGVK			
1314.7416	1314.7267	-0.0149	-11	99	110	EHALLAYTLGVK			
1404.7269	1404.729	0.0021	1	49	60	YYVTIIDAPGHR			
1908.0013	1907.9967	-0.0046	-2	49	64	YYVTIIDAPGHRDFIK			
1997.0126	1997.0341	0.0215	11	44	60	FETSKYYVTIIDAPGHR			
2515.3838	2515.387	0.0032	1	231	254	VETGVLKPGMVVTFAPVNVTTEVK			
2515.3838	2515.387	0.0032	1	231	254	VETGVLKPGMVVTFAPVNVTTEVK			
2852.4167	2852.4299	0.0132	5	65	93	NMITGTSQADCAVLIVAAGVGEFEAGISK			
2938.3782	2938.3789	0.0007	0	360	387	SGDAAIVDMVPGKPMCVESFSDYPPLGR			
2938.3782	2938.3789	0.0007	0	360	387	SGDAAIVDMVPGKPMCVESFSDYPPLGR			

Spot Idx/Pos	161/G2	17	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	electron-transfer-flavoprotein, beta polypeptide isoform 1 [Homo sapiens]	gi|4503609	27826.2	135	100	14	78.09

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
828.5301	828.5347	0.0046	6	249	255	LKEIGRI			
853.5253	853.5312	0.0059	7	99	106	LGPLQVAR			
1050.5652	1050.5626	-0.0026	-2	192	200	YATLPNIMK			
1054.6255	1054.6179	-0.0076	-7	177	186	LPAVVTADLR			
1102.5739	1102.5786	0.0047	4	165	174	EIDGGLETLR			

1102.5739	1102.5786	0.0047	4	165	174	EIDGGLETLR	4	0	
1295.8044	1295.8088	0.0044	3	175	186	LKLPAVVTADLR			
1295.8044	1295.8088	0.0044	3	175	186	LKLPAVVTADLR	5	0	
1339.7216	1339.7217	0.0001	0	222	233	LSVISVEDPPQR			
1339.7216	1339.7217	0.0001	0	222	233	LSVISVEDPPQR			
1403.7277	1403.735	0.0073	5	86	98	GIHVEVPPAEAER	5	0	
1403.7277	1403.735	0.0073	5	86	98	GIHVEVPPAEAER			
1470.8274	1470.8271	-0.0003	0	22	35	VKPDRTGVVTDGVK			
1486.7859	1486.7898	0.0039	3	162	174	VEREIDGGLETLR			
1554.9464	1554.9446	-0.0018	-1	111	124	LAEKEKVDLVLLGK			
1683.9526	1683.9391	-0.0135	-8	206	221	IEVIKPGDLGVDLTSK			
1831.8464	1831.8707	0.0243	13	36	51	HSMNPFCEIAVEEAVR			
1831.8464	1831.8707	0.0243	13	36	51	HSMNPFCEIAVEEAVR			
1905.1279	1905.1251	-0.0028	-1	175	191	LKLPAVVTADLRLNEPR			
2238.2351	2238.2393	0.0042	2	86	106	GIHVEVPPAEAERLGPLQVAR			
2688.3118	2688.3362	0.0244	9	27	51	TGVVTDGVKHSMNPFCEIAVEEAVR			

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
4	PREDICTED: similar to Adenylate kinase isoenzyme 4, mitochondrial (Adenylate kinase 3-like 1) (ATP-	gi|113423642	25224.2	84	99.998	7	5.016

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
949.5002	949.506	0.0058	6	127	134	WIHPPSGR			
949.5002	949.506	0.0058	6	127	134	WIHPPSGR			
1045.5524	1045.5605	0.0081	8	93	102	TLGQAEALDK			
1105.6013	1105.6149	0.0136	12	126	134	RWIHPPSGR			
1122.5282	1122.5358	0.0076	7	72	80	LMMSELENR			
1122.5282	1122.5358	0.0076	7	72	80	LMMSELENR			
1249.7262	1249.7363	0.0101	8	61	71	SLLVPDHVITR	4	0	
1249.7262	1249.7363	0.0101	8	61	71	SLLVPDHVITR			
1278.6293	1278.6471	0.0178	14	72	81	LMMSELENRR			
1325.6749	1325.6909	0.016	12	82	92	GQHWLLDGFPR			
1325.6749	1325.6909	0.016	12	82	92	GQHWLLDGFPR	3	0	
1639.8948	1639.9193	0.0245	15	8	24	AVILGPPGSGKGTVCQR			
1925.0139	1925.0304	0.0165	9	25	41	IAQNFGLQHLSSGHFLR			
1925.0139	1925.0304	0.0165	9	25	41	IAQNFGLQHLSSGHFLR			
2409.2786	2409.2932	0.0146	6	25	45	IAQNFGLQHLSSGHFLRENIK			
3984.936	3984.9592	0.0232	6	135	170	VYNLDFNPPHVHGIDDVTGEPLVQQEDDKPEAVAAR			

Spot Idx/Pos	162/G4	18	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	electron-transfer-flavoprotein, beta polypeptide isoform 1 [Homo sapiens]	gi|4503609	27826.2	92	100	24	97.868

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
853.5253	853.5281	0.0028	3	99	106	LGPLQVAR			
1102.5739	1102.5658	-0.0081	-7	165	174	EIDGGLETLR			
1102.5739	1102.5658	-0.0081	-7	165	174	EIDGGLETLR			
1295.8044	1295.8074	0.003	2	175	186	LKLPAVVTADLR			
1295.8044	1295.8074	0.003	2	175	186	LKLPAVVTADLR	18	90.519	
1339.7216	1339.7192	-0.0024	-2	222	233	LSVISVEDPPQR			
1339.7216	1339.7192	-0.0024	-2	222	233	LSVISVEDPPQR			
1403.7277	1403.7322	0.0045	3	86	98	GIHVEVPPAEAER			
1403.7277	1403.7322	0.0045	3	86	98	GIHVEVPPAEAER	6	0	
1831.8464	1831.8613	0.0149	8	36	51	HSMNPFCEIAVEEAVR			
1831.8464	1831.8613	0.0149	8	36	51	HSMNPFCEIAVEEAVR			
1905.1279	1905.1244	-0.0035	-2	175	191	LKLPAVVTADLRLNEPR			
1905.1279	1905.1244	-0.0035	-2	175	191	LKLPAVVTADLRLNEPR			
2238.2351	2238.2378	0.0027	1	86	106	GIHVEVPPAEAERLGPLQVAR			
2290.1606	2290.1719	0.0113	5	77	98	TALAMGADRGIHVEVPPAEAER			

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
4	PREDICTED: similar to Adenylate kinase isoenzyme 4, mitochondrial (Adenylate kinase 3-like 1) (ATP-	gi|113423642	25224.2	69	99.906		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
949.5002	949.5016	0.0014	1	127	134	WIHPPSGR			
949.5002	949.5016	0.0014	1	127	134	WIHPPSGR			
1105.6013	1105.5948	-0.0065	-6	126	134	RWIHPPSGR			
1249.7262	1249.7294	0.0032	3	61	71	SLLVPDHVITR			
1249.7262	1249.7294	0.0032	3	61	71	SLLVPDHVITR			
1278.6293	1278.6423	0.013	10	72	81	LMMSELENRR			
1325.6749	1325.6772	0.0023	2	82	92	GQHWLLDGFPR			
1325.6749	1325.6772	0.0023	2	82	92	GQHWLLDGFPR			
1481.776	1481.7815	0.0055	4	81	92	RGQHWLLDGFPR			
1639.8948	1639.8844	-0.0104	-6	8	24	AVILGPPGSGKGTVCQR			
1925.0139	1925.0172	0.0033	2	25	41	IAQNFGLQHLSSGHFLR			
1925.0139	1925.0172	0.0033	2	25	41	IAQNFGLQHLSSGHFLR			
2409.2786	2409.2827	0.0041	2	25	45	IAQNFGLQHLSSGHFLRENIK			

Spot Idx/Pos	163/G6	19	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	7

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %

Spot Idx/Pos	164/G8	20	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
3	myosin, heavy polypeptide 9, non-muscle [Homo sapiens]	gi|12667788	226391.6	33	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1045.571	1045.5795	0.0085	8	1558	1566	LEVNLQAMK			
1155.6632	1155.6715	0.0083	7	1924	1933	GDLPFVVPRR			
1155.6632	1155.6715	0.0083	7	1923	1932	RGDLPFVVPR			
1524.8057	1524.8043	-0.0014	-1	290	301	TDLLLEPYNKYR			
1558.8588	1558.8754	0.0166	11	719	731	QRYEILTPNSIPK			
1571.854	1571.8658	0.0118	8	374	387	VSHLLGINVTDFTR			
1571.854	1571.8658	0.0118	8	374	387	VSHLLGINVTDFTR			
1579.8438	1579.834	-0.0098	-6	765	778	AGVLAHLEEERDLK			
1615.8181	1615.8287	0.0106	7	328	341	IMGIPEEEQMGLLR			
1615.8181	1615.8287	0.0106	7	328	341	IMGIPEEEQMGLLR			
1623.839	1623.8448	0.0058	4	706	718	QGFPNRVVFQEFR			
1643.8097	1643.8097	0	0	1	14	MAQQAADKYLYVDK			
1643.8097	1643.8097	0	0	1	14	MAQQAADKYLYVDK			
1727.856	1727.8778	0.0218	13	126	139	NLPIYSEEIVEMYK			
1815.9082	1815.9271	0.0189	10	1816	1830	IAQLEEQLDNETKER			
1869.9664	1869.9609	-0.0055	-3	1755	1770	ANLQIDQINTDLNLER			
1949.9927	1950.0028	0.0101	5	1418	1433	LQQELDDLLVDLDHQR			
1949.9927	1950.0028	0.0101	5	1418	1433	LQQELDDLLVDLDHQR			
2048.9626	2048.9705	0.0079	4	1677	1694	SMEAEMIQLQEELAAAER			

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
2048.9626	2048.9705	0.0079	4	1677	1694	SMEAEMIQLQEELAAAER			
2299.1345	2299.1677	0.0332	14	1175	1193	TLEEEAKTHEAQIQEMRQK			
2333.0562	2333.0798	0.0236	10	941	959	MQQNIQELEEQLEEEESAR			
2749.3274	2749.3521	0.0247	9	1302	1324	DFSALESQLQDTQELLQEENRQK			
3017.4797	3017.47	-0.0097	-3	1136	1162	DLGEELEALKTELEDTLDSTAAQQELR			

7 KIAA0678 protein [Homo sapiens] gi|71891673 255972.3 30 0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1045.5887	1045.5795	-0.0092	-9	105	113	TELLTEALR			
1083.5656	1083.5759	0.0103	10	1406	1414	YAGYPMLIR			
1491.7437	1491.7435	-0.0002	0	1457	1469	ENGLEVLQEAFSR			
1504.6854	1504.708	0.0226	15	864	874	SYEFFNELYHR			
1504.6854	1504.708	0.0226	15	864	874	SYEFFNELYHR			
1513.7756	1513.7799	0.0043	3	114	126	FRTDFSEGKITGR			
1550.7849	1550.7935	0.0086	6	225	236	EPLEFEQYLNLR			
1586.8285	1586.8195	-0.009	-6	207	221	SAIDHAGNYIGISLR			
1586.8285	1586.8195	-0.009	-6	207	221	SAIDHAGNYIGISLR			
1643.7958	1643.8097	0.0139	8	627	640	HLHTAMFTISSDQR			
1643.7958	1643.8097	0.0139	8	627	640	HLHTAMFTISSDQR			
1647.8448	1647.8569	0.0121	7	1456	1469	RENGLEVLQEAFSR			
1699.9026	1699.9037	0.0011	1	1	14	GWSLSSLPRRFEHK			
1712.9329	1712.9464	0.0135	8	193	206	LHLFASEQREEIIK			
1736.8754	1736.8877	0.0123	7	375	390	FLATPPNGNFADAVFR			
1736.8754	1736.8877	0.0123	7	375	390	FLATPPNGNFADAVFR			
1916.9487	1916.96	0.0113	6	240	256	YSTDESITSLAEFVVQK			
1940.0269	1940.0266	-0.0003	0	967	984	ATVPLQSNVIEAAPDMKR			
1948.0176	1948.0352	0.0176	9	2099	2116	AMASLETIGPLMNGMKKR			
1958.9817	1958.9923	0.0106	5	1603	1620	LGGYLAEEQATPENPTIR			
2087.0767	2087.0789	0.0022	1	1603	1621	LGGYLAEEQATPENPTIRK			
2110.0637	2110.072	0.0083	4	357	374	WGLLSMPVDEEVESLHLR			
2266.219	2266.2039	-0.0151	-7	140	160	KPVILEVTPGGFDQINPATNR			
2266.219	2266.2039	-0.0151	-7	140	160	KPVILEVTPGGFDQINPATNR			
2511.334	2511.3438	0.0098	4	669	691	ILPPGLLAYLESSDLVPEKDADR			

11 DnaJ (Hsp40) homolog, subfamily C, member 13 [Homo sapiens] gi|112421122 254252.4 26 0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1045.5887	1045.5795	-0.0092	-9	91	99	TELLTEALR			
1083.5656	1083.5759	0.0103	10	1392	1400	YAGYPMLIR			
1491.7437	1491.7435	-0.0002	0	1443	1455	ENGLEVLQEAFSR			
1504.6854	1504.708	0.0226	15	850	860	SYEFFNELYHR			
1504.6854	1504.708	0.0226	15	850	860	SYEFFNELYHR			
1513.7756	1513.7799	0.0043	3	100	112	FRTDFSEGKITGR			
1550.7849	1550.7935	0.0086	6	211	222	EPLEFEQYLNLR			
1586.8285	1586.8195	-0.009	-6	193	207	SAIDHAGNYIGISLR			
1586.8285	1586.8195	-0.009	-6	193	207	SAIDHAGNYIGISLR			
1643.7958	1643.8097	0.0139	8	613	626	HLHTAMFTISSDQR			
1643.7958	1643.8097	0.0139	8	613	626	HLHTAMFTISSDQR			
1647.8448	1647.8569	0.0121	7	1442	1455	RENGLEVLQEAFSR			
1712.9329	1712.9464	0.0135	8	179	192	LHLFASEQREEIIK			
1736.8754	1736.8877	0.0123	7	361	376	FLATPPNGNFADAVFR			
1736.8754	1736.8877	0.0123	7	361	376	FLATPPNGNFADAVFR			
1916.9487	1916.96	0.0113	6	226	242	YSTDESITSLAEFVVQK			
1940.0269	1940.0266	-0.0003	0	953	970	ATVPLQSNVIEAAPDMKR			
1948.0176	1948.0352	0.0176	9	2085	2102	AMASLETIGPLMNGMKKR			
1958.9817	1958.9923	0.0106	5	1589	1606	LGGYLAEEQATPENPTIR			
2087.0767	2087.0789	0.0022	1	1589	1607	LGGYLAEEQATPENPTIRK			
2110.0637	2110.072	0.0083	4	343	360	WGLLSMPVDEEVESLHLR			
2266.219	2266.2039	-0.0151	-7	126	146	KPVILEVTPGGFDQINPATNR			
2266.219	2266.2039	-0.0151	-7	126	146	KPVILEVTPGGFDQINPATNR			
2511.334	2511.3438	0.0098	4	655	677	ILPPGLLAYLESSDLVPEKDADR			

Spot Idx/Pos	165/G10	21	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1 [Homo sapiens]	gi|4826686	82379.8	82	99.996	7	35.986

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
975.5006	975.5065	0.0059	6	452	458	TDRLWER			
1048.6149	1048.6255	0.0106	10	491	499	ILKGEYAVR			
1111.6832	1111.6978	0.0146	13	320	330	ELLIIGGVAAR			
1111.6832	1111.6978	0.0146	13	320	330	ELLIIGGVAAR	7	35.986	
1380.8684	1380.8784	0.01	7	318	330	LRELLIIGGVAAR			
1386.7239	1386.7271	0.0032	2	422	432	IMHFPTWVDLK			
1467.7664	1467.7736	0.0072	5	211	223	DLGLAFEIPPHMK			
1610.8068	1610.8232	0.0164	10	387	400	MHNQIPQVTSDGKR			
1663.8948	1663.8997	0.0049	3	563	577	KGDVRFLICTDVAAR			
1766.9258	1766.9036	-0.0222	-13	208	223	NGKDLGLAFEIPPHMK			
1916.0421	1916.0293	-0.0128	-7	400	416	RLQVIVCSATLHSFDVK			
1968.0396	1968.0426	0.003	2	331	349	DQLSVLENGVDIVVGTPGR			
1968.0396	1968.0426	0.003	2	331	349	DQLSVLENGVDIVVGTPGR			
2002.9287	2002.9384	0.0097	5	473	490	DNTRPGANSPEMWSEAIK			
2002.9287	2002.9384	0.0097	5	473	490	DNTRPGANSPEMWSEAIK			
2025.0399	2025.0447	0.0048	2	433	451	GEDSVPDTVHHVVVPVNPK			
2079.1121	2079.1104	-0.0017	-1	578	596	GIDIHGVPYVINVTLPDEK			
2134.1079	2134.1169	0.009	4	721	738	EAQTSFLHLGYLPNQLFR			
2134.1079	2134.1169	0.009	4	721	738	EAQTSFLHLGYLPNQLFR			
2138.1814	2138.1704	-0.011	-5	289	307	ALIVEPSRELAEQTLNNIK			
2372.1768	2372.178	0.0012	1	366	386	FLVLDEADGLLSQGYSDFINR			
2372.1768	2372.178	0.0012	1	366	386	FLVLDEADGLLSQGYSDFINR			
2876.5051	2876.4907	-0.0144	-5	578	602	GIDIHGVPYVINVTLPDEKQNYVHR			

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
2876.5051	2876.4907	-0.0144	-5	578	602	GIDIHGVPYVINVTLPDEKQNYVHR			
2896.5261	2896.4885	-0.0376	-13	331	358	DQLSVLENGVDIVVGTPGRLDDLVSTGK			

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
3	chaperone protein HSP90 beta [Homo sapiens]	gi|9082289	72827.8	58	98.916		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
829.5505	829.5417	-0.0088	-11	106	112	VKEVVKK			
886.5468	886.5516	0.0048	5	358	364	RLSELLR			
1236.6371	1236.6489	0.0118	10	246	255	RAPFDLFENK			
1237.6283	1237.6427	0.0144	12	77	88	ADHGEPIGRGTK			
1348.6643	1348.6775	0.0132	10	228	238	HFSVEGQLEFR			
1348.6643	1348.6775	0.0132	10	228	238	HFSVEGQLEFR			
1513.7856	1513.8082	0.0226	15	287	300	GVVDSEDLPLNISR			
1649.8744	1649.8676	-0.0068	-4	180	192	IKEKYIDQEELNK			
1782.9497	1782.9545	0.0048	3	533	547	HLEINPDHPIVETLR			
1782.9497	1782.9545	0.0048	3	533	547	HLEINPDHPIVETLR			
1808.9581	1808.9552	-0.0029	-2	113	127	HSQFIGYPITLYLEK			
1911.0446	1911.0511	0.0065	3	532	547	KHLEINPDHPIVETLR			
2015.0443	2015.0457	0.0014	1	89	104	VILHLKEDQTEYLEER			
2015.0443	2015.0457	0.0014	1	89	104	VILHLKEDQTEYLEER			
2171.1455	2171.146	0.0005	0	89	105	VILHLKEDQTEYLEERR			
2176.9451	2176.9678	0.0227	10	365	383	YHTSQSGDEMTSLSEYVSR			
2176.9451	2176.9678	0.0227	10	365	383	YHTSQSGDEMTSLSEYVSR			
2255.9587	2255.9744	0.0157	7	57	76	HNDDEQYAWESSAGGSFTVR			
2255.9587	2255.9744	0.0157	7	57	76	HNDDEQYAWESSAGGSFTVR			
2317.1243	2317.0999	-0.0244	-11	268	286	VFIMDSCDELIPEYLNFIR			
2391.1826	2391.1809	-0.0017	-1	390	410	SIYYITGESKEQVANSAFVER			

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
4	ribonucleotide reductase M1 subunit [Homo sapiens]	gi|5006420	89984.5	58	98.839		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1096.5819	1096.5847	0.0028	3	13	21	VMFDKITSR			
1126.6003	1126.6104	0.0101	9	71	80	HPDYAILAAR			
1344.748	1344.7441	-0.0039	-3	119	130	STLDIVLANKDR			
1367.7035	1367.7137	0.0102	7	163	173	VAERPQHMLMR			
1367.7035	1367.7137	0.0102	7	163	173	VAERPQHMLMR			
1509.7842	1509.7776	-0.0066	-4	10	21	QERVMFDKITSR			
1570.87	1570.869	-0.001	-1	741	754	TRPAANPIQFTLNK			
1693.9635	1693.9425	-0.021	-12	629	643	VLSGEFQIVNPHLLK			
1828.0074	1827.9912	-0.0162	-9	741	756	TRPAANPIQFTLNKEK			
1850.0646	1850.0602	-0.0044	-2	628	643	RVLSGEFQIVNPHLLK			
2064.1533	2064.1414	-0.0119	-6	498	516	HRPIGIGVQGLADAFILMR			
2093.0444	2093.0535	0.0091	4	257	277	ATGSYIAGTNGNSNGLVPMLR			
2108.0845	2108.0823	-0.0022	-1	480	497	IIDINYYPVPEACLSNKR			
2302.1462	2302.1604	0.0142	6	699	719	GAFIDQSQSLNIHIAEPNYGK			
2333.1235	2333.1125	-0.011	-5	131	149	LNSAIIYDRDFSYNYFGFK			
2391.2019	2391.1809	-0.021	-9	140	158	DFSYNYFGFKTLERSYLLK			
2572.3252	2572.3203	-0.0049	-2	174	196	VSVGIHKEDIDAAIETYNLLSER			
3579.7998	3579.7856	-0.0142	-4	595	627	NSLLIAPMPTASTAQILGNNESIEPYTSNIYTR			

Spot Idx/Pos	166/G12	22	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	heat shock 90kDa protein 1, beta [Homo sapiens]	gi|20149594	83212.1	134	100	1	0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
829.5294	829.5364	0.007	8	331	337	ALLFIPR			
886.5468	886.5482	0.0014	2	450	456	RLSELLR			
901.5254	901.524	-0.0014	-2	285	291	TKPIWTR			
1194.6477	1194.6538	0.0061	5	73	82	IDIIPNPQER			
1236.6371	1236.6494	0.0123	10	338	347	RAPFDLFENK			
1249.6171	1249.635	0.0179	14	492	502	EQVANSAFVER			
1348.6643	1348.6707	0.0064	5	320	330	HFSVEGQLEFR			
1348.6643	1348.6707	0.0064	5	320	330	HFSVEGQLEFR	1	0	
1364.7321	1364.7297	-0.0024	-2	338	348	RAPFDLFENKK			
1513.7856	1513.7952	0.0096	6	379	392	GVVDSEDLPLNISR			
1513.7856	1513.7952	0.0096	6	379	392	GVVDSEDLPLNISR			
1544.8278	1544.8197	-0.0081	-5	42	55	ELISNASDALDKIR			
1564.8693	1564.8527	-0.0166	-11	70	82	ELKIDIIPNPQER			
1649.8744	1649.8595	-0.0149	-9	272	284	IKEKYIDQEELNK			
1782.9497	1782.9604	0.0107	6	625	639	HLEINPDHPIVETLR			
1782.9497	1782.9604	0.0107	6	625	639	HLEINPDHPIVETLR			
1808.9581	1808.9512	-0.0069	-4	205	219	HSQFIGYPITLYLEK			
1847.797	1847.8038	0.0068	4	292	306	NPDDITQEEYGEFYK			
1911.0446	1911.0476	0.003	2	624	639	KHLEINPDHPIVETLR			
1911.0446	1911.0476	0.003	2	624	639	KHLEINPDHPIVETLR			
2015.0443	2015.0425	-0.0018	-1	181	196	VILHLKEDQTEYLEER			
2015.0443	2015.0425	-0.0018	-1	181	196	VILHLKEDQTEYLEER			
2034.0654	2034.0372	-0.0282	-14	276	291	YIDQEELNKTKPIWTR			
2059.0051	2059.009	0.0039	2	412	428	CLELFSELAEDKENYKK			
2171.1455	2171.155	0.0095	4	181	197	VILHLKEDQTEYLEERR			
2176.9451	2176.9622	0.0171	8	457	475	YHTSQSGDEMTSLSEYVSR			
2176.9451	2176.9622	0.0171	8	457	475	YHTSQSGDEMTSLSEYVSR			
2255.9587	2255.97	0.0113	5	149	168	HNDDEQYAWESSAGGSFTVR			
2255.9587	2255.97	0.0113	5	149	168	HNDDEQYAWESSAGGSFTVR			
2317.1243	2317.1086	-0.0157	-7	360	378	VFIMDSCDELIPEYLNFIR			
2358.1968	2358.1667	-0.0301	-13	379	399	GVVDSEDLPLNISREMLQQSK			
2369.1882	2369.1697	-0.0185	-8	429	448	FYEAFSKNLKLGIHEDSTNR			
2391.1826	2391.1763	-0.0063	-3	482	502	SIYYITGESKEQVANSAFVER			
2988.5312	2988.5474	0.0162	5	653	679	DLVVLLFETALLSSGFSLEDPQTHSNR			

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1 [Homo sapiens]	gi|4826686	82379.8	87	99.999	1	0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
901.5253	901.524	-0.0013	-1	455	461	LWERLGK			
975.5006	975.4911	-0.0095	-10	452	458	TDRLWER			

1048.6149	1048.6185	0.0036	3	491	499	ILKGEYAVR		
1111.6832	1111.6936	0.0104	9	320	330	ELLIIGGVAAR		
1111.6832	1111.6936	0.0104	9	320	330	ELLIIGGVAAR	1	0
1380.8684	1380.8829	0.0145	11	318	330	LRELLIIGGVAAR		
1386.7239	1386.7163	-0.0076	-5	422	432	IMHFPTWVDLK		
1467.7664	1467.7673	0.0009	1	211	223	DLGLAFEIPPHMK		
1610.8068	1610.8152	0.0084	5	387	400	MHNQIPQVTSDGKR		
1663.8948	1663.8977	0.0029	2	563	577	KGDVRFLICTDVAAR		
1759.941	1759.9385	-0.0025	-1	401	416	LQVIVCSATLHSFDVK		
1766.9258	1766.9109	-0.0149	-8	208	223	NGKDLGLAFEIPPHMK		
1968.0396	1968.0535	0.0139	7	331	349	DQLSVLENGVDIVVGTPGR		
1968.0396	1968.0535	0.0139	7	331	349	DQLSVLENGVDIVVGTPGR		
1972.0724	1972.047	-0.0254	-13	417	432	KLSEKIMHFPTWVDLK		
2002.9287	2002.9343	0.0056	3	473	490	DNTRPGANSPEMWSEAIK		
2002.9287	2002.9343	0.0056	3	473	490	DNTRPGANSPEMWSEAIK		
2079.1121	2079.095	-0.0171	-8	578	596	GIDIHGVPYVINVTLPDEK		
2134.1079	2134.1172	0.0093	4	721	738	EAQTSFLHLGYLPNQLFR		
2134.1079	2134.1172	0.0093	4	721	738	EAQTSFLHLGYLPNQLFR		
2138.1814	2138.1819	0.0005	0	289	307	ALIVEPSRELAEQTLNNIK		
2372.1768	2372.179	0.0022	1	366	386	FLVLDEADGLLSQGYSDFINR		
2372.1768	2372.179	0.0022	1	366	386	FLVLDEADGLLSQGYSDFINR		
2564.3606	2564.3567	-0.0039	-2	53	75	TGAFSIPVIQIVYETLKDQQEGK		
2876.5051	2876.5066	0.0015	1	578	602	GIDIHGVPYVINVTLPDEKQNYVHR		
2896.5261	2896.5046	-0.0215	-7	331	358	DQLSVLENGVDIVVGTPGRLDDLVSTGK		

Spot Idx/Pos	167/G14	23	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	crystallin, zeta variant [Homo sapiens]	gi|62089008	35384.7	83	99.996	10	70.02

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1054.564	1054.5559	-0.0081	-8	235	244	DLSLLSHGGR			
1221.6512	1221.6334	-0.0178	-15	15	25	VFEFGGPEVLK			
1221.6512	1221.6334	-0.0178	-15	15	25	VFEFGGPEVLK			
1249.6755	1249.6769	0.0014	1	1	11	ITMATGQKLMR			
1527.7954	1527.7863	-0.0091	-6	127	140	QGAAIGIPYFTAYR			
1527.7954	1527.7863	-0.0091	-6	127	140	QGAAIGIPYFTAYR	10	70.02	
1557.7842	1557.7848	0.0006	0	44	57	VHACGVNPVETYIR			
1633.8557	1633.8478	-0.0079	-5	190	203	IVLQNGAHEVFNHR			
1633.8557	1633.8478	-0.0079	-5	190	203	IVLQNGAHEVFNHR			
1773.0269	1773.0081	-0.0188	-11	28	43	SDIAVPIPKDHQVLIK			
2123.1025	2123.1028	0.0003	0	150	172	AGESVLVHGASGGVGLAACQIAR			
2123.1025	2123.1028	0.0003	0	150	172	AGESVLVHGASGGVGLAACQIAR			
2391.26	2391.2693	0.0093	4	37	57	DHQVLIKVHACGVNPVETYIR			
2551.2351	2551.2666	0.0315	12	95	118	VFTSSTISGGYAEYALAADHTVYK			
2716.4192	2716.4446	0.0254	9	64	90	KPLLPYTPGSDVAGVIEAVGDNASAFK			
2804.4436	2804.4668	0.0232	8	178	203	VLGTAGTEEGQKIVLQNGAHEVFNHR			
2844.5142	2844.4875	-0.0267	-9	64	91	KPLLPYTPGSDVAGVIEAVGDNASAFKK			

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
2	mitochondrial malate dehydrogenase 2, NAD [Homo sapiens]	gi|89574129	31948.8	77	99.986	20	97.029

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1147.6581	1147.6473	-0.0108	-9	171	182	VNVPVIGGHAGK			
1233.7201	1233.7104	-0.0097	-8	145	155	IFGVTTLDIVR			
1233.7201	1233.7104	-0.0097	-8	145	155	IFGVTTLDIVR	14	87.003	
1281.6982	1281.6901	-0.0081	-6	71	83	GCDVVVIPAGVPR			
1454.7056	1454.6948	-0.0108	-7	221	236	AGAGSATLSMAYAGAR			
1454.7056	1454.6948	-0.0108	-7	221	236	AGAGSATLSMAYAGAR			
1560.8016	1560.7906	-0.011	-7	195	208	VDFPQDQLTALTGR	6	30.843	
1560.8016	1560.7906	-0.011	-7	195	208	VDFPQDQLTALTGR			
1793.0894	1793.0842	-0.0052	-3	6	24	VAVLGASGGIGQPLSLLLK			
1916.9309	1916.9399	0.009	5	259	275	SQETECTYFSTPLLLGK			
2143.1658	2143.1716	0.0058	3	137	155	HGVYNPNKIFGVTTLDIVR			
2143.1658	2143.1716	0.0058	3	137	155	HGVYNPNKIFGVTTLDIVR			
2365.2397	2365.2437	0.004	2	32	53	LTLYDIAHTPGVAADLSHIETK			
2365.2397	2365.2437	0.004	2	32	53	LTLYDIAHTPGVAADLSHIETK			
2695.3945	2695.4033	0.0088	3	58	83	GYLGPEQLPDCLKGCDVVVIPAGVPR			
2855.5334	2855.554	0.0206	7	183	208	TIIPLISQCTPKVDFPQDQLTALTGR			

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
7	glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]	gi|31645	36031.4	72	99.957		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1330.6493	1330.6451	-0.0042	-3	324	335	VVDLMAHMASKE			
1473.7729	1473.7878	0.0149	10	235	248	VPTANVSVVDLTCR			
1613.9009	1613.8972	-0.0037	-2	67	80	LVINGNPITIFQER			
1613.9009	1613.8972	-0.0037	-2	67	80	LVINGNPITIFQER			
1646.8933	1646.8862	-0.0071	-4	220	234	VIPELDGKLTGMAFR			
1763.8022	1763.7977	-0.0045	-3	310	323	LISWYDNEFGYSNR			
1763.8022	1763.7977	-0.0045	-3	310	323	LISWYDNEFGYSNR			
2041.1075	2041.1089	0.0014	1	67	84	LVINGNPITIFQERDPSK			
2041.1075	2041.1089	0.0014	1	67	84	LVINGNPITIFQERDPSK			
2113.1399	2113.1384	-0.0015	-1	62	80	AENGKLVINGNPITIFQER			
2277.0378	2277.0623	0.0245	11	87	107	WGDAGAEYVVESTGVFTTMEK			
2369.2104	2369.2415	0.0311	13	118	139	RVIISAPSADAPMFVMGVNHEK			
2518.2168	2518.2429	0.0261	10	85	107	IKWGDAGAEYVVESTGVFTTMEK			
2540.3467	2540.3274	-0.0193	-8	62	84	AENGKLVINGNPITIFQERDPSK			
2595.3599	2595.3623	0.0024	1	163	186	VIHDNFGIVEGLMTTVHAITATQK			

2933.4534	2933.4802	0.0268	9	119	145	VIISAPSADAPMFVMGVNHEKYDNSLK

12	uracil DNA glycosylase [Homo sapiens]	gi|35053	35470.1	57	98.784

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1473.7729	1473.7878	0.0149	10	234	247	VPTANVSVVDLTCR			
1613.9009	1613.8972	-0.0037	-2	67	80	LVINGNPITIFQER			
1613.9009	1613.8972	-0.0037	-2	67	80	LVINGNPITIFQER			
1763.8022	1763.7977	-0.0045	-3	309	322	LISWYDNEFGYSNR			
1763.8022	1763.7977	-0.0045	-3	309	322	LISWYDNEFGYSNR			
2041.1075	2041.1089	0.0014	1	67	84	LVINGNPITIFQERDPSK			
2041.1075	2041.1089	0.0014	1	67	84	LVINGNPITIFQERDPSK			
2113.1399	2113.1384	-0.0015	-1	62	80	AENGKLVINGNPITIFQER			
2277.0378	2277.0623	0.0245	11	87	107	WGDAGAEYVVESTGVFTTMEK			
2369.2104	2369.2415	0.0311	13	118	139	RVIISAPSADAPMFVMGVNHEK			
2518.2168	2518.2429	0.0261	10	85	107	IKWGDAGAEYVVESTGVFTTMEK			
2540.3467	2540.3274	-0.0193	-8	62	84	AENGKLVINGNPITIFQERDPSK			
2595.3599	2595.3623	0.0024	1	163	186	VIHDNFGIVEGLMTTVHAITATQK			
2933.4534	2933.4802	0.0268	9	119	145	VIISAPSADAPMFVMGVNHEKYDNSLK			

Spot Idx/Pos	168/G16	24	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]	gi|89573929	24604.7	107	100	2	0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1473.7729	1473.845	0.0721	49	210	223	VPTANVSVVDLTCR			
1613.9009	1613.9684	0.0675	42	42	55	LVINGNPITIFQER			
1613.9009	1613.9684	0.0675	42	42	55	LVINGNPITIFQER	2	0	
1645.9093	1645.9619	0.0526	32	195	209	VIPELNGKLTGMAFR			
2041.1075	2041.1807	0.0732	36	42	59	LVINGNPITIFQERDPSK			
2041.1075	2041.1807	0.0732	36	42	59	LVINGNPITIFQERDPSK			
2113.1399	2113.2173	0.0774	37	37	55	AENGKLVINGNPITIFQER			
2213.1091	2213.1819	0.0728	33	94	114	VIISAPSADAPMFVMGVNHEK			
2213.1091	2213.1819	0.0728	33	94	114	VIISAPSADAPMFVMGVNHEK			
2277.0378	2277.1165	0.0787	35	62	82	WGDAGAEYVVESTGVFTTMEK			
2369.2104	2369.3091	0.0987	42	93	114	RVIISAPSADAPMFVMGVNHEK			
2518.2168	2518.3201	0.1033	41	60	82	IKWGDAGAEYVVESTGVFTTMEK			
2540.3467	2540.3562	0.0095	4	37	59	AENGKLVINGNPITIFQERDPSK			
2595.3599	2595.4463	0.0864	33	138	161	VIHDNFGIVEGLMTTVHAITATQK			
2595.3599	2595.4463	0.0864	33	138	161	VIHDNFGIVEGLMTTVHAITATQK			
2617.5034	2617.417	-0.0864	-33	176	202	GALQNIIPASTGAAKAVGKVIPELNGK			
2933.4534	2933.5596	0.1062	36	94	120	VIISAPSADAPMFVMGVNHEKYDNSLK			
3308.5642	3308.6765	0.1123	34	3	30	VDIVAINDPFIDLNYMVYMFQYDSTHGK			

10	MDH2 [Homo sapiens]	gi|49168580	35536.8	70	99.935	16	78.164

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1221.6837	1221.6976	0.0139	11	325	335	ASIKKGEDFVK			
1233.7201	1233.7793	0.0592	48	166	176	IFGVTTLDIVR			
1233.7201	1233.7793	0.0592	48	166	176	IFGVTTLDIVR	16	78.164	
1281.6982	1281.7611	0.0629	49	92	104	GCDVVVIPAGVPR			
1327.6714	1327.7172	0.0458	34	258	269	FVFSLVDAMNGK			
1352.8372	1352.7809	-0.0563	-42	2	14	LSALVRPVSAALR			
1454.7056	1454.7694	0.0638	44	242	257	AGAGSATLSMAYAGAR			
1515.8451	1515.8148	-0.0303	-20	315	328	MISDAIPELKASIK			
1560.8016	1560.8658	0.0642	41	216	229	VDFPQDQLTALTGR			
1560.8016	1560.8658	0.0642	41	216	229	VDFPQDQLTALTGR			
1601.8645	1601.8942	0.0297	19	177	191	ANTFVAELKGLDPAR			
1793.0894	1793.1414	0.052	29	27	45	VAVLGASGGIGQPLSLLLK			
2143.1658	2143.2273	0.0615	29	158	176	HGVYNPNKIFGVTTLDIVR			
2365.2397	2365.3191	0.0794	34	53	74	LTLYDIAHTPGVAADLSHIETK			
2365.2397	2365.3191	0.0794	34	53	74	LTLYDIAHTPGVAADLSHIETK			

4	uracil DNA glycosylase [Homo sapiens]	gi|35053	35470.1	52	96.065

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1645.9093	1645.9619	0.0526	32	219	233	VIPELNGKLTGMAFR			
1763.8022	1763.8685	0.0663	38	309	322	LISWYDNEFGYSNR			
1763.8022	1763.8685	0.0663	38	309	322	LISWYDNEFGYSNR			
2041.1075	2041.1807	0.0732	36	67	84	LVINGNPITIFQERDPSK			
2041.1075	2041.1807	0.0732	36	67	84	LVINGNPITIFQERDPSK			
2113.1399	2113.2173	0.0774	37	62	80	AENGKLVINGNPITIFQER			
2213.1091	2213.1819	0.0728	33	119	139	VIISAPSADAPMFVMGVNHEK			
2213.1091	2213.1819	0.0728	33	119	139	VIISAPSADAPMFVMGVNHEK			
2277.0378	2277.1165	0.0787	35	87	107	WGDAGAEYVVESTGVFTTMEK			
2540.3467	2540.3562	0.0095	4	62	84	AENGKLVINGNPITIFQERDPSK			
2595.3599	2595.4463	0.0864	33	163	186	VIHDNFGIVEGLMTTVHAITATQK			
2595.3599	2595.4463	0.0864	33	163	186	VIHDNFGIVEGLMTTVHAITATQK			
2933.4534	2933.5596	0.1062	36	119	145	VIISAPSADAPMFVMGVNHEKYDNSLK			
3308.5642	3308.6765	0.1123	34	28	55	VDIVAINDPFIDLNYMVYMFQYDSTHGK			

Spot Idx/Pos	169/G18	25	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein	Protein	Total Ion	Total Ion

				Score	C. I. %	Score	C. I. %
1	NME1-NME2 protein [Homo sapiens]	gi|66392203	30117.6	172	100	14	88.077

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
977.5964	977.5933	-0.0031	-3	150	157	LVAMKFLR			
984.6199	984.6278	0.0079	8	134	142	GLVGEIIKR			
984.6199	984.6278	0.0079	8	19	27	GLVGEIIKR			
1069.5636	1069.5635	-0.0001	0	230	239	NIIHGSDSVK			
1175.6571	1175.6639	0.0068	6	172	181	DRPFFPGLVK			
1175.6571	1175.6639	0.0068	6	172	181	DRPFFPGLVK			
1344.7633	1344.7697	0.0064	5	122	133	TFIAIKPDGVQR			
1344.7633	1344.7697	0.0064	5	7	18	TFIAIKPDGVQR	15	90.107	
1516.8845	1516.8929	0.0084	6	19	31	GLVGEIIKRFEQK			
1516.8845	1516.8929	0.0084	6	134	146	GLVGEIIKRFEQK			
1710.8809	1710.8773	-0.0036	-2	158	171	ASEEHLKQHYIDLK			
1785.9163	1785.9221	0.0058	3	204	220	VMLGETNPADSKPGTIR			
1785.9163	1785.9221	0.0058	3	89	105	VMLGETNPADSKPGTIR			
1895.9789	1895.9728	-0.0061	-3	244	258	EISLWFKPEELVDYK			
2073.1279	2073.1257	-0.0022	-1	165	181	QHYIDLKDRPFFPGLVK			
2073.1279	2073.1257	-0.0022	-1	165	181	QHYIDLKDRPFFPGLVK			
2093.0557	2093.0549	-0.0008	0	182	200	YMNSGPVVAMVWEGLNVVK			
2311.1855	2311.1824	-0.0031	-1	240	258	SAEKEISLWFKPEELVDYK			
2311.1855	2311.1824	-0.0031	-1	240	258	SAEKEISLWFKPEELVDYK			
2407.2261	2407.2288	0.0027	1	182	203	YMNSGPVVAMVWEGLNVVKTGR			
2867.5203	2867.5078	-0.0125	-4	158	181	ASEEHLKQHYIDLKDRPFFPGLVK			
2867.5203	2867.5078	-0.0125	-4	158	181	ASEEHLKQHYIDLKDRPFFPGLVK			
3361.7312	3361.741	0.0098	3	230	258	NIIHGSDSVKSAEKEISLWFKPEELVDYK			

4	Putative nucleoside diphosphate kinase (NDK) (NDP kinase)	gi|3914116	15519	51	95.159		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1069.5636	1069.5635	-0.0001	0	100	109	NIIHGSDSVK			
1175.6571	1175.6639	0.0068	6	42	51	DRPFFPGLVK			
1175.6571	1175.6639	0.0068	6	42	51	DRPFFPGLVK			
1785.9163	1785.9221	0.0058	3	74	90	VMLGETNPADSKPGTIR			
1785.9163	1785.9221	0.0058	3	74	90	VMLGETNPADSKPGTIR			
2073.1279	2073.1257	-0.0022	-1	35	51	QHYIDLKDRPFFPGLVK			
2073.1313	2073.1257	-0.0056	-3	17	34	GFRLVAMKFLPASEEHLK			
2093.0557	2093.0549	-0.0008	0	52	70	YMNSGPVVAMVWEGLNVVK			
2407.2261	2407.2288	0.0027	1	52	73	YMNSGPVVAMVWEGLNVVKTGR			

Spot Idx/Pos	170/G20	26	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	NME1-NME2 protein [Homo sapiens]	gi|66392203	30117.6	163	100	29	99.785

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
911.4733	911.4702	-0.0031	-3	143	149	FEQKGFR			
984.6199	984.6236	0.0037	4	19	27	GLVGEIIKR	6	52.426	
984.6199	984.6236	0.0037	4	134	142	GLVGEIIKR			
994.4774	994.4841	0.0067	7	221	229	GDFCIQVGR			
994.4774	994.4841	0.0067	7	106	114	GDFCIQVGR	9	76.913	
1069.5636	1069.5569	-0.0067	-6	230	239	NIIHGSDSVK			
1175.6571	1175.6576	0.0005	0	172	181	DRPFFPGLVK			
1175.6571	1175.6576	0.0005	0	172	181	DRPFFPGLVK			
1344.7633	1344.764	0.0007	1	122	133	TFIAIKPDGVQR			
1344.7633	1344.764	0.0007	1	7	18	TFIAIKPDGVQR	17	96.204	
1516.8845	1516.88	-0.0045	-3	134	146	GLVGEIIKRFEQK			
1710.8809	1710.8801	-0.0008	0	158	171	ASEEHLKQHYIDLK			
1785.9163	1785.9178	0.0015	1	89	105	VMLGETNPADSKPGTIR			
1785.9163	1785.9178	0.0015	1	204	220	VMLGETNPADSKPGTIR			
1895.9789	1895.9713	-0.0076	-4	244	258	EISLWFKPEELVDYK			
2073.1279	2073.1345	0.0066	3	165	181	QHYIDLKDRPFFPGLVK			
2093.0557	2093.0532	-0.0025	-1	182	200	YMNSGPVVAMVWEGLNVVK			
2311.1855	2311.1882	0.0027	1	240	258	SAEKEISLWFKPEELVDYK			
2761.376	2761.376	0	0	204	229	VMLGETNPADSKPGTIRGDFCIQVGR			
2867.5203	2867.4978	-0.0225	-8	158	181	ASEEHLKQHYIDLKDRPFFPGLVK			

7	Putative nucleoside diphosphate kinase (NDK) (NDP kinase)	gi|3914116	15519	63	99.649	9	76.913

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
911.4733	911.4702	-0.0031	-3	13	19	FEQKGFR			
994.4774	994.4841	0.0067	7	91	99	GDFCIQVGR			
994.4774	994.4841	0.0067	7	91	99	GDFCIQVGR	9	76.913	
1069.5636	1069.5569	-0.0067	-6	100	109	NIIHGSDSVK			
1175.6571	1175.6576	0.0005	0	42	51	DRPFFPGLVK			
1175.6571	1175.6576	0.0005	0	42	51	DRPFFPGLVK			
1785.9163	1785.9178	0.0015	1	74	90	VMLGETNPADSKPGTIR			
1785.9163	1785.9178	0.0015	1	74	90	VMLGETNPADSKPGTIR			
2073.1313	2073.1345	0.0032	2	17	34	GFRLVAMKFLPASEEHLK			
2093.0557	2093.0532	-0.0025	-1	52	70	YMNSGPVVAMVWEGLNVVK			
2761.376	2761.376	0	0	74	99	VMLGETNPADSKPGTIRGDFCIQVGR			

8	RNA binding motif protein 3 isoform a [Homo sapiens]	gi|5803137	17160	41	41.804		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
867.4067	867.4026	-0.0041	-5	132	138	SRDYNGR			
1437.5665	1437.5724	0.0059	4	146	157	YSGGNYRDNYDN			
1437.5665	1437.5724	0.0059	4	146	157	YSGGNYRDNYDN			
1606.6992	1606.7145	0.0153	10	139	152	NQGGYDRYSGGNYR			
1730.7556	1730.754	-0.0016	-1	117	131	YYDSRPGGYGYGYGR			
1730.7556	1730.754	-0.0016	-1	117	131	YYDSRPGGYGYGYGR			
1981.9589	1981.9657	0.0068	3	48	65	GFGFITFTNPEHASVAMR			
1981.9589	1981.9657	0.0068	3	48	65	GFGFITFTNPEHASVAMR			
2225.092	2225.1077	0.0157	7	46	65	SRGFGFITFTNPEHASVAMR			
2227.9023	2227.9102	0.0079	4	139	157	NQGGYDRYSGGNYRDNYDN			
2227.9023	2227.9102	0.0079	4	139	157	NQGGYDRYSGGNYRDN			

YDN

Spot Idx/Pos	171/G22	27	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	type 1 RNA helicase pNORF1	gi|1885356	122976	202	100	1	0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
942.5843	942.5868	0.0025	3	858	865	RLNVALTR			
952.5502	952.5402	-0.01	-10	342	349	IAYFTLPK			
1099.5742	1099.5775	0.0033	3	245	253	IPSEQEQLR			
1107.5792	1107.5828	0.0036	3	678	687	AGLSQSLFER			
1129.6476	1129.64	-0.0076	-7	333	341	WDLGLNKKR			
1135.7673	1135.7693	0.002	2	688	697	LVVLGIRPIR			
1135.7673	1135.7693	0.002	2	688	697	LVVLGIRPIR			
1182.6953	1182.6874	-0.0079	-7	918	928	KLVNTINPGAR			
1182.6953	1182.6874	-0.0079	-7	918	928	KLVNTINPGAR			
1206.5282	1206.5366	0.0084	7	929	938	FMTTAMYDAR			
1206.5282	1206.5366	0.0084	7	929	938	FMTTAMYDAR	1	0	
1219.6317	1219.6475	0.0158	13	939	949	EAIIPGSVYDR			
1219.6317	1219.6475	0.0158	13	939	949	EAIIPGSVYDR			
1222.6249	1222.6318	0.0069	6	908	917	ESLMQFSKPR			
1286.7578	1286.7528	-0.005	-4	866	877	ARYGVIIVGNPK			
1286.7578	1286.7528	-0.005	-4	866	877	ARYGVIIVGNPK			
1322.7136	1322.7274	0.0138	10	833	843	EKDFIILSCVR			
1380.6542	1380.6582	0.004	3	1106	1118	AYQHGGVTGLSQY			
1431.7954	1431.8054	0.01	7	499	511	TVTSATIVYHLAR			
1431.7954	1431.8054	0.01	7	499	511	TVTSATIVYHLAR			
1490.7822	1490.7893	0.0071	5	149	162	GNTSGSHIVNHLVR			
1490.7822	1490.7893	0.0071	5	149	162	GNTSGSHIVNHLVR			
1531.8074	1531.809	0.0016	1	320	332	LKESQTQDNITVR			
1567.7611	1567.761	-0.0001	0	844	857	ANEHQGIGFLNDPR			
1567.7611	1567.761	-0.0001	0	844	857	ANEHQGIGFLNDPR			
1603.7961	1603.8101	0.014	9	383	396	VPDNYGDEIAIELR			
1657.8254	1657.8335	0.0081	5	342	355	IAYFTLPKTDSDMR			
1723.8622	1723.8701	0.0079	5	844	858	ANEHQGIGFLNDPRR			
1816.8751	1816.8944	0.0193	11	429	444	TFAVDETSVSGYIYHK			
1824.9126	1824.9191	0.0065	4	817	832	LYQEVEIASVDAFQGR			
1824.9126	1824.9191	0.0065	4	817	832	LYQEVEIASVDAFQGR			
1862.0857	1862.0919	0.0062	3	481	498	TVLQRPLSLIQGPPGTGK			
1862.0857	1862.0919	0.0062	3	481	498	TVLQRPLSLIQGPPGTGK			
1896.8933	1896.9064	0.0131	7	1089	1105	SQIDVALSQDSTYQGER			
1910.0129	1910.0242	0.0113	6	550	566	EAIDSPVSFLALHNQIR			
1910.0129	1910.0242	0.0113	6	550	566	EAIDSPVSFLALHNQIR			
1914.0078	1914.0186	0.0108	6	783	800	AGAKPDQIGIITPYEGQR			
1947.9486	1947.9583	0.0097	5	296	311	YEDAYQYQNIFGPLVK			
1953.0118	1953.0227	0.0109	6	656	673	QLILVGDHCQLGPVVMCK			
1988.0236	1988.0309	0.0073	4	463	480	FTAQGLPDLNHSQVYAVK			
2000.946	2000.9686	0.0226	11	221	236	DINWDSSQWQPLIQDR			
2047.0302	2047.0461	0.0159	8	577	594	LQQLKDETGELSSADEKR			
2082.05	2082.0237	-0.0263	-13	817	834	LYQEVEIASVDAFQGREK			
2144.1245	2144.1235	-0.001	0	462	480	RFTAQGLPDLNHSQVYAVK			
2246.124	2246.1479	0.0239	11	397	416	SSVGAPVEVTHNFQVDFVWK			
2253.1543	2253.1572	0.0029	1	512	533	QGNGPVLVCAPSNIAVDQLTEK			
2308.2295	2308.2256	-0.0039	-2	376	396	GIGHVIKVPDNYGDEIAIELR			
2530.2778	2530.3091	0.0313	12	632	655	SILIDESTQATEPECMVPVVLGAK			
2538.1406	2538.157	0.0164	6	96	116	TSQLLAELNFEEDEEDTYYTK			
2815.4106	2815.4187	0.0081	3	271	295	ENPSATLEDLEKPGVDEEPQHVLLR			

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
31	transcription activator	gi|292496	114659.1	22	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1094.6027	1094.597	-0.0057	-5	427	435	VLIFSQMTR			
1115.5844	1115.6006	0.0162	15	229	237	YLVIDEAHR			
1159.6371	1159.646	0.0089	8	865	873	YKAPFHQLR			
1159.6371	1159.646	0.0089	8	865	873	YKAPFHQLR			
1174.6327	1174.6414	0.0087	7	102	111	GGPLRDYQIR			
1222.6248	1222.6318	0.007	6	182	192	VICFVGDKDAR			
1237.6575	1237.6388	-0.0187	-15	467	476	FLEVEFLGQR			
1305.6909	1305.7035	0.0126	10	740	751	NPDIPNPALAQR			
1308.6946	1308.6876	-0.007	-5	774	784	LLTQGFTNWTK			
1397.8223	1397.8152	-0.0071	-5	562	573	LRLDSIVIQQGR			
1619.7964	1619.8162	0.0198	12	705	717	QPNVQDFQFFPPR			
1645.8809	1645.87	-0.0109	-7	867	880	APFHQLRIQYGTSK			
1670.9119	1670.9052	-0.0067	-4	837	850	IMAQIERGEARIQR			
1686.902	1686.8951	-0.0069	-4	544	557	LITDNTVEERIVER			
1819.9297	1819.9084	-0.0213	-12	740	755	NPDIPNPALAQREEQK			

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
43	Tax1-binding protein 2 [Homo sapiens]	gi|76560593	148167.9	21	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1159.6317	1159.646	0.0143	12	245	255	ETLTGELAGLR			
1159.6317	1159.646	0.0143	12	245	255	ETLTGELAGLR			
1190.6375	1190.6339	-0.0036	-3	411	421	STVNALTSELR			
1320.6212	1320.637	0.0158	12	453	463	DSCLREAEELR			
1333.6957	1333.6971	0.0014	1	945	956	EVLDASESRTVK			
1407.7703	1407.7583	-0.012	-9	682	693	QQLDHARGLELK			
1486.772	1486.7902	0.0182	12	487	498	LRESQEGREVQR			
1540.7754	1540.7549	-0.0205	-13	1299	1313	RSSAPFSPPSGPPEK			
1584.8088	1584.8094	0.0006	0	1195	1208	SHEDTVRLSAEKGR			
1669.9119	1669.8969	-0.015	-9	56	69	LDLNRLVAQLEEEK			
1670.9071	1670.9052	-0.0019	-1	61	75	LVAQLEEEKSALQGR			
1747.9224	1747.9001	-0.0223	-13	207	221	LEKEALEGSLFEVQR			
1947.9552	1947.9583	0.0031	2	833	849	TQTSALNRQLAEMEAER			
2000.9744	2000.9686	-0.0058	-3	489	505	ESQEGREVQRQEAGELR			
2284.1638	2284.176	0.0122	5	1124	1143	QRQEGEAAALNTVQKLQDER			
2287.2039	2287.1743	-0.0296	-13	210	229	EALEGSLFEVQRQLAQLEAR			

Spot Idx/Pos	172/G24	28	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	Regulator of nonsense transcripts 1 (ATP-dependent helicase RENT1) (Nonsense mRNA reducing factor 1	gi|17380291	124266.7	216	100		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
942.5843	942.5738	-0.0105	-11	869	876	RLNVALTR			

952.5502	952.5398	-0.0104	-11	342	349	IAYFTLPK
1059.6196	1059.6069	-0.0127	-12	879	888	YGVIIVGNPK
1099.5742	1099.5876	0.0134	12	245	253	IPSEQEQLR
1107.5792	1107.5837	0.0045	4	689	698	AGLSQSLFER
1135.7673	1135.7666	-0.0007	-1	699	708	LVVLGIRPIR
1135.7673	1135.7666	-0.0007	-1	699	708	LVVLGIRPIR
1182.6953	1182.7019	0.0066	6	929	939	KLVNTINPGAR
1206.5282	1206.5421	0.0139	12	940	949	FMTTAMYDAR
1206.5282	1206.5421	0.0139	12	940	949	FMTTAMYDAR
1218.7244	1218.7244	0	0	190	200	NVFLLGFIPAK
1222.6249	1222.6359	0.011	9	919	928	ESLMQFSKPR
1223.7106	1223.699	-0.0116	-9	908	918	VLVEGPLNNLR
1223.7106	1223.699	-0.0116	-9	908	918	VLVEGPLNNLR
1286.7578	1286.7611	0.0033	3	877	888	ARYGVIIVGNPK
1286.7578	1286.7611	0.0033	3	877	888	ARYGVIIVGNPK
1364.7783	1364.7693	-0.009	-7	456	467	LLGHEVEDVIIK
1380.6542	1380.671	0.0168	12	1117	1129	AYQHGGVTGLSQY
1431.7954	1431.8002	0.0048	3	510	522	TVTSATIVYHLAR
1431.7954	1431.8002	0.0048	3	510	522	TVTSATIVYHLAR
1490.7822	1490.7894	0.0072	5	149	162	GNTSGSHIVNHLVR
1490.7822	1490.7894	0.0072	5	149	162	GNTSGSHIVNHLVR
1567.7611	1567.7598	-0.0013	-1	855	868	ANEHQGIGFLNDPR
1567.7611	1567.7598	-0.0013	-1	855	868	ANEHQGIGFLNDPR
1588.827	1588.8282	0.0012	1	893	904	QPLWNHLLNYYK
1603.7961	1603.7972	0.0011	1	394	407	VPDNYGDEIAIELR
1630.8435	1630.8455	0.002	1	350	363	TDSGNEDLVIIWLR
1723.8622	1723.861	-0.0012	-1	855	869	ANEHQGIGFLNDPRR
1723.8622	1723.861	-0.0012	-1	855	869	ANEHQGIGFLNDPRR
1816.8751	1816.8787	0.0036	2	440	455	TFAVDETSVSGYIYHK
1824.9126	1824.9178	0.0052	3	828	843	LYQEVEIASVDAFQGR
1824.9126	1824.9178	0.0052	3	828	843	LYQEVEIASVDAFQGR
1862.0857	1862.0867	0.001	1	492	509	TVLQRPLSLIQGPPGTGK
1862.0857	1862.0867	0.001	1	492	509	TVLQRPLSLIQGPPGTGK
1888.9261	1888.934	0.0079	4	812	827	SYLVQYMQFSGSLHTK
1910.0129	1910.0179	0.005	3	561	577	EAIDSPVSFLALHNQIR
1910.0129	1910.0179	0.005	3	561	577	EAIDSPVSFLALHNQIR
1914.0078	1914.0145	0.0067	4	794	811	AGAKPDQIGIITPYEGQR
1947.9486	1947.9462	-0.0024	-1	296	311	YEDAYQYQNIFGPLVK
1988.0236	1988.0115	-0.0121	-6	474	491	FTAQGLPDLNHSQVYAVK
2000.946	2000.9602	0.0142	7	221	236	DINWDSSQWQPLIQDR
2047.0302	2047.033	0.0028	1	588	605	LQQLKDETGELSSADEKR
2144.1245	2144.1265	0.002	1	473	491	RFTAQGLPDLNHSQVYAVK
2153.146	2153.1426	-0.0034	-2	559	577	SREAIDSPVSFLALHNQIR
2308.2295	2308.23	0.0005	0	387	407	GIGHVIKVPDNYGDEIAIELR
2308.2295	2308.23	0.0005	0	387	407	GIGHVIKVPDNYGDEIAIELR
2538.1406	2538.147	0.0064	3	96	116	TSQLLAELNFEEDEEDTYYTK
2815.4106	2815.4021	-0.0085	-3	271	295	ENPSATLEDLEKPGVDEEPQHVLLR
2893.3936	2893.3936	0	0	715	741	MHPALSAFPSNIFYEGSLQNGVTAADR

Spot Idx/Pos	187/H2	29	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	**Protein Name**	**Accession No.**	**Protein MW**	**Protein Score**	**Protein C. I. %**	**Total Ion Score**	**Total Ion C. I. %**
1	glutamate dehydrogenase 1 variant [Homo sapiens]	gi|62897195	61301.2	107	100	13	86.964

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
956.52	956.5281	0.0081	8	454	460	LTFKYER			
956.52	956.5281	0.0081	8	454	460	LTFKYER			
963.5258	963.5309	0.0051	5	528	535	YNLGLDLR			
995.5342	995.5436	0.0094	9	204	211	RFTMELAK			
1000.4556	1000.4669	0.0113	11	69	76	MVEGFFDR			
1000.4556	1000.4669	0.0113	11	69	76	MVEGFFDR			
1059.533	1059.5468	0.0138	13	445	453	NLNHVSYGR			
1059.533	1059.5468	0.0138	13	445	453	NLNHVSYGR			
1394.746	1394.748	0.002	1	524	535	TAMKYNLGLDLR			
1425.6281	1425.6279	-0.0002	0	125	136	DDGSWEVIEGYR			
1425.6281	1425.6279	-0.0002	0	125	136	DDGSWEVIEGYR	1	0	
1488.828	1488.8413	0.0133	9	35	50	GQPAAAPQPGLALAAR			
1491.726	1491.7263	0.0003	0	504	516	DIVHSGLAYTMER			
1543.8325	1543.8275	-0.005	-3	77	90	GASIVEDKLVEDLR			
1543.8325	1543.8275	-0.005	-3	77	90	GASIVEDKLVEDLR	12	81.881	
1581.7291	1581.7305	0.0014	1	124	136	RDDGSWEVIEGYR			
1737.8918	1737.8822	-0.0096	-6	481	496	HGGTIPIVPTAEFQDR			
1737.8918	1737.8822	-0.0096	-6	481	496	HGGTIPIVPTAEFQDR			
1748.89	1748.8826	-0.0074	-4	303	318	TFVVQGFGNVGLHSMR			
1748.89	1748.8826	-0.0074	-4	303	318	TFVVQGFGNVGLHSMR			
1837.0516	1837.0535	0.0019	1	108	123	IIKPCNHVLSLSFPIR			
1837.0516	1837.0535	0.0019	1	108	123	IIKPCNHVLSLSFPIR			
1915.9218	1915.9131	-0.0087	-5	213	231	GFIGPGIDVPAPDMSTGER			
1920.912	1920.9061	-0.0059	-3	461	476	DSNYHLLMSVQESLER			
1920.912	1920.9061	-0.0059	-3	461	476	DSNYHLLMSVQESLER			
1958.0381	1958.0212	-0.0169	-9	347	363	ELEDFKLQHGSILGFPK			
1993.1527	1993.1251	-0.0276	-14	108	124	IIKPCNHVLSLSFPIRR			
2044.0167	2044.0094	-0.0073	-4	212	231	KGFIGPGIDVPAPDMSTGER			
2049.0068	2049.0005	-0.0063	-3	461	477	DSNYHLLMSVQESLERK			
2164.0703	2164.0613	-0.009	-4	497	516	ISGASEKDIVHSGLAYTMER			
2164.0703	2164.0613	-0.009	-4	497	516	ISGASEKDIVHSGLAYTMER			
2242.1714	2242.1565	-0.0149	-7	400	420	IIAEGANGPTTPEADKIFLER			
2242.1714	2242.1565	-0.0149	-7	400	420	IIAEGANGPTTPEADKIFL			

7	ATP synthase, H+ transporting, mitochondrial F1 complex, beta subunit precursor [Homo sapiens]	gi|32189394	56524.6	40	25.028		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1385.7092	1385.7094	0.0002	0	144	155	IMNVIGEPIDER			
1406.681	1406.6974	0.0164	12	226	239	AHGGYSVFAGVGER			
1435.7539	1435.7715	0.0176	12	311	324	FTQAGSEVSALLGR			
1439.7892	1439.7858	-0.0034	-2	282	294	VALTGLTVAEYFR			
1601.8103	1601.8223	0.012	7	265	279	VALVYGQMNEPPGAR			
1650.9172	1650.9092	-0.008	-5	95	109	LVLEVAQHLGESTVR			
1650.9172	1650.9092	-0.008	-5	95	109	LVLEVAQHLGESTVR			
1780.9625	1780.9495	-0.013	-7	144	159	IMNVIGEPIDERGPIK			
1815.8694	1815.8885	0.0191	11	407	422	IMDPNIVGSEHYDVAR			
1988.0334	1988.0197	-0.0137	-7	388	406	AIAELGIYPAVDPLDSTSR			
2023.0105	2023.0178	0.0073	4	463	480	FLSQPFQVAEVFTGHMGK			
2266.0842	2266.0862	0.002	1	325	345	IPSAVGYQPTLATDMGTMQER			
2318.1445	2318.1326	-0.0119	-5	240	259	TREGNDLYHEMIESGVIN			

Calc. Mass		Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
							LK			
3338.7014		3338.7253	0.0239	7	295	324	DQEGQDVLLFIDNIFRFTQAGSEVSALLGR			

Spot Idx/Pos	188/H4	30	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	Chain A, Structure Of Human Glutamate Dehydrogenase-Apo Form	gi|20151	55973.4	198	100	23	#

Peptide Information

Calc. Mass		Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
905.4323	905.4658		0.0335	37	40	46	ESEEQKR			
956.52	956.5453		0.0253	26	401	407	LTFKYER			
956.52	956.5453		0.0253	26	401	407	LTFKYER			
963.5258	963.5499		0.0241	25	475	482	YNLGLDLR			
1000.4556	1000.4904		0.0348	35	16	23	MVEGFFDR	6	0	
1000.4556	1000.4904		0.0348	35	16	23	MVEGFFDR			
1059.533	1059.5614		0.0284	27	392	400	NLNHVSYGR			
1394.746	1394.7701		0.0241	17	471	482	TAMKYNLGLDLR			
1425.6281	1425.6548		0.0267	19	72	83	DDGSWEVIEGYR			
1425.6281	1425.6548		0.0267	19	72	83	DDGSWEVIEGYR	6	0	
1491.726	1491.7567		0.0307	21	451	463	DIVHSGLAYTMER			
1543.8325	1543.8599		0.0274	18	24	37	GASIVEDKLVEDLR	10	37.458	
1543.8325	1543.8599		0.0274	18	24	37	GASIVEDKLVEDLR			
1581.7291	1581.7565		0.0274	17	71	83	RDDGSWEVIEGYR			
1737.8918	1737.9161		0.0243	14	428	443	HGGTIPIVPTAEFQDR			
1737.8918	1737.9161		0.0243	14	428	443	HGGTIPIVPTAEFQDR			
1748.89	1748.9139		0.0239	14	250	265	TFVVQGFGNVGLHSMR			
1748.89	1748.9139		0.0239	14	250	265	TFVVQGFGNVGLHSMR			
1837.0516	1837.0806		0.029	16	55	70	IIKPCNHVLSLSFPIR			
1837.0516	1837.0806		0.029	16	55	70	IIKPCNHVLSLSFPIR			
1915.9218	1915.9493		0.0275	14	160	178	GFIGPGIDVPAPDMSTGER			
1920.912	1920.9424		0.0304	16	408	423	DSNYHLLMSVQESLER			
1920.912	1920.9424		0.0304	16	408	423	DSNYHLLMSVQESLER			
1933.0024	1932.9475		-0.0549	-28	131	147	AGVKINPKNYTDNELEK			
1958.0381	1958.0604		0.0223	11	294	310	ELEDFKLQHGSILGFPK			
1958.0381	1958.0604		0.0223	11	294	310	ELEDFKLQHGSILGFPK			
1993.1527	1993.1589		0.0062	3	55	71	IIKPCNHVLSLSFPIRR			
2044.0167	2044.0457		0.029	14	159	178	KGFIGPGIDVPAPDMSTGER			
2044.0167	2044.0457		0.029	14	159	178	KGFIGPGIDVPAPDMSTGER			
2049.0068	2049.0439		0.0371	18	408	424	DSNYHLLMSVQESLERK			
2164.0703	2164.1028		0.0325	15	444	463	ISGASEKDIVHSGLAYTMER			
2164.0703	2164.1028		0.0325	15	444	463	ISGASEKDIVHSGLAYTMER			
2242.1714	2242.2017		0.0303	14	347	367	IIAEGANGPTTPEADKIFLER			
2242.1714	2242.2017		0.0303	14	347	367	IIAEGANGPTTPEADKIFLER			
2318.1975	2318.209		0.0115	5	250	269	TFVVQGFGNVGLHSMRYLHR			
2441.3035	2441.3164		0.0129	5	345	367	AKIIAEGANGPTTPEADKIFLER			
2497.2139	2497.2927		0.0788	32	405	424	YERDSNYHLLMSVQESLERK			
2603.3384	2603.3323		-0.0061	-2	95	118	GGIRYSTDVSVDEVKALASLMTYK			
2742.4211	2742.4666		0.0455	17	368	391	NIMVIPDLYLNAGGVTVSYFEWLK			
3045.4885	3045.5374		0.0489	16	266	293	YLHRFGAKCIAVGESDGSIWNPDGIDPK			
3782.9363	3782.9573		0.021	6	368	400	NIMVIPDLYLNAGGVTVSYFEWLKNLNHVSYGR			

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
6	ATP synthase, H+ transporting, mitochondrial F1 complex, beta subunit precursor [Homo sapiens]	gi|32189	56524.6	84	99.997		

Peptide Information

Calc. Mass		Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1385.7092	1385.7341		0.0249	18	144	155	IMNVIGEPIDER			
1406.681	1406.7242		0.0432	31	226	239	AHGGYSVFAGVGER			
1435.7539	1435.782		0.0281	20	311	324	FTQAGSEVSALLGR			
1439.7892	1439.8136		0.0244	17	282	294	VALTGLTVAEYFR			
1601.8103	1601.8384		0.0281	18	265	279	VALVYGQMNEPPGAR			
1650.9172	1650.9451		0.0279	17	95	109	LVLEVAQHLGESTVR			
1748.8561	1748.9139		0.0578	33	45	62	DYAAQTSPSPKAGAATGR			
1748.8561	1748.9139		0.0578	33	45	62	DYAAQTSPSPKAGAATGR			
1780.9625	1780.9805		0.018	10	144	159	IMNVIGEPIDERGPIK			
1815.8694	1815.9052		0.0358	20	407	422	IMDPNIVGSEHYDVAR			
1988.0334	1988.0648		0.0314	16	388	406	AIAELGIYPAVDPLDSTSR			
2023.0105	2023.0638		0.0533	26	463	480	FLSQPFQVAEVFTGHMGK			
2060.9956	2061.0601		0.0645	31	242	259	EGNDLYHEMIESGVINLK			
2164.1145	2164.1028		-0.0117	-5	35	55	AAPTAVHPVRDYAAQTSPSPK			
2164.1145	2164.1028		-0.0117	-5	35	55	AAPTAVHPVRDYAAQTSPSPK			
2228.1128	2228.1885		0.0757	34	407	426	IMDPNIVGSEHYDVARGVQK			
2266.0842	2266.1287		0.0445	20	325	345	IPSAVGYQPTLATDMGTMQER			
2318.1445	2318.209		0.0645	28	240	259	TREGNDLYHEMIESGVINLK			
2732.6045	2732.5076		-0.0969	-35	19	44	RLTPSASLPPAQLLLRAAPTAVHPVR			
3031.6824	3031.5806		-0.1018	-34	63	91	IVAVIGAVVDVQFDEGLPPILNALEVQGR			
3714.886	3714.8579		-0.0281	-8	352	387	GSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSR			

Spot Idx/Pos	189/H6	31	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	lactate dehydrogenase A [Homo sapiens]	gi|5031857	36665.4	150	100	21	97.755

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
833.3748	833.3673	-0.0075	-9	100	106	QQEGESR			
913.5829	913.5765	-0.0064	-7	91	99	LVIITAGAR			
913.5829	913.5765	-0.0064	-7	91	99	LVIITAGAR	21	97.755	
1071.5404	1071.5294	-0.011	-10	170	177	FRYLMGER			
1071.5404	1071.5294	-0.011	-10	170	177	FRYLMGER			

1134.5636	1134.5571	-0.0065	-6	306	315	VTLTSEEEAR			
1167.6666	1167.6621	-0.0045	-4	269	278	RVHPVSTMIK			
1167.6666	1167.6621	-0.0045	-4	269	278	RVHPVSTMIK			
1191.5786	1191.5812	0.0026	2	158	169	VIGSGCNLDSAR			
1494.748	1494.7413	-0.0067	-4	158	171	VIGSGCNLDSARFR			
1556.8138	1556.8066	-0.0072	-5	100	112	QQEGESRLNLVQR			
1633.7825	1633.7809	-0.0016	-1	60	73	GEMMDLQHGSLFLR			
1633.7825	1633.7809	-0.0016	-1	60	73	GEMMDLQHGSLFLR			
1644.9835	1644.9662	-0.0173	-11	113	126	NVNIFKFIIPNVVK			
1874.9614	1874.9647	0.0033	2	58	73	LKGEMMDLQHGSLFLR			
1874.9614	1874.9647	0.0033	2	58	73	LKGEMMDLQHGSLFLR			
1906.0392	1906.0281	-0.0111	-6	82	99	DYNVTANSKLVIITAGAR			
1910.9606	1910.9519	-0.0087	-5	213	228	TLHPDLGTDKDKEQWK			
2074.0815	2074.0828	0.0013	1	6	22	DQLIYNLLKEEQTPQNK			
2112.0681	2112.0447	-0.0234	-11	246	265	GYTSWAIGLSVADLAESIMK			
2232.158	2232.1401	-0.0179	-8	285	305	DDVFLSVPCILGQNGISDLVK			
2353.2471	2353.2388	-0.0083	-4	244	265	LKGYTSWAIGLSVADLAESIMK			
2390.3401	2390.3481	0.008	3	77	99	IVSGKDYNVTANSKLVIITAGAR			
2863.5273	2863.5417	0.0144	5	279	305	GLYGIKDDVFLSVPCILGQNGISDLVK			

4	heterogeneous nuclear ribonucleoprotein A2/B1 isoform A2 [Homo sapiens]	gi|4504447	35983.9	48	89.163

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1013.4434	1013.4584	0.015	15	192	201	GGNFGFGDSR			
1377.6293	1377.627	-0.0023	-2	202	216	GGGGNFGPGPGSNFR			
1377.6293	1377.627	-0.0023	-2	202	216	GGGGNFGPGPGSNFR			
1410.6873	1410.6952	0.0079	6	162	173	YHTINGHNAEVR			
1798.9221	1798.938	0.0159	9	11	26	LFIGGLSFETTEESLR			
1879.9659	1879.9691	0.0032	2	102	117	LFVGGIKEDTEEHHLR			
1927.017	1927.0332	0.0162	8	10	26	KLFIGGLSFETTEESLR			
2189.9053	2189.9114	0.0061	3	314	338	NMGGPYGGGNYGPGGSGGSGGYGGR			
2189.9053	2189.9114	0.0061	3	314	338	NMGGPYGGGNYGPGGSGGSGGYGGR			
2220.0706	2220.0769	0.0063	3	118	135	DYFEEYGKIDTIEIITDR			
2277.155	2277.1479	-0.0071	-3	142	161	GFGFVTFDDHDPVDKIVLQK			
2495.0393	2495.0474	0.0081	3	227	254	GFGDGYNGYGGGPGGGNFGGSPGYGGGR			

32	Phosphodiesterase 6A, cGMP-specific, rod, alpha [Homo sapiens]	gi|112180437	99482.8	22	0

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
929.5665	929.5605	-0.006	-6	32	40	LISDLLGAK			
1011.5581	1011.5488	-0.0093	-9	621	629	LHGSSILER			
1542.8525	1542.8413	-0.0112	-7	318	330	VIDYILHGKEDIK			
1784.9146	1784.9069	-0.0077	-4	751	765	TVLQQNPIPMMDRNK			
1784.9146	1784.9069	-0.0077	-4	751	765	TVLQQNPIPMMDRNK			
1886.9969	1886.9821	-0.0148	-8	198	213	VDGSHFTKRDEEILLK			
2249.1138	2249.0938	-0.02	-9	12	29	FLDSNIGFAKQYYNLHYR			
2438.2529	2438.2637	0.0108	4	751	771	TVLQQNPIPMMDRNKADELPK			
2806.4246	2806.4207	-0.0039	-1	556	579	ITYHNWRHGFNVGQTMFSLLVTGK			
2934.5195	2934.5176	-0.0019	-1	555	579	KITYHNWRHGFNVGQTMFSLLVTGK			
3682.876	3682.8433	-0.0327	-9	207	236	DEEILLKYLNFANLIMKVYHLSYLHNCETR			

Spot Idx/Pos	190/H8	32	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.			Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	lactate dehydrogenase A [Homo sapiens]	gi|50318	36665.4	119	100				

Peptide Information

Calc. Mass		Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
833.4152	833.4354		0.0202	24	223	228	DKEQWK			
1011.5656	1011.6007		0.0351	35	270	278	VHPVSTMIK			
1264.6782	1264.7018		0.0236	19	233	243	QVVESAYEVIK			
1644.9835	1645.0377		0.0542	33	113	126	NVNIFKFIIPNVVK			
1657.853	1657.8906		0.0376	23	43	57	DLADELALVDVIEDK			
1799.0359	1799.0052		-0.0307	-17	269	284	RVHPVSTMIKGLYGIK			
1899.032	1899.064		0.032	17	43	59	DLADELALVDVIEDKLK			
1906.0392	1906.1049		0.0657	34	82	99	DYNVTANSKLVIITAGAR			
1910.9606	1911.0211		0.0605	32	213	228	TLHPDLGTDKDKEQWK			
1933.0682	1933.118		0.0498	26	23	42	ITVVGVGAVGMACAISILMK			
1944.1204	1944.1799		0.0595	31	133	149	LLIVSNPVDILTYVAWK			
2112.0681	2112.1367		0.0686	32	246	265	GYTSWAIGLSVADLAESIMK			
2112.0681	2112.1367		0.0686	32	246	265	GYTSWAIGLSVADLAESIMK			
2353.2471	2353.3394		0.0923	39	244	265	LKGYTSWAIGLSVADLAESIMK			
2390.3401	2390.4207		0.0806	34	77	99	IVSGKDYNVTANSKLVIITAGAR			
2495.2961	2495.2114		-0.0847	-34	246	268	GYTSWAIGLSVADLAESIMKNLR			
2863.5273	2863.6221		0.0948	33	279	305	GLYGIKDDVFLSVPCILGQNGISDLVK			
3513.7966	3513.8669		0.0703	20	43	73	DLADELALVDVIEDKLKGEMMDLQHGSLFLR			
3611.7886	3611.8848		0.0962	27	178	212	LGVHPLSCHGWVLGEHGDSSVPVWSGMNVAGVSLK			

Spot Idx/Pos	191/H10	33	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	NME1-NME2 protein [Homo sapiens]	gi|66392203	30117.6	118	100		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
994.4774	994.4921	0.0147	15	106	114	GDFCIQVGR			
994.4774	994.4921	0.0147	15	221	229	GDFCIQVGR			
1149.6415	1149.6565	0.015	13	57	66	DRPFFAGLVK			
1149.6415	1149.6565	0.015	13	57	66	DRPFFAGLVK			
1181.587	1181.5825	-0.0045	-4	40	49	FMQASEDLLK			
1344.7633	1344.7744	0.0111	8	122	133	TFIAIKPDGVQR			
1344.7633	1344.7744	0.0111	8	7	18	TFIAIKPDGVQR			

1516.8845	1516.8854	0.0009	1	134	146	GLVGEIIKRFEQK			
1516.8845	1516.8854	0.0009	1	19	31	GLVGEIIKRFEQK			
1785.9163	1785.927	0.0107	6	89	105	VMLGETNPADSKPGTIR			
1785.9163	1785.927	0.0107	6	204	220	VMLGETNPADSKPGTIR			
2034.0806	2034.0894	0.0088	4	50	66	EHYVDLKDRPFFAGLVK			
2034.0806	2034.0894	0.0088	4	50	66	EHYVDLKDRPFFAGLVK			
2066.0261	2066.0259	-0.0002	0	40	56	FMQASEDLLKEHYVDLK			
2066.0261	2066.0259	-0.0002	0	40	56	FMQASEDLLKEHYVDLK			
2116.0718	2116.074	0.0022	1	67	85	YMHSGPVVAMVWEGLNVVK			
2116.0718	2116.074	0.0022	1	67	85	YMHSGPVVAMVWEGLNVVK			
3196.6499	3196.6282	-0.0217	-7	40	66	FMQASEDLLKEHYVDLKDRPFFAGLVK			

11	Chain A, Nucleoside Triphosphate, Nucleoside Diphosphate Mol_id: 1; Molecule: Nucleoside Diphosphat	gi|1421609	17155.9	25	0		

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
994.4774	994.4921	0.0147	15	105	113	GDFCIQVGR			
994.4774	994.4921	0.0147	15	105	113	GDFCIQVGR			
1344.7633	1344.7744	0.0111	8	6	17	TFIAIKPDGVQR			
1344.7633	1344.7744	0.0111	8	6	17	TFIAIKPDGVQR			
1516.8845	1516.8854	0.0009	1	18	30	GLVGEIIKRFEQK			
1516.8845	1516.8854	0.0009	1	18	30	GLVGEIIKRFEQK			
1785.9163	1785.927	0.0107	6	88	104	VMLGETNPADSKPGTIR			
1785.9163	1785.927	0.0107	6	88	104	VMLGETNPADSKPGTIR			

Spot Idx/Pos	192/H12	34	**Instr./Spot Origin**	ab4700/042810	**Process Status**	Analysis Succeeded
Plate [#] Name	[1] 042810		**4700 Sample Name**		**Spectra**	13

Rank	Protein Name	Accession No.	Protein MW	Protein Score	Protein C. I. %	Total Ion Score	Total Ion C. I. %
1	NME1-NME2 protein [Homo sapiens]	gi|66392203	30117.6	135	100	17	86.888

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
911.4733	911.4838	0.0105	12	143	149	FEQKGFR			
984.6199	984.6309	0.011	11	19	27	GLVGEIIKR	9	5.908	
984.6199	984.6309	0.011	11	134	142	GLVGEIIKR			
1149.6415	1149.6497	0.0082	7	57	66	DRPFFAGLVK			
1149.6415	1149.6497	0.0082	7	57	66	DRPFFAGLVK			
1344.7633	1344.7748	0.0115	9	122	133	TFIAIKPDGVQR			
1344.7633	1344.7748	0.0115	9	7	18	TFIAIKPDGVQR	10	31.837	
1516.8845	1516.8903	0.0058	4	134	146	GLVGEIIKRFEQK			
1516.8845	1516.8903	0.0058	4	19	31	GLVGEIIKRFEQK			
1785.9163	1785.9252	0.0089	5	204	220	VMLGETNPADSKPGTIR			
1785.9163	1785.9252	0.0089	5	89	105	VMLGETNPADSKPGTIR			
2034.0806	2034.0925	0.0119	6	50	66	EHYVDLKDRPFFAGLVK			
2034.0806	2034.0925	0.0119	6	50	66	EHYVDLKDRPFFAGLVK			
2066.0261	2066.0303	0.0042	2	40	56	FMQASEDLLKEHYVDLK			
2116.0718	2116.0618	-0.01	-5	67	85	YMHSGPVVAMVWEGLNVVK			
2116.0718	2116.0618	-0.01	-5	67	85	YMHSGPVVAMVWEGLNVVK			

23	nucleoside diphosphate kinase B	gi|924935	2058.1	21	0	10	31.837

Peptide Information

Calc. Mass	Obsrv. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence	Ion Score	C. I. %	Modification
1344.7633	1344.7748	0.0115	9	7	18	TFIAIKPDGVQR			
1344.7633	1344.7748	0.0115	9	7	18	TFIAIKPDGVQR	10	31.837	