

GEL ID PROTEIN	Gene ID	MW	pI	MASCOT				ALDENTE					
				RANK	SCORE	PEPTIDE	COVERAGE %	MASS VALUES	RANK	SCORE	PEPTIDE	COVERAGE %	MASS VALUES
1 Endoplasmic reticulum chaperone protein	Hsp90b1	90	4.7	1	54	30	38	200	18	4	14	19	200
2 Heat shock protein HSP 90-alpha	Hsp90aa1	85	4.9	10	36	20	35	200	5	2	11	20	200
4 Calreticulin	Calr	46	4.3	12	31	10	31	150	1	2	6	25	150
5 Rab GTPase-binding effector protein 2	Rabep2	62	4.9	4	51	14	19	100	4	4	8	14	100
6 Protein disulfide-isomerase	P4hb	55	4.8	1*	87	21	48	150	1*	15	9	22	70
8 ATP synthase subunit beta, mitochondrial	Atp5b	52	5	1*	64	17	35	100	1*	24	12	29	100
9 SPARC	Sparc	33	4.7	1*	66	13	41	100	1*	12	9	28	100
10 Annexin A5	Anxa5	36	4.8	1*	63	13	43	100	1*	16	11	31	100
14 ATP synthase subunit d, mitochondrial	Atp5h	19	5.5	4	41	8	67	150	1	2	6	43	200
15 26S proteasome non-ATPase regulatory subunit 10	Psmd10	25	5.7	1	46	10	53	200	5	1.2	6	39	200
16 N-acetyltransferase 9	Nat9	28	5.2	3	38	11	41	200	5	2	6	32	200
17 Prohibitin	Phb	30	5.5	12	35	7	37	100	1	5	5	29	100
18 TIP41-like protein	Tipr1	31	5.4	15	31	7	32	100	1	5	6	32	100
19 Nuclear distribution protein nudE homolog 1	Nde1	36	5.3	8	31	12	40	200	3	7	10	29	200
20 Annexin A4	Anxa4	36	5.4	2	37	9	34	75	1*	14	11	38	150
25 T-complex protein 1 subunit theta	Cct8	59	5.4	7	38	11	27	100	1	6	11	29	100
28 T-complex protein 1 subunit theta	Cct8	59	5.4	13	34	10	18	100	4	2	6	15	100
29 T-complex protein 1 subunit theta	Cct8	59	5.4	6	38	10	19	75	2	10	12	22	100
30 RuvB-like 2	Ruvb12	51	5.5	10	36	16	40	200	5	3	8	21	200
32 Tubulin alpha-1C chain	Tuba1c	50	5	1*	62	11	32	80	1	12	8	24	80
33 Na(+)/H(+) exchange regulatory cofactor NHE-RF3	Pdzk1	56	5.3	15	35	14	38	200	8	2	9	25	200
35 ATP synthase subunit beta, mitochondrial	Atp5b	52	5	24	31	11	33	150	1	8	9	29	150
36 Actin, cytoplasmic 2	Actg1	42	5.3	2	52	11	35	100	3	4	6	24	100
37 Actin, cytoplasmic 2	Actg1	42	5.3	1*	64	13	45	100	2	7	8	33	100
38 Actin, cytoplasmic 2	Actg1	42	5.3	12	36	15	46	250	1	5	12	39	250
43 Protein disulfide-isomerase A3	Pdia3	54	5.7	1	45	12	29	100	5	7	9	21	100
40 Homer protein homolog 1	Homer1	41	5.4	16	26	11	31	200	6	2	7	21	200
41 Activator of 90 kDa heat shock protein ATPase homolog 1	Ahsa1	38	5.4	10	39	12	37	150	5	4	8	26	150
42 Guanine nucleotide-binding protein subunit alpha-11	Gna11	42	5.7	39	26	8	30	100	12	2	7	29	200
44 Baculoviral IAP repeat-containing protein 4	Xiap	56	5.7	15	36	16	32	200	1	8	14	27	200
45 Protein disulfide-isomerase A3	Pdia3	54	5.7	1*	65	14	26	60	1*	20	9	19	60
47 Annexin A6	Anxa6	76	5.3	41	29	23	30	200	1	5	12	22	200
48 RNA polymerase I-specific transcription initiation factor RRN3	Rrn3	75	5.3	1	46	10	21	70	2	5	7	17	70
49 Collagen type IV alpha-3-binding protein	Col4a3bp	71	5.3	2	44	8	20	50	5	3	5	15	50
50 Calpain-9	Capn9	79	5.1	45	26	13	26	200	14	2	9	18	200
51 Heat shock cognate 71 kDa protein	Hspa8	71	5.4	1*	78	13	26	50	1*	28	10	22	50
52 Cytochrome P450 2D11	Cyp2d11	57	6.2	2	36	16	43	250	35	1.4	7	21	250
53 Pyruvate kinase isozymes M1/M2	Pkm2	58	6.7	14	33	15	38	200	1	7	14	31	200
54 5-azacytidine-induced protein 2	Azi2	46	6.2	29	30	8	24	120	1	4	9	25	120
56 Ornithine aminotransferase, mitochondrial	Oat	46	5.7	15	29	8	20	75	4	7	6	16	75
57 Transcobalamin-2	Tcn2	46	5.9	1*	57	11	36	80	1	4	6	15	100
58 WNT1-inducible-signaling pathway protein 1	Wispr1	43	6	21	29	6	23	70	30	3	7	33	150
60 Alpha-enolase	Eno1	47	6.4	1*	61	13	38	75	1*	19	11	32	100
62 Cytosolic 5'-nucleotidase 3	Nt5c3	37	6.2	5	45	11	46	150	4	4	7	34	150
63 Ankyrin repeat domain-containing protein 16	Ankrd16	40	6.5	26	30	8	28	100	2	6	6	27	100
Control Serum albumin		66	5.6	1*	129	19	32	50	1*	32	12	24	50

(* indicates p<0.05)

(* indicates p<0.05)

1 Endoplasmin

Number of mass values searched: **200**

Number of mass values matched: **30**

Sequence Coverage: **38%**

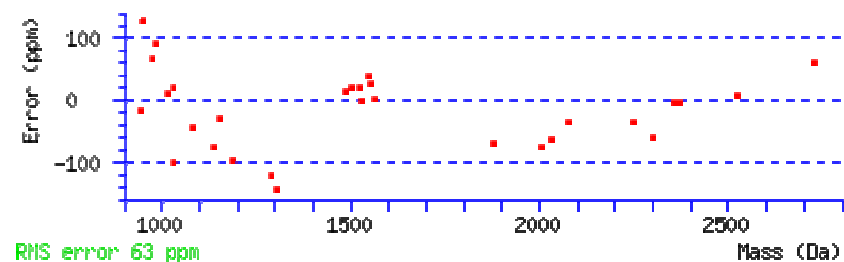
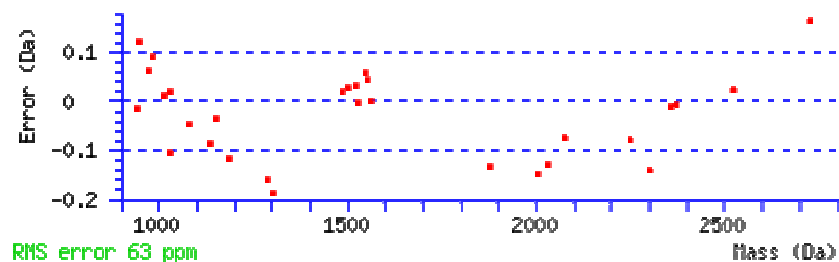
Matched peptides shown in **Bold Red**

1 MRVLWVLGLC CVLLTFGFVR ADDEVVDVGT VEEDLGKSRE GSRTDDEVVQ
51 REEEAIQLDG LNASQIR ELR EKSEKFAFQA EVNRMMKLII NSLYKNKEIF
101 LRELISNASD ALDKIRLISL TDENALAGNE ELTVKIKCDK EKNLLHVTDT
151 GVGMTREELV KNLGTIAKSG TSEFLNK MTE AQEDGQSTSE LIGQFVGVGFY
201 SAFLVADKVI VTSKHNDTQ HIWESDSNEF SVIADPRGNT LGRGTTITLV
251 LKEEASDYLE LDTIKNLVRK YSQFINFPIY VWSSKTETVE EPLEEDEAAK
301 EEKEESDDEA AVEEEEEEEK PKTKKVEKTV WDWELMNDIK PIWQRPSKEV
351 EEDEYKAFYK SFSKESDDPM AYIHFTAEGE VTFK SILFVP TSAPRGLFDE
401 YGSKKSDYIK LYVRRVITD DFHDMMPKYL NFVKGVVSD DLPLNVSRET
451 LQQHKLLKVI RKKLVKRLTD MIKKIADEKY NDTFWKEFGT NIKLGVIEDH
501 SNRTRLAKLL RFQSSHSTD ITSLDQYVER MKEKQDKIYF MAGSSRKEAE
551 SSPFVERLLK KGYEVIYLTE PVDEYCIQAL PEFDGKRFQN VAKEGVKFDE
601 SEKTKESREA TEKEFEPLLN WMKDKALKDK IEKAVVSQRL TESPICALVAS
651 QYGWSGNMER IMKAQAYQTG KDISTNYAS QKKTFEINPR HPLIRDMLRR
701 IKEDEDDKTV MDLAVVLFET ATRSGYLLP DTKAYGDR IE RMLRSLNID
751 PEAQVEEPE EEPEDTSEDA EDSEQDEGEE MDAGTEEEEE ETEKESTEKD
801 EL

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
44 - 67	2728.5059	2727.4986	2727.3311	0.1675	1	R.TDDEVVQREEEAIQLDGLNASQIR.E
76 - 84	1081.4958	1080.4885	1080.5352	-0.0467	0	K.FAFQAEVNR.M
115 - 135	2299.1104	2298.1031	2298.2430	-0.1399	1	K.IRLISLTDENALAGNEELTVK.I
117 - 135	2029.9357	2028.9284	2029.0579	-0.1295	0	R.LISLTDENALAGNEELTVK.I
143 - 156	1529.7711	1528.7638	1528.7668	-0.0030	0	K.NLLHVTDGVMTR.E Oxidation (M)
169 - 177	982.5743	981.5670	981.4767	0.0903	0	K.SGTSEFLNK.M
244 - 252	945.5840	944.5767	944.5906	-0.0139	0	R.GTTITLVLK.E
253 - 265	1525.7590	1524.7517	1524.7195	0.0322	0	K.EEASDYLELDTIK.N
253 - 269	2007.8750	2006.8677	2007.0160	-0.1483	1	K.EEASDYLELDTIKNLVR.K
271 - 285	1878.8118	1877.8045	1877.9352	-0.1307	0	K.YSQFINFPIYVWSSK.T
286 - 303	2075.8767	2074.8694	2074.9429	-0.0735	1	K.TETVEEPEEDEAAKEEK.E
385 - 395	1187.5620	1186.5547	1186.6710	-0.1163	0	K.SILFVPTSAPR.G
396 - 404	1015.4853	1014.4780	1014.4658	0.0122	0	R.GLFDEYGSK.K

435 - 448	1485.7764	1484.7691	1484.7471	0.0220	0	K.GVVSDDDLPLNVSR.E
480 - 486	973.5068	972.4995	972.4341	0.0654	0	K.YNDTFWK.E
494 - 503	1139.4948	1138.4875	1138.5731	-0.0856	0	K.LGVIEDHSNR.T
512 - 530	2249.9668	2248.9595	2249.0349	-0.0754	0	R.FQSSHSTDITSLDQYVER.M
512 - 532	2525.1978	2524.1905	2524.1653	0.0253	1	R.FQSSHSTDITSLDQYVERMK.E Oxidation (M)
538 - 546	1031.5186	1030.5113	1030.4906	0.0207	0	K.IYFMAGSSR.K
548 - 557	1150.5045	1149.4972	1149.5302	-0.0330	0	K.EAESSPFVER.L
548 - 560	1504.8314	1503.8241	1503.7933	0.0308	1	K.EAESSPFVERLLK.K
606 - 613	949.5800	948.5727	948.4512	0.1215	1	K.ESREATEK.E
614 - 623	1306.4618	1305.4545	1305.6427	-0.1882	0	K.EFEPLLNMWK.D
614 - 625	1549.8325	1548.8252	1548.7646	0.0606	1	K.EFEPLLNMWKDK.A
614 - 625	1565.7687	1564.7614	1564.7595	0.0019	1	K.EFEPLLNMWKDK.A Oxidation (M)
631 - 639	1029.5012	1028.4939	1028.5978	-0.1039	1	K.IEKAVVSQR.L
640 - 660	2356.0581	2355.0508	2355.0623	-0.0115	0	R.LTESPCALVASQYGWGSGNMER.I
640 - 660	2372.0566	2371.0493	2371.0573	-0.0079	0	R.LTESPCALVASQYGWGSGNMER.I Oxidation (M)
672 - 682	1289.4431	1288.4358	1288.5935	-0.1577	0	K.DISTNYYASQK.K
725 - 738	1555.8196	1554.8123	1554.7678	0.0445	1	R.SGYLLPDTKAYGDR.I

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2 Heat shock protein HSP 90-alpha

Number of mass values searched: **200**

Number of mass values matched: **20**

Sequence Coverage: **35%**

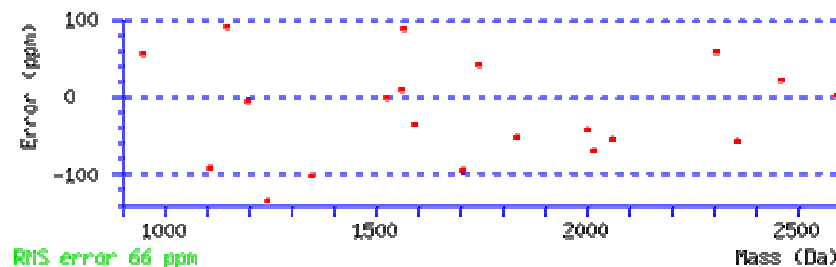
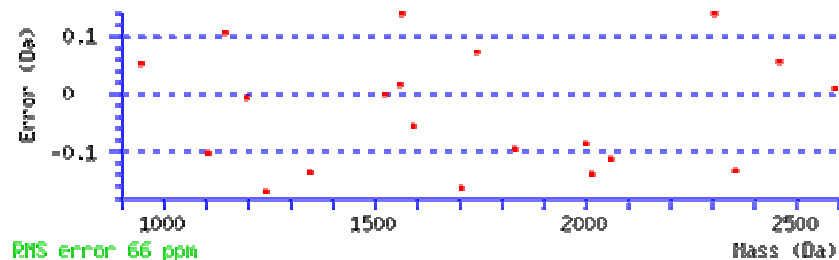
Matched peptides shown in **Bold Red**

1 MPEETQTQDQ PMEEEEVETF AFQAEIAQLM SLIINTFYNS KEIFLRELIS
51 NSSDALDKIR YESLTDPSKL DSGK**ELHINL IPSKQDR**TLT IVDTGIGMTK
101 **ADLINNLGTI AK**SGTKAFME ALQAGADISM IGQFGVGFYS AYLVAEKVTV
151 ITKHNDDEQY AWESSAGGSF TVRTDTGEPM GRGTV**VILHL KEDQTEYLEE**
201 **RRIKEIVKHH SQFIGYPITL FVEKERDKEV SDDEAEEK**EE KEEEEKEEEK
251 **ESDDKPEIED VGSDEEEEEK** KDGDKDKKKK IKEKYIDQEE LNKTKPIWT
301 **NPDDITNEEY GEFYK**SLTND WEEHLAVKHF SVEGQLEFRA LLFVPRR**APF**
351 **DLFENR**KKKN NIKLYVRRVF IMDNCEELIP EYLNFI**RGVV DSEDLPLNIS**
401 **REMLQQSK**IL KVIRKNLVK**K CLELFTELAE DKENYK**KFYE QFSKNIK**LGI**
451 **HEDSQNR**KKL SELLR**YYTSA SGDEMVS**LKD YCTRM**ENQK HIYFITGETK**
501 DQVANS**AFVE RLRKHGLEVI YMI**EPIDE**YC VQQLK**EFEGK TLVSVTKEGL
551 ELPEDEEEK KQEEK**TKFE NLCKIMK**DIL EKKVEKVVVS **NRLVTS****PCCI**
601 **VTSTY**GW**TAN MERIMKAQAL RDNSTMGYMA AKK**HLEINPD HSIETLRQK
651 AEADKNDKSV KDLVILLYET ALLSSGF**SLE DPQ**THANRIY RMIK**LGLGID**
701 EDDPTVDDTS AAVTEEM**PPL EGDD**DTSRME EV**D**

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
75 - 87	1562.8802	1561.8729	1561.8576	0.0153	1	K.ELHINLIPSKQDR.T
101 - 112	1242.5383	1241.5310	1241.6979	-0.1669	0	K.ADLINNLGTIAK.S
186 - 201	2014.9066	2013.8993	2014.0371	-0.1378	1	K.VILHLKEDQTEYLEER.R
210 - 226	2063.9800	2062.9727	2063.0840	-0.1113	1	K.HSQFIGYPITLFVEKER.D
229 - 238	1150.5803	1149.5730	1149.4673	0.1057	0	K.EVSDDEAEEK.E
251 - 270	2308.0857	2307.0784	2306.9397	0.1387	0	K.ESDDKPEIEDVGSDEEEEEK.K
301 - 315	1833.6860	1832.6787	1832.7741	-0.0953	0	R.NPDDITNEEYGEFYK.S
348 - 356	1108.4401	1107.4328	1107.5349	-0.1021	0	R.APFDLFENR.K
388 - 408	2358.0645	2357.0572	2357.1897	-0.1324	1	R.GVVSDLPLNISREMLQQSK.I
420 - 432	1595.7428	1594.7355	1594.7912	-0.0557	1	K.KCLELFTELAEDK.E
421 - 436	2001.8607	2000.8534	2000.9401	-0.0866	1	K.CLELFTELAEDKENYK.K
445 - 457	1523.7910	1522.7837	1522.7852	-0.0014	1	K.NIKLGIHEDSQNR.K
466 - 479	1566.8386	1565.8313	1565.6919	0.1394	0	R.YYTASGDEMVS LK .D Oxidation (M)
487 - 500	1707.7086	1706.7013	1706.8628	-0.1614	1	K.ENQKHIYFITGETK.D
515 - 535	2593.2766	2592.2693	2592.2604	0.0089	0	K.HGLEVIYMI EPIDE YCVQQLK.E Oxidation (M)

569 - 577 1198.5901 1197.5828 1197.5886 -0.0058 1 K.FENLCKIMK.D Oxidation (M)
593 - 613 2462.1699 2461.1626 2461.1076 0.0550 0 R.LVTSPCCIVTSTYGWTANMER.I Oxidation (M)
614 - 621 946.6027 945.5954 945.5429 0.0525 1 R.IMKAQALR.D Oxidation (M)
617 - 632 1743.8872 1742.8799 1742.8080 0.0720 1 K.AQALRDNSTMGYMAAK.K Oxidation (M)
622 - 633 1348.4518 1347.4445 1347.5799 -0.1353 1 R.DNSTMGYMAAKK.H 2 Oxidation (M)

No match to: 905.1322, 911.5391, 913.6351, 916.6147, 922.3146, 926.6247, 931.6022, 937.6257, 938.6370, 944.2769, 952.5798, 954.6281, 959.6088, 965.5944, 968.6093, 974.6243, 982.6179, 985.5740, 992.1921, 996.6216, 1002.5772, 1014.1541, 1025.5760, 1028.1254, 1030.1190, 1034.1290, 1045.5608, 1052.0900, 1058.5321, 1066.0558, 1072.0669, 1078.0608, 1082.0175, 1088.5122, 1098.5613, 1102.5226, 1106.4880, 1115.9926, 1118.5068, 1126.5658, 1132.6097, 1142.5297, 1148.5917, 1165.6237, 1173.5479, 1180.5522, 1185.5884, 1189.4896, 1191.5179, 1203.6086, 1218.4485, 1222.6334, 1233.4554, 1244.9908, 1254.9529, 1260.9618, 1269.5767, 1276.9219, 1283.9353, 1292.9001, 1299.9122, 1307.4783, 1319.6143, 1326.5609, 1329.4984, 1334.6248, 1339.5380, 1355.5925, 1362.4708, 1372.5652, 1375.5679, 1383.5094, 1391.6058, 1405.6389, 1411.7155, 1419.7850, 1436.7915, 1448.8839, 1455.8240, 1464.8641, 1475.8011, 1482.8552, 1487.8823, 1489.8978, 1507.8655, 1514.8324, 1528.8334, 1531.8483, 1540.8770, 1547.8287, 1549.8472, 1555.8306, 1571.7968, 1577.8169, 1588.8392, 1593.7883, 1604.8569, 1612.8353, 1618.7588, 1630.8510, 1634.8784, 1643.8306, 1650.8287, 1655.8545, 1660.8257, 1669.8156, 1678.8480, 1686.8853, 1699.9137, 1717.7644, 1722.8396, 1735.7548, 1750.7284, 1762.7433, 1766.6803, 1780.7074, 1790.7363, 1794.7073, 1808.8204, 1818.7179, 1838.7988, 1847.7115, 1861.7329, 1873.8247, 1890.8479, 1910.8903, 1922.8085, 1940.8173, 1961.8336, 1970.8190, 1978.8943, 1983.7762, 1993.8625, 2022.9215, 2045.9213, 2084.8772, 2097.9211, 2107.8452, 2149.9839, 2167.0146, 2184.0059, 2193.9854, 2207.9839, 2225.0330, 2234.0117, 2248.9958, 2254.9795, 2266.0544, 2268.9666, 2271.9531, 2282.0994, 2292.9812, 2297.1130, 2299.0964, 2313.0962, 2322.0869, 2336.0842, 2345.0574, 2388.0774, 2399.0481, 2409.1226, 2421.1846, 2432.1287, 2447.1606, 2458.2083, 2481.1763, 2487.1868, 2503.1936, 2509.1982, 2527.1589, 2536.2502, 2548.1843, 2568.2397, 2584.2493, 2609.3225, 2636.3230, 2652.3452, 2664.3545, 2707.5398, 2779.6150



4 Calreticulin

Number of mass values searched: **150**

Number of mass values matched: **10**

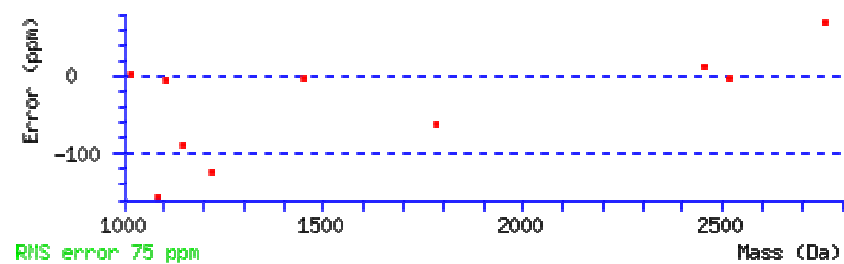
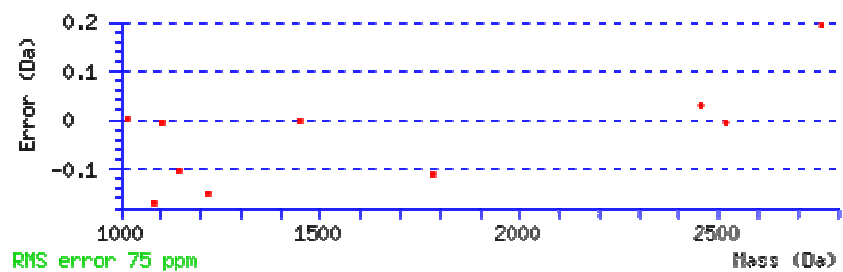
Sequence Coverage: **31%**

Matched peptides shown in **Bold Red**

1 MLLSVPLLLG LLGLAADPA IYFK**EQFLDG DAWTNR**WVES KHKSDFGK FV
51 LSSGKFY GDL EKDKGLQTSQ DARFYALSAK FEPFSNK**GQT LVVQFTV**KHE
101 QNIDCGGGYV KLFPSGLDQK **DMHGDSEYNI MFGPDICGPG TKKVHVIFNY**
151 **KGKNVLINKD IRCKDDEFTH** LYTLIVRPDN TYEVK**IDNSQ VESGSLEDDW**
201 **DFLPPKKIKD PDAAKPEDWD ERAKIDDPD SKPEDWDKPE HIPDPDAK**KP
251 EDWDEEMDGE WEPPIQNPE YKGEWKPRQI DNPDKGTWI HPEIDNPEYS
301 PDANIYAYDS FAVLGLDLWQ VKSGTIFDNF LITNDEAYAE EFGNETWGV
351 KAAEKQMKDK QDEEQRLKEE EEDKKR**KEEE EAEDK**EDDDD RDEDEDEEDE
401 KEEDEEESPG QAKDEL

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
25 - 36	1451.6514	1450.6441	1450.6477	-0.0036	0	K.EQFLDGDAWTNR.W
88 - 98	1219.5522	1218.5449	1218.6972	-0.1523	0	K.GQTLVVQFTV.K.H
121 - 142	2457.0437	2456.0364	2456.0083	0.0281	0	K.DMHGDSEYNI MFGPDICGPGTK.K Oxidation (M)
143 - 151	1147.5591	1146.5518	1146.6550	-0.1031	1	K.KVHVIFNYK.G
144 - 151	1019.5690	1018.5617	1018.5600	0.0017	0	K.VHVIFNYK.G
154 - 162	1084.4779	1083.4706	1083.6400	-0.1694	1	K.NVLINKDIR.C
186 - 207	2519.1885	2518.1812	2518.1864	-0.0051	1	K.IDNSQVESGSLEDDWDFLPPKK.I
208 - 222	1784.7324	1783.7251	1783.8377	-0.1125	1	K.IKDPDAAKPEDWDER.A
225 - 248	2760.4563	2759.4490	2759.2562	0.1928	0	K.IDDPDTSKPEDWDKPEHIPDPDAK.K
377 - 385	1106.4795	1105.4722	1105.4775	-0.0052	1	R.KEEEEAE DK.E

No match to: 904.5634, 911.5720, 919.5899, 923.6359, 926.6425, 931.5907, 938.6382, 942.6124, 948.6053, 951.5952, 959.5609, 967.5212, 973.5989, 985.5552, 995.5775, 1000.5576, 1002.5673, 1031.5319, 1052.0858, 1058.5194, 1065.9270, 1068.4999, 1074.5187, 1089.5112, 1095.4814, 1102.5139, 1109.4355, 1118.4951, 1130.4995, 1140.4773, 1157.5092, 1165.5222, 1173.4818, 1179.4917, 1186.5319, 1193.4805, 1201.4750, 1227.4708, 1233.4768, 1242.5375, 1265.4633, 1277.5436, 1300.3481, 1307.4832, 1320.3833, 1329.4572, 1339.5253, 1346.4513, 1354.3467, 1365.4271, 1373.4209, 1383.4600, 1390.4880, 1407.5332, 1421.6102, 1427.6881, 1433.6188, 1458.7473, 1466.6816, 1475.7732, 1487.8535, 1489.8757, 1497.7645, 1507.8551, 1514.7355, 1531.8418, 1546.8037, 1549.8403, 1555.8303, 1571.7905, 1578.8268, 1585.7284, 1594.7534, 1604.8096, 1630.7831, 1634.8246, 1646.7344, 1657.7228, 1668.7291, 1675.7971, 1699.7365, 1707.6813, 1716.7585, 1738.7253, 1748.6572, 1765.6331, 1791.6398, 1794.6936, 1816.7086, 1837.8301, 1856.8038, 1890.8287, 1940.8112, 1948.8322, 1963.8606, 1977.8038, 1993.8394, 2015.8312, 2022.7856, 2050.8801, 2063.8894, 2077.8718, 2082.8523, 2094.9075, 2117.8982, 2133.9277, 2170.9121, 2186.9434, 2210.9949, 2225.0146, 2233.9988, 2239.0300, 2248.9817, 2264.0000, 2283.0791, 2298.0959, 2321.0630, 2342.9268, 2367.1980, 2383.9175, 2393.0537, 2400.1406, 2421.1550, 2448.1396, 2473.9968, 2487.1672, 2503.1626, 2510.1428, 2533.1936, 2565.2166, 2637.2976, 2705.2888, 2737.4688, 2747.5715, 2774.4675, 2839.5774, 2856.6282, 2872.6536, 2895.6689, 2902.6985



6 Protein disulfide-isomerase

Number of mass values searched: **150**

Number of mass values matched: **21**

Sequence Coverage: **48%**

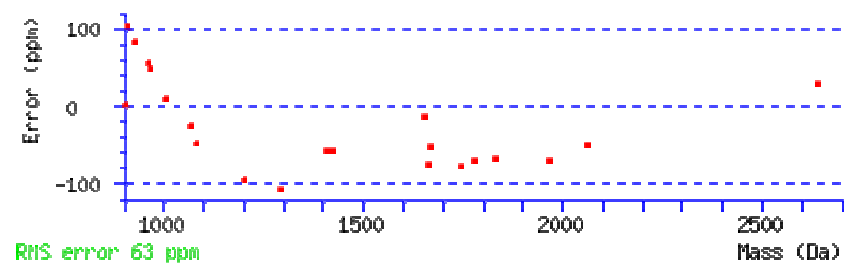
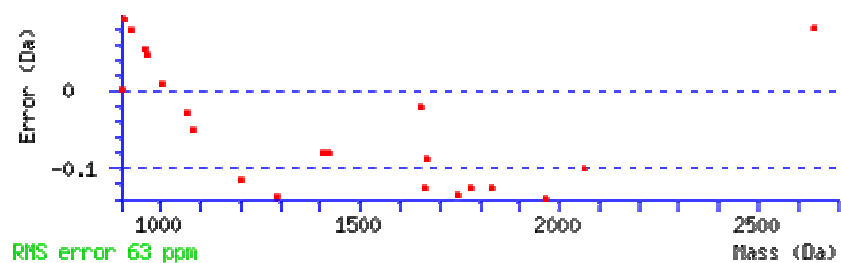
Matched peptides shown in **Bold Red**

1 MLSRALLCLA LAWAARVGAD ALEEDNVLV LKKSNFEEAL AAHKYLLVEF
51 YAPWCGHCKA LAPEYAKRAA **KLKAEGSEIR LAKVDATEES DLAQQYGVRG**
101 YPTIKFFKNG DTASPKEYTA **GREADDIVNW LKKRTGPAAT TLSDTAAAES**
151 LVDSSEVTVI GFFKDVESDS **AKQFLLAEEA IDDIPFGITS NSGVFSKYQL**
201 **DKDGVVLFKK FDEGRNNFEG EITKEKLLDF IKHNQLPLVI EFTEQTAPK**
251 FGGEIK**THIL LFLPK**SVSDY DGLSSFKRA AEGFKG**KILF IFIDSDHTDN**
301 **QRILEFFGLK KEECPAVRLI TLEEEMTKYK PEDELTAEK ITEFCHRFL**
351 GKIKPHLMSQ EVPEDWDKQP **VKVLVGANFE EVAFDEK**KNV FVEFYAPWCG
401 HCK**QLAPIWD KLGETYKDHE NIIIAKMDST ANEVEAVKVH SFPTLKFFPA**
451 **SADRTVIDYN GERTLDGFKK FLESGGQDGA GDEDLLEE ALEPDMEEDD**
501 DQKAVKDEL

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
72 - 80	1002.5675	1001.5602	1001.5505	0.0097	1	K.LKAEGSEIR.L
84 - 99	1780.7120	1779.7047	1779.8275	-0.1228	0	K.VDATEESDLAQQYGVR.G
123 - 132	1202.4922	1201.4849	1201.5979	-0.1130	0	R.EADDIVNWLK.K
173 - 197	2640.4368	2639.4295	2639.3483	0.0812	0	K.QFLLAEEAIDDIPFGITSNSGVFSK.Y
198 - 209	1424.6982	1423.6909	1423.7711	-0.0802	1	K.YQLDKDGVVLFK.K
203 - 210	905.5485	904.5412	904.5382	0.0030	1	K.DGVVLFKK.F
211 - 224	1655.7452	1654.7379	1654.7587	-0.0208	1	K.FDEGRNNFEGEITK.E
233 - 249	1964.9060	1963.8987	1964.0367	-0.1380	0	K.HNQLPLVIEFTEQTAPK.I
257 - 265	1081.6265	1080.6192	1080.6695	-0.0503	0	K.THILLFLPK.S
288 - 302	1833.7896	1832.7823	1832.9057	-0.1234	0	K.ILFIFIDSDHTDNQR.I
303 - 310	966.6129	965.6056	965.5586	0.0470	0	R.ILEFFGLK.K
312 - 328	2063.8984	2062.8911	2062.9915	-0.1003	1	K.EECPAVRLITLEEEMTK.Y Oxidation (M)
329 - 340	1409.5995	1408.5922	1408.6722	-0.0799	0	K.YKPESDELTAEK.I
341 - 347	962.5057	961.4984	961.4440	0.0544	0	K.ITEFCHR.F
373 - 387	1666.7460	1665.7387	1665.8250	-0.0863	0	K.VLVGANFEEVAFDEK.K
404 - 417	1661.7660	1660.7587	1660.8824	-0.1237	1	K.QLAPIWDKLGETYK.D
412 - 426	1743.7927	1742.7854	1742.9203	-0.1348	1	K.LGETYKDHENIIIAK.M
427 - 438	1293.4622	1292.4549	1292.5918	-0.1369	0	K.MDSTANEVEAVK.V
439 - 446	928.6041	927.5968	927.5178	0.0790	0	K.VHSFPTLK.F

447 - 454 910.5364 909.5291 909.4345 0.0947 0 K.FFPASADR.T
455 - 463 1066.4899 1065.4826 1065.5091 -0.0265 0 R.TVIDYNGER.T

No match to: 902.3400, 917.3734, 923.5850, 935.5857, 939.5625, 953.5679, 976.5244, 985.5616, 996.6130, 1000.5526, 1016.5523, 1029.5316, 1031.5358, 1034.1272, 1045.5526, 1058.5236, 1068.4943, 1074.5137, 1089.5072, 1102.5100, 1106.4868, 1118.4998, 1125.4934, 1130.5190, 1142.5093, 1151.5708, 1157.5131, 1165.4907, 1173.4908, 1179.4954, 1186.4875, 1191.4742, 1209.5210, 1217.4481, 1233.4583, 1244.4706, 1265.4832, 1277.5366, 1301.4905, 1307.4730, 1320.3965, 1329.4542, 1339.5260, 1354.4640, 1365.4221, 1383.4718, 1391.5096, 1436.7760, 1460.7373, 1465.7969, 1475.7761, 1489.8789, 1496.7589, 1507.8531, 1516.7498, 1531.8398, 1549.8322, 1555.8248, 1564.7863, 1571.7820, 1578.8217, 1593.7650, 1597.7408, 1604.8334, 1621.7086, 1637.7402, 1680.7614, 1694.7700, 1707.6920, 1716.7612, 1732.7819, 1750.7241, 1762.7269, 1764.6514, 1766.6641, 1777.7091, 1791.6478, 1794.7103, 1809.7410, 1817.7563, 1825.7583, 1849.7900, 1860.8376, 1876.8354, 1890.8098, 1912.7305, 1928.7294, 1940.7909, 1948.8385, 1956.7617, 1972.8126, 1978.9080, 1986.8207, 1993.8556, 2013.8026, 2022.8860, 2035.9230, 2050.8845, 2076.8955, 2082.8606, 2094.9043, 2110.8806, 2133.9646, 2149.9578, 2165.9822, 2192.9902, 2225.0264, 2234.0193, 2239.0498, 2265.0581, 2297.1040, 2311.9924, 2342.9485, 2367.1895, 2383.9165, 2399.0632, 2421.1831, 2434.1780, 2447.1670, 2481.1885, 2487.1772, 2509.1912, 2653.4214, 2707.5381, 2717.2700, 2746.5847, 2766.6226, 2779.6399, 2985.8958



8 ATP synthase subunit beta, mitochondrial

Number of mass values searched: **100**

Number of mass values matched: **17**

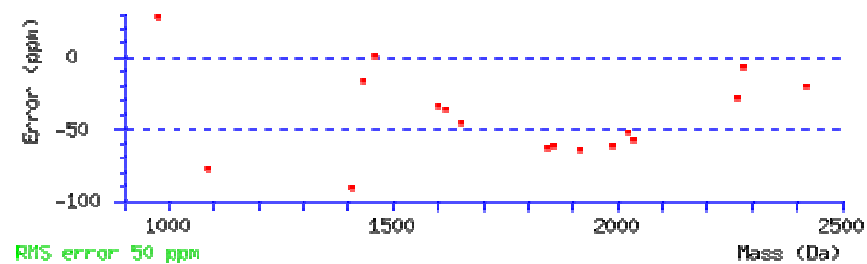
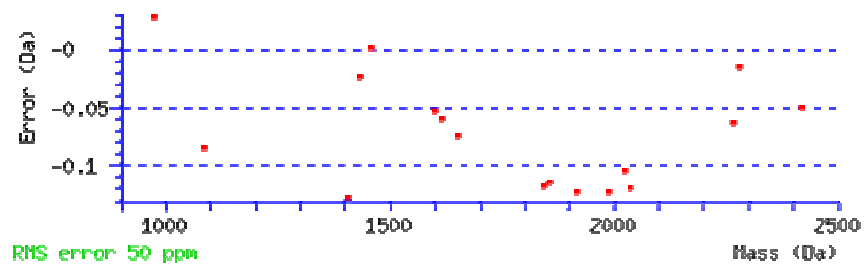
Sequence Coverage: **35%**

Matched peptides shown in **Bold Red**

1 MLSLVGRVAS ASASGALRGL SPSAALPQAQ LLLRAAPAGV HPARDYAAQA
51 SAAPKAGTAT GRIVAVIGAV VDVQFDEGLP PILNALEVQG RDSRL**LVLEVA**
101 **QHLGESTVRT** IAMDGTEGLV RGQK**VLD**SGA **PIKIPVGPET LGR**IMNVIGE
151 PIDERGIPT KQFAPIHAEA PEFIEMSVEQ EILVTGIK**VV DLLAPYAK**GG
201 **KIGLFGGAGV GKT**VLIMELI **NNVAKAHGGY SVFAGVGERT** REGNDLYHEM
251 IESGVINLKD ATSK**VALVYG QMNEPPGARA** RVALTGLTVA EYFRDQEGQD
301 VLLFIDNIFR **FTQAGSEVSA LLGRIPSAVG YQPTLATDMG TMQER**ITTTK
351 KGSITSVQAI YVPADDLTDP APATTFAHLD ATTVLSR**AIA ELGIYPAVDP**
401 **LDSTSRIMDP NIVGNEHYDV ARGVQKILQD** YKSLQDIIAI LGMDELSEED
451 KLTVSRARKI **QRFLSQPFQV AEVFTGHMGK** LVPLKETIKG FQQILAGEYD
501 HLPEQAFYMV GPIEEAVAKA DKLAEEHGS

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
95 - 109	1650.8419	1649.8346	1649.9101	-0.0754	0	R.LVLEVA QHLGESTVR .T
125 - 143	1918.9727	1917.9654	1918.0888	-0.1233	1	K.VLD SGAPIKIPVGPETLGR .I
189 - 198	1088.5510	1087.5437	1087.6277	-0.0840	0	K.V VDLLAPYAK .G
202 - 212	975.5900	974.5827	974.5549	0.0278	0	K.I GLFGGAGV GK.T
213 - 225	1457.8405	1456.8332	1456.8323	0.0009	0	K.T VLIMELINNVAK .A
226 - 239	1406.5529	1405.5456	1405.6739	-0.1283	0	K.A HGGYSVFAGVGER .T
265 - 279	1601.7563	1600.7490	1600.8031	-0.0541	0	K.V ALVYGMNEPPGAR .A
265 - 279	1617.7461	1616.7388	1616.7981	-0.0592	0	K.V ALVYGMNEPPGAR .A Oxidation (M)
311 - 324	1435.7311	1434.7238	1434.7467	-0.0229	0	R.F TQAGSEVSALLGR .I
325 - 345	2266.0210	2265.0137	2265.0770	-0.0632	0	R.I PSAVGYQPTLATDMGMTQER .I
325 - 345	2282.0642	2281.0569	2281.0719	-0.0149	0	R.I PSAVGYQPTLATDMGMTQER .I Oxidation (M)
388 - 406	1987.9115	1986.9042	1987.0262	-0.1220	0	R.A IAELGIYPAVDPLDSTSR .I
407 - 422	1842.7629	1841.7556	1841.8730	-0.1174	0	R.I MDPNIVGNEHYDVAR .G
407 - 422	1858.7614	1857.7541	1857.8679	-0.1138	0	R.I MDPNIVGNEHYDVAR .G Oxidation (M)
460 - 480	2420.2039	2419.1966	2419.2471	-0.0505	1	K.I QRFLSQPFQVAEVFTGHMGK .L
463 - 480	2022.9054	2021.8981	2022.0033	-0.1052	0	R.F LSQPFQVAEVFTGHMGK .L
463 - 480	2038.8867	2037.8794	2037.9983	-0.1188	0	R.F LSQPFQVAEVFTGHMGK .L Oxidation (M)

No match to: 903.3585, 909.1082, 917.3708, 925.3575, 931.5544, 939.3627, 947.5124, 955.5194, 961.3792, 971.5813, 985.5535, 995.5023, 1000.5446, 1002.5604, 1031.5273, 1034.1312, 1045.5488, 1052.0925, 1058.5211, 1066.0615, 1072.0675, 1082.0237, 1097.5128, 1108.4202, 1118.4863, 1127.4496, 1143.5148, 1179.4891, 1212.4800, 1233.4327, 1260.9740, 1276.9426, 1307.4540, 1320.3856, 1329.4556, 1339.4965, 1354.3271, 1362.4515, 1385.4971, 1400.5548, 1415.6436, 1420.6241, 1442.7318, 1449.7668, 1463.7333, 1475.7797, 1489.8760, 1507.8588, 1549.8296, 1555.8330, 1571.7976, 1578.8237, 1595.7512, 1615.7716, 1633.7832, 1638.7843, 1664.8483, 1678.8370, 1707.7136, 1766.6686, 1791.6351, 1794.7191, 1851.8059, 1868.8496, 1932.9861, 1975.9380, 2001.9265, 2009.9244, 2054.8794, 2224.0295, 2233.0156, 2248.9858, 2284.0984, 2299.0330, 2383.9187, 2448.1826, 2487.2205, 2503.2249, 2690.5330, 2705.3325, 2780.6841, 3032.1311, 3046.1436



10 Annexin A5

Number of mass values searched: **100**

Number of mass values matched: **13**

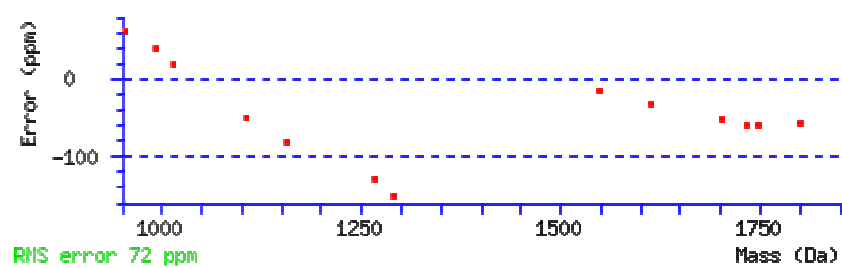
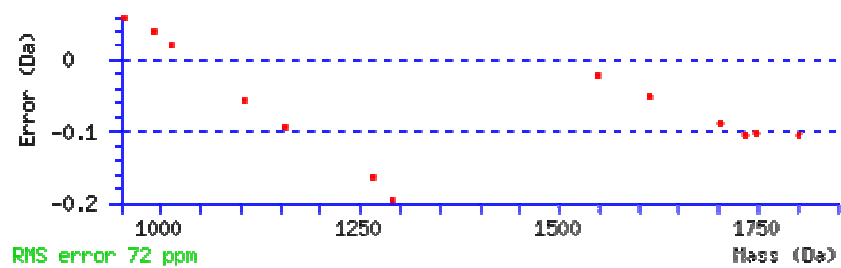
Sequence Coverage: **43%**

Matched peptides shown in **Bold Red**

1 MATR**GTVD**F **PGFDGR**ADAE VLRKAMK**GLG TDEDSILNLL** T**SR**SNAQR**QE**
51 **IAQEFK**TLFG RDLVDDLKSE LTGK**FEKLIV** **AMMKPSRLYD** **AYELK**HALKG
101 AGTDEKVLTE IASRTPEEL SAIKQVYEEE YGSNLEDDVV GDTSGYYQ**RM**
151 **LVVLLQANRD** PDTAIDDAQV ELDAQALFQA GELKWGTDEE **KFITIFGTRS**
201 VSHLRRVFDK **YMTISGFQIE** **ETIDRETS**GN **LEQLLAVVK** SIRSIPAYLA
251 **ETLYYAMK**GGA GTDDHTLIRV VVSR**SEIDLF** **NIRKEFRKNF** **ATSLYS**MIK**G**
301 DTSGDYK**KAL** LLLCGGEDD

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
5 - 16	1268.4264	1267.4191	1267.5834	-0.1642	0	R.GTVD FPGFDGR .A
28 - 43	1703.7925	1702.7852	1702.8737	-0.0885	0	K.G LGTDEDSILNLL T SR .S
49 - 56	992.5438	991.5365	991.4974	0.0391	0	R.QE IAQEFK .T
75 - 87	1549.8364	1548.8291	1548.8520	-0.0229	1	K.FE KLIV AMMK PSR .L
88 - 95	1014.5341	1013.5268	1013.5069	0.0199	0	R.LY DAYELK .H
150 - 159	1156.5919	1155.5846	1155.6798	-0.0952	0	R.M LVVLLQANR .D
192 - 199	954.5996	953.5923	953.5335	0.0589	0	K.F ITIFGTR .S
211 - 225	1802.7581	1801.7508	1801.8556	-0.1048	0	K.Y MTISGFQIE ET IDR .E
226 - 240	1613.8595	1612.8522	1612.9036	-0.0513	0	R.E TSGNLEQLL AV VK .S
244 - 258	1733.7778	1732.7705	1732.8745	-0.1040	0	R.S IPAYLA ET LYAMK .G
244 - 258	1749.7743	1748.7670	1748.8695	-0.1024	0	R.S IPAYLA ET LYAMK .G Oxidation (M)
275 - 283	1106.5277	1105.5204	1105.5768	-0.0563	0	R.S EIDLFNIR .K
289 - 299	1290.4448	1289.4375	1289.6326	-0.1950	0	K.N FATSLYS MIK G Oxidation (M)

No match to: 905.5695, 910.6422, 917.3578, 926.6440, 931.5986, 939.6024, 975.5441, 985.5634, 996.6005, 1000.5661, 1002.5697, 1028.5310, 1031.5397, 1034.1202, 1044.0648, 1052.0824, 1058.5245, 1066.0463, 1074.5117, 1082.0104, 1088.5062, 1098.5189, 1118.4994, 1120.5370, 1143.5317, 1165.5929, 1179.5046, 1189.4829, 1224.4697, 1233.4479, 1277.5184, 1307.4675, 1339.5393, 1353.5701, 1383.4703, 1436.7860, 1475.7855, 1489.8878, 1507.8668, 1531.8442, 1555.8230, 1571.7850, 1578.8318, 1595.8381, 1604.8395, 1623.8035, 1638.7972, 1660.7903, 1677.8059, 1717.8010, 1764.6586, 1766.6705, 1780.7144, 1791.6401, 1794.6987, 1817.7498, 1831.7661, 1839.8051, 1851.8075, 1856.8047, 1940.7982, 1993.8673, 2008.9977, 2149.9736, 2192.9724, 2225.0322, 2234.0190, 2248.9851, 2266.0403, 2282.0923, 2284.0940, 2298.1013, 2307.0669, 2342.9619, 2383.9192, 2399.0247, 2420.1772, 2448.1672, 2487.1763, 2503.1833, 2687.4175, 2705.3113, 2780.6472, 2898.5437, 2914.5640, 2929.6018, 2943.6233



14 ATP synthase subunit d, mitochondrial

Number of mass values searched: **150**

Number of mass values matched: **8**

Sequence Coverage: **67%**

Matched peptides shown in **Bold Red**

1 MAGRKLALKT IDWVSFVEVM PQNQKAIGNA LKSWNETFHA RLASLSEKPP

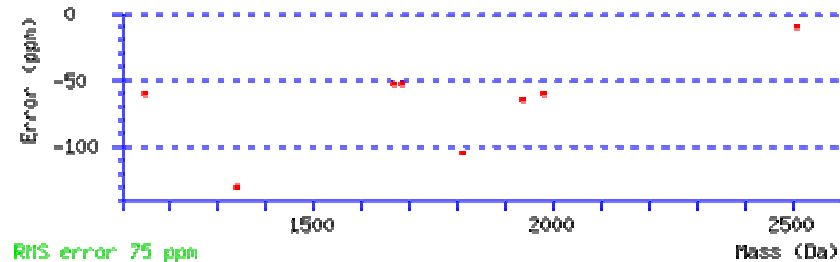
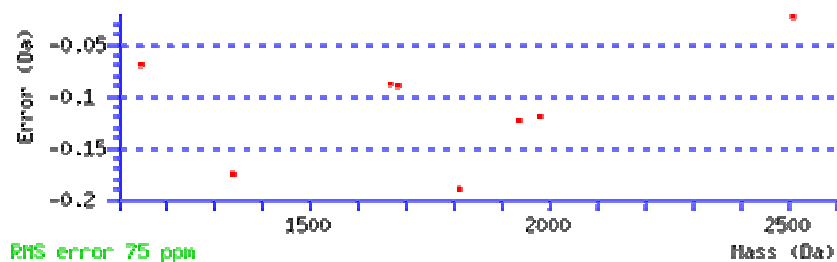
51 AIDWAYYRAN VAKPGLVDDF EKYNALKIP VPEDKYTALV DQEEKEDVKS

101 CAEFVSGSQL RIQEYEQLE KMRNIIPFDQ MTIDDLNEIF PETKLDKKKY

151 PYWPHQPIEN L

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
10 - 25	1936.8241	1935.8168	1935.9401	-0.1232	0	K.TIDWVSFVEVMPQNK.A Oxidation (M)
26 - 41	1814.7393	1813.7320	1813.9223	-0.1903	1	K.AIGNALKSWNETFHAR.L
33 - 41	1147.4589	1146.4516	1146.5206	-0.0690	0	K.SWNETFHAR.L
42 - 58	1979.9032	1978.8959	1979.0152	-0.1193	0	R.LASLSEKPPAIDWAYYR.A
86 - 99	1666.7284	1665.7211	1665.8097	-0.0886	1	K.YTALVDQEEKEDVK.S
100 - 111	1340.4508	1339.4435	1339.6190	-0.1755	0	K.SCAEFVSGSQLR.I
124 - 144	2509.1948	2508.1875	2508.2094	-0.0219	0	R.NIIPFDQMTIDDLNEIFPETK.L Oxidation (M)
149 - 161	1684.7595	1683.7522	1683.8409	-0.0887	1	K.KYPYWPHQPIENL.-

No match to: 900.3402, 906.5959, 915.3600, 917.3668, 923.5369, 926.5962, 931.5869, 933.3480, 939.3262, 947.5634, 952.6024, 955.3016, 961.3044, 967.5056, 971.5976, 977.2591, 985.5657, 1000.5555, 1002.5640, 1016.5448, 1028.5488, 1031.5244, 1034.1283, 1045.5507, 1052.0839, 1058.5228, 1066.0538, 1072.5325, 1084.4735, 1088.5188, 1089.5043, 1096.4912, 1103.5095, 1106.4724, 1109.4396, 1118.5009, 1124.4475, 1130.4602, 1142.5109, 1157.5010, 1165.4971, 1173.4948, 1179.4921, 1189.4740, 1194.4952, 1204.4558, 1217.4536, 1233.4580, 1242.5551, 1262.4578, 1265.4987, 1277.5402, 1300.3571, 1307.4741, 1320.3993, 1339.5453, 1354.4724, 1365.4218, 1383.4708, 1391.5486, 1410.6625, 1434.7455, 1436.7848, 1443.6805, 1458.7479, 1469.8577, 1475.7863, 1487.8678, 1489.8856, 1507.8624, 1516.7925, 1531.8380, 1540.9054, 1547.8232, 1549.8419, 1555.8191, 1563.8087, 1571.7832, 1578.8257, 1593.7690, 1595.7451, 1604.8522, 1634.8525, 1657.7339, 1675.8142, 1692.7637, 1699.7480, 1707.6941, 1716.7557, 1741.7010, 1750.7180, 1762.7275, 1764.6554, 1766.6686, 1777.6697, 1780.6873, 1791.6566, 1794.7014, 1838.8149, 1851.8051, 1890.8488, 1921.8054, 1940.7982, 1961.8646, 1993.8615, 2017.8478, 2045.8843, 2063.8875, 2082.8513, 2149.9697, 2167.0110, 2183.9993, 2193.9814, 2225.0205, 2233.9934, 2248.9966, 2266.0452, 2280.0667, 2283.0928, 2298.1028, 2307.0779, 2322.0691, 2336.1055, 2342.9521, 2353.1443, 2367.1899, 2383.9441, 2399.0112, 2421.1753, 2447.1636, 2456.1721, 2474.0139, 2487.1814, 2503.2190, 2526.1838, 2565.2556, 2637.3240, 2705.3354, 2746.6128, 2780.6450, 2872.6743, 3053.0813



15 26S proteasome non-ATPase regulatory subunit 10

Number of mass values searched: **200**

Number of mass values matched: **10**

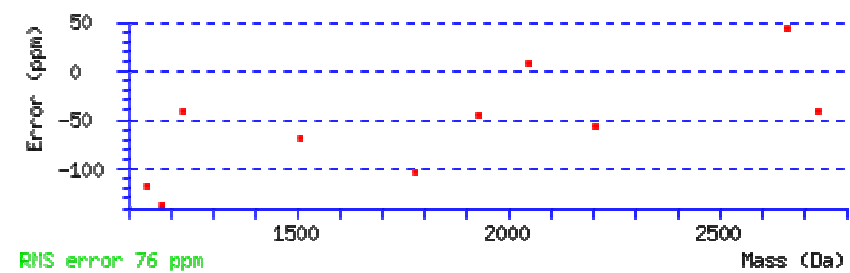
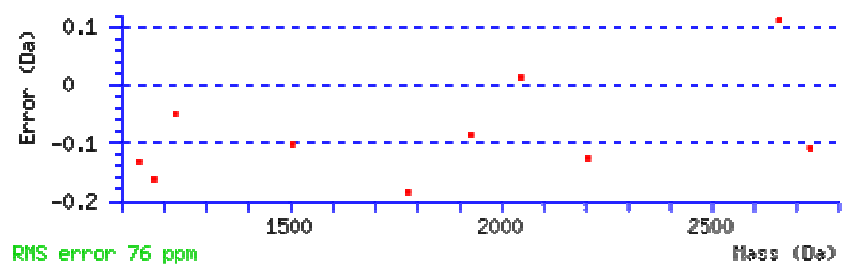
Sequence Coverage: **53%**

Matched peptides shown in **Bold Red**

1 MEGCVSNIMI CNLAYSGKLD ELKERILADK SLATRTDQDS RTALHWACS
51 GHTEIVEFLL QLGVPVNDKD DAGWSPLHIA ASAGRDEIVK ALLVKGAVHN
101 AVNQNGCTPL HYAASKNRHE IAVMLLEGGA NPDAKDHYDA TAMHRAAAKG
151 NLKMOVHILLF YKASTNIQDT EGNTPLHLAC DEERVEEAKF LVTQGASIYI
201 ENKEEKTPLQ VAKGGLGLIL KRLAEGEEAS M

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
1 - 18	2046.9258	2045.9185	2045.9043	0.0143	0	-.MEGCVSNIMICNLAYSGK.L
1 - 23	2661.3513	2660.3440	2660.2318	0.1122	1	-.MEGCVSNIMICNLAYSGKLDLDELK.E Oxidation (M)
2 - 18	1931.7795	1930.7722	1930.8587	-0.0865	0	M.EGCVSNIMICNLAYSGK.L Oxidation (M)
70 - 90	2207.9792	2206.9719	2207.0971	-0.1252	1	K.DDAGWSPLHIAASAGRDEIVK.A
91 - 116	2733.3152	2732.3079	2732.4180	-0.1101	1	K.ALLVKGAVHNAVNQNGCTPLHYAASK.N
119 - 135	1780.7059	1779.6986	1779.8825	-0.1839	0	R.HEIAVMLLEGGANPDAK.D Oxidation (M)
136 - 145	1232.4598	1231.4525	1231.5040	-0.0515	0	K.DHYDATAMHR.A Oxidation (M)
154 - 162	1179.4990	1178.4917	1178.6522	-0.1605	0	K.MVHILLFYK.A Oxidation (M)
204 - 213	1142.5079	1141.5006	1141.6343	-0.1336	1	K.EEKTPLQVAK.G
207 - 221	1507.8539	1506.8466	1506.9497	-0.1031	1	K.TPLQVAKGGLGLILK.R

No match to: 900.3644, 906.5753, 913.5676, 916.6031, 922.6007, 925.5959, 928.5309, 935.5721, 938.5342, 941.5845, 948.5187, 954.3199, 960.5219, 963.5454, 968.6084, 971.3471, 977.6231, 982.5153, 985.5707, 996.6103, 1000.5548, 1002.5684, 1012.5680, 1016.5661, 1029.5419, 1031.5337, 1034.1263, 1040.5659, 1045.5588, 1052.0840, 1058.5236, 1065.9028, 1068.5065, 1074.5033, 1082.5470, 1089.5013, 1095.5142, 1102.5121, 1106.4840, 1109.4501, 1118.4954, 1125.4956, 1132.4751, 1139.4692, 1148.5221, 1151.6125, 1157.5060, 1165.6262, 1173.5217, 1191.4716, 1202.5277, 1210.5258, 1218.4580, 1225.4498, 1233.4426, 1242.5345, 1251.4763, 1263.4777, 1277.5328, 1284.4130, 1292.4723, 1302.5071, 1309.4733, 1320.3860, 1329.4855, 1339.5221, 1350.4656, 1357.4895, 1365.4424, 1383.4633, 1393.5481, 1410.6370, 1422.6089, 1436.7743, 1443.7432, 1450.6858, 1459.7644, 1464.8152, 1469.8455, 1475.7705, 1487.8674, 1489.8835, 1514.8231, 1522.7964, 1531.8386, 1546.8053, 1549.8311, 1555.8248, 1565.8049, 1571.7866, 1578.8204, 1585.7192, 1593.7654, 1604.8370, 1613.7240, 1622.7639, 1634.8442, 1638.7952, 1652.8221, 1660.7820, 1669.7804, 1677.7965, 1681.8007, 1699.7417, 1707.6747, 1716.7644, 1724.7715, 1735.6794, 1740.6359, 1750.7169, 1764.6361, 1766.6586, 1791.6179, 1794.6929, 1807.7968, 1819.6547, 1836.8147, 1838.8049, 1851.8031, 1859.8204, 1867.7911, 1879.7777, 1899.7875, 1910.7589, 1922.7797, 1940.8005, 1949.8368, 1965.9214, 1978.8486, 1993.8479, 2001.8749, 2014.8552, 2022.9125, 2030.8977, 2055.8884, 2077.9014, 2096.8513, 2105.9434, 2121.9312, 2135.9998, 2149.9595, 2166.9878, 2185.9692, 2194.9309, 2225.0173, 2234.0042, 2250.0308, 2266.0232, 2282.0881, 2284.0779, 2298.0916, 2307.0693, 2318.0771, 2328.0830, 2336.0791, 2349.1470, 2358.0867, 2368.1155, 2374.1138, 2383.8975, 2398.9802, 2417.1870, 2420.1738, 2432.1580, 2446.1729, 2448.1553, 2457.1958, 2462.1841, 2482.1694, 2487.1594, 2501.2454, 2510.1592, 2565.3320, 2584.2529, 2594.2908, 2609.2959, 2626.3350, 2636.3113, 2651.4614, 2692.5637, 2705.2827, 2720.4263, 2780.6279, 2831.4231, 2872.6416, 2888.6665, 2902.6963, 2932.8181, 2981.8923, 3053.0422



16 N-acetyltransferase 9

Number of mass values searched: **200**

Number of mass values matched: **11**

Sequence Coverage: **41%**

Matched peptides shown in **Bold Red**

1 MKLNQNTMLV GKKVVLVPYT SEHVPYHEW **MKSEELR**HLT ASEQLTLQQE

51 YEMQCSWCED EDKCTFIVLD AEKWAQPRP PEESCMVGDV NLFLTDLEDP

101 TLGEIEVMIA EPSYRRQGLG TEASLLIMSY GVTKLGLTKF EAKIGQENEP

151 SIRMFQKLHF KQVAMSNVFQ EVTLRLAVSE PERKWILEQT SHMEERPVRT

201 RKAEPVTATL SEQKSWNCPL PRPDGCMGDT SAVSSVCARL S

Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence

1 - 12 1376.5750 1375.5677 1375.7316 -0.1638 1 -.MKLNQNTMLVGK.K

3 - 12 1133.6028 1132.5955 1132.5910 0.0045 0 K.LNQNNTMLVGK.K Oxidation (M)

27 - 37 1507.8574 1506.8501 1506.6925 0.1576 1 R.YHEWMKSEELR.H

27 - 37 1523.8492 1522.8419 1522.6874 0.1545 1 R.YHEWMKSEELR.H Oxidation (M)

140 - 153 1617.7576 1616.7503 1616.8158 -0.0655 1 K.FEAKIGQENEPSIR.M

144 - 153 1142.5140 1141.5067 1141.5727 -0.0660 0 K.IGQENEPSIR.M

144 - 157 1676.8112 1675.8039 1675.8352 -0.0312 1 K.IGQENEPSIRMFQK.L

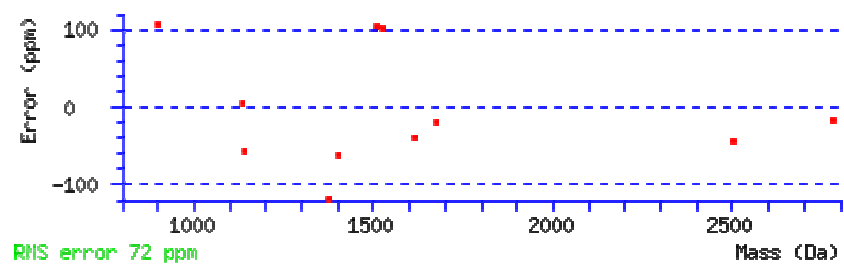
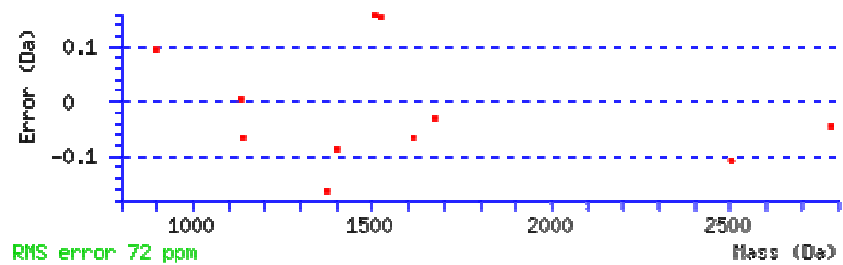
162 - 183 2503.1875 2502.1802 2502.2900 -0.1098 1 K.QVAMSNVFQEVTLRLAVSEPER.K

176 - 183 900.5750 899.5677 899.4712 0.0965 0 R.LAVSEPER.K

202 - 214 1401.6724 1400.6651 1400.7511 -0.0860 1 R.KAEPVTATLSEQK.S

215 - 239 2780.1545 2779.1472 2779.1935 -0.0463 0 K.SWNCPLPRPDGCMGDTSAVSSVCAR.L

No match to: 906.5345, 909.0938, 910.6434, 917.3564, 924.6210, 926.6180, 931.5905, 937.5581, 940.6033, 947.6476, 950.5831, 956.6492, 958.5587, 964.5879, 971.5845, 976.6078, 982.5979, 985.5601, 996.6107, 1000.5515, 1002.5607, 1013.5504, 1029.5452, 1031.5265, 1034.1281, 1044.5321, 1045.5519, 1052.0909, 1058.5214, 1066.0316, 1072.5259, 1074.5211, 1082.0197, 1084.4675, 1089.4978, 1097.5245, 1102.5087, 1106.4767, 1112.4570, 1118.4990, 1125.5664, 1137.5472, 1148.5446, 1159.4950, 1165.6100, 1173.4840, 1179.4863, 1191.4762, 1200.5238, 1215.5497, 1218.4252, 1225.4904, 1233.4443, 1242.5505, 1255.5734, 1260.9679, 1268.5453, 1277.5399, 1295.5298, 1302.5310, 1307.4946, 1314.5453, 1320.4025, 1335.6484, 1339.5251, 1354.4729, 1364.4512, 1383.4739, 1393.5691, 1410.6526, 1417.7589, 1427.6837, 1434.7767, 1436.7815, 1443.7201, 1463.8158, 1469.8658, 1475.7794, 1487.8729, 1489.8871, 1515.7711, 1527.8312, 1531.8423, 1544.9702, 1547.8007, 1549.8361, 1555.8276, 1565.8209, 1571.7906, 1578.8313, 1586.8000, 1593.7640, 1595.7448, 1604.8441, 1624.6813, 1634.8428, 1649.7988, 1655.7828, 1660.8080, 1669.8069, 1695.7955, 1704.7847, 1707.6990, 1716.7566, 1734.7078, 1750.7072, 1762.7203, 1764.6462, 1766.6653, 1777.6819, 1780.6890, 1791.6431, 1794.7030, 1802.7133, 1816.6776, 1832.6726, 1837.8291, 1851.7939, 1861.7999, 1884.7656, 1899.8408, 1913.8495, 1940.8002, 1948.8171, 1960.8273, 1968.7963, 1983.7482, 1993.8577, 2007.8208, 2025.8634, 2036.8702, 2044.9174, 2050.8826, 2063.9097, 2082.8701, 2094.9194, 2112.8691, 2154.9314, 2167.0054, 2185.9998, 2193.9797, 2207.9937, 2222.0569, 2225.0259, 2234.0110, 2249.9912, 2263.0400, 2265.0505, 2280.0750, 2283.0962, 2296.1064, 2298.1055, 2307.0715, 2322.0889, 2336.1072, 2342.9648, 2353.1555, 2367.1882, 2383.9150, 2399.0608, 2421.1829, 2434.1609, 2446.1904, 2448.1638, 2457.1931, 2462.2144, 2481.1672, 2487.1792, 2511.2017, 2525.1890, 2543.2598, 2558.2981, 2565.2505, 2592.2944, 2609.3147, 2637.3235, 2652.3406, 2662.4849, 2689.4727, 2705.3130, 2720.4409, 2737.5159, 2747.5793, 2758.6272, 2814.6250, 2872.6436, 2902.7009, 2951.7778, 2965.7861



17 Prohibitin

Number of mass values searched: **100**

Number of mass values matched: **7**

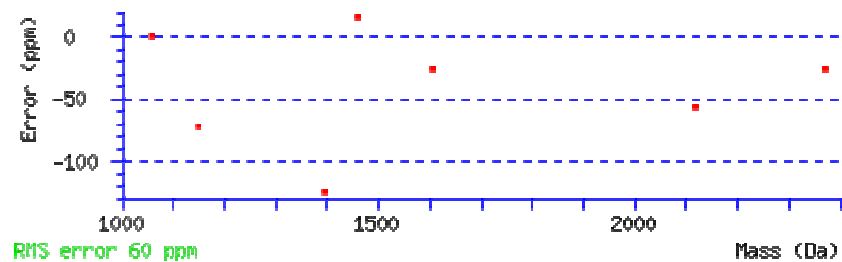
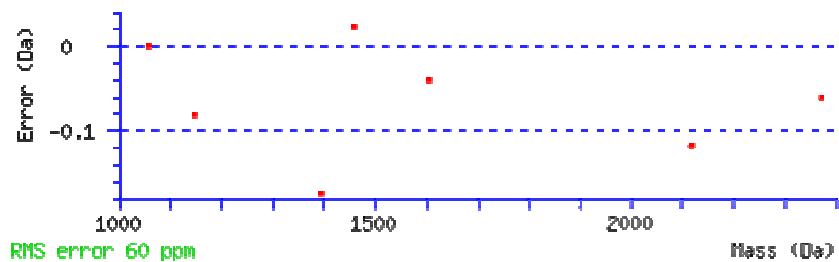
Sequence Coverage: **37%**

Matched peptides shown in **Bold Red**

1 MAAKVFESIG **KFGLALAVAG GVVNSALYNV DAGHRAVIFD** RFRGVQDIVV
51 GEGTHFLIPW VQKPIIFDCR SRPRNPVIT GSKDLQNVNI TLR**ILFRPVA**
101 **SQLPRIYTSI GEDYDER**VLP SITTEILKSV VAR**FDAGELI TQRELVSRQV**
151 SDDLTER**AAT FGLILDDVSL THLTFGKEFT** EAVEAK**QVAQ QEAERARFVV**
201 EKAEQQKAA IISAEGDSKA AELIANSLAT AGDGLIEL**RK LEAAEDIAYQ**
251 **LSR**SRNITYL PAGQSVLLQL PQ

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
12 - 35	2371.1909	2370.1836	2370.2444	-0.0608	0	K.FGLALAVAGGVVNSALYNVDAGHR.A
94 - 105	1396.6680	1395.6607	1395.8350	-0.1743	0	R.ILFRPVASQLPR.I
106 - 117	1460.6779	1459.6706	1459.6467	0.0239	0	R.IYTSIGEDYDER.V
134 - 143	1149.5079	1148.5006	1148.5826	-0.0820	0	R.FDAGELITQR.E
158 - 177	2119.0251	2118.0178	2118.1361	-0.1183	0	R.AATFGLILDDVSLTHLTFGK.E
187 - 195	1058.5226	1057.5153	1057.5152	0.0001	0	K.QVAQQEAER.A
240 - 253	1606.8033	1605.7960	1605.8362	-0.0402	1	R.KLEAAEDIAYQLSR.S

No match to: 910.6238, 915.5768, 920.5528, 926.6274, 931.5954, 941.6123, 949.5977, 958.5903, 985.5637, 996.6186, 1000.5536, 1002.5673, 1029.5404, 1031.5350, 1034.1337, 1045.5547, 1052.0923, 1066.0437, 1074.5144, 1084.4730, 1089.5061, 1106.4911, 1118.5052, 1142.5106, 1163.5127, 1173.5074, 1179.4996, 1186.5367, 1191.4905, 1218.4469, 1233.4480, 1242.5549, 1277.5366, 1307.4734, 1320.4009, 1339.5403, 1354.5302, 1436.7802, 1474.7271, 1487.8754, 1489.8889, 1507.8597, 1531.8433, 1549.8402, 1555.8237, 1562.8181, 1571.7871, 1578.8301, 1593.7590, 1604.8502, 1620.7998, 1634.8531, 1648.8066, 1660.8152, 1669.7982, 1678.8263, 1699.7516, 1707.7014, 1716.7633, 1765.6523, 1780.6987, 1791.6367, 1794.7002, 1837.8344, 1851.8066, 1940.7999, 1993.8557, 2011.9702, 2149.9807, 2166.9944, 2193.9895, 2225.0215, 2234.0093, 2248.9778, 2265.0483, 2282.0859, 2284.0852, 2298.0901, 2307.0747, 2322.0723, 2354.1365, 2383.9204, 2421.1790, 2446.1707, 2448.1599, 2487.1680, 2503.1738, 2525.1604, 2565.2380, 2609.3035, 2637.3110, 2705.2937, 2780.6377



18 TIP41-like protein

Number of mass values searched: **100**

Number of mass values matched: **7**

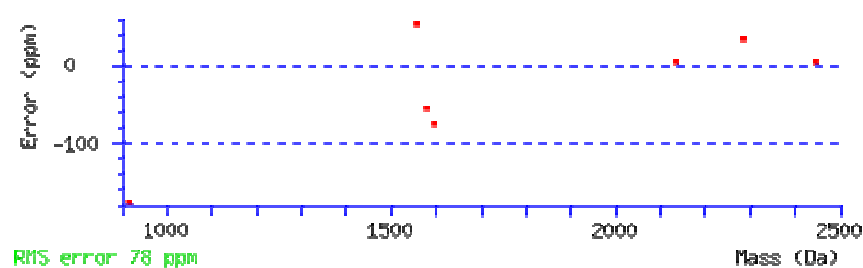
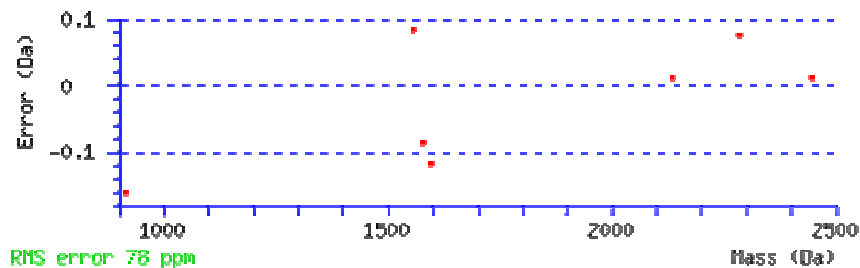
Sequence Coverage: **32%**

Matched peptides shown in **Bold Red**

1 MMIHGFQSSH QDFSFGPWK TASKTHIMKS ADVEK**LADEL HMPSLPEMMF**
51 GDNVLRIQHG SGFGIEFNAT DALRCVNNYQ GMLKVACAAE WQESRTEGEH
101 SKEVIKPYDW TYTTDYK**GL LGESLKLKVV PTTDHIDTEK LK**AREQIKFF
151 EEVLLFEDEL HDHGVSSLSV KIRVMPSSFF LLLRFFLRID GVLIRMNDTR
201 LYHEADKTYM LREYTSRESK IANLMHVPPS LFTEPNEISQ YLPIKEAVCE
251 KLVFPERIDP NPVDSQSTPS E

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
1 - 19	2283.0869	2282.0796	2282.0038	0.0759	0	-.MMIHGFQSSHQDFSFGPWK.L Oxidation (M)
2 - 19	2135.9873	2134.9800	2134.9684	0.0117	0	M.MIHGFQSSHQDFSFGPWK.L
36 - 56	2447.1533	2446.1460	2446.1331	0.0130	0	K.LADELHMPSLPEMMFGDNVLR.I 2 Oxidation (M)
118 - 126	917.3693	916.3620	916.5229	-0.1609	0	K.GTLLGESLK.L
129 - 142	1595.7458	1594.7385	1594.8566	-0.1181	1	K.VVPTTDHIDTEK.LK.A
172 - 184	1578.8314	1577.8241	1577.9116	-0.0875	1	K.IRVMPSSFFLLLR.F
201 - 212	1555.8402	1554.8329	1554.7500	0.0829	1	R.LYHEADKTYMLR.E Oxidation (M)

No match to: 905.5483, 911.6208, 926.6006, 931.5907, 940.6144, 948.5227, 954.5648, 968.6176, 982.6210, 985.5685, 996.6229, 1001.5633, 1030.5509, 1034.1282, 1045.5642, 1052.0907, 1058.5316, 1066.0530, 1068.5076, 1074.5179, 1084.4882, 1088.5220, 1106.4834, 1108.4161, 1118.5062, 1125.4896, 1132.4779, 1142.5087, 1150.4523, 1165.6134, 1173.5037, 1179.5028, 1191.4863, 1217.4708, 1233.4490, 1260.9608, 1277.5498, 1307.4872, 1320.4063, 1339.5424, 1350.4784, 1383.4742, 1436.7903, 1475.7877, 1489.8899, 1507.8710, 1531.8561, 1549.8500, 1562.8350, 1571.8037, 1593.7742, 1604.8457, 1617.7338, 1624.6820, 1634.8373, 1638.7954, 1659.6559, 1676.8215, 1699.7543, 1707.7002, 1716.7683, 1766.6678, 1780.7062, 1791.6403, 1794.7006, 1816.7245, 1837.8071, 1851.8101, 1899.8243, 1913.8098, 1940.8141, 1959.7721, 1993.8442, 2098.8999, 2192.9622, 2225.0212, 2233.9976, 2248.9966, 2266.0520, 2272.9521, 2298.0991, 2307.0706, 2322.0693, 2346.0481, 2383.9138, 2420.1638, 2487.1672, 2501.2249, 2510.1855, 2527.1516, 2584.2654, 2705.3140, 2779.6067



19 Nuclear distribution protein nudE homolog 1

Number of mass values searched: **200**

Number of mass values matched: **12**

Sequence Coverage: **40%**

Matched peptides shown in **Bold Red**

1 MEDSGKTFES EEEETNYWRD LAMTYKQRAE NTQEELREFQ EGSREYEAEEL

51 EAQLQIETR NRDLLSENNR LRMELESVKE KFEMQHSEGY RQISALEDDL

101 AQTKAIKQDL QKYIRELEQA NDDLERAKRA** TIMSLED**FEQ** RLNQAIERNA**

151 FLESELDEKE NLLESVQRLK DEARDLRQEL** AVQ**QKQDKPR** TPMPG**SGQAK****

201 RTDMAVQATG SVPSTPVAHR GPSSGLNTPG MFRRGLDSSST SGTPLTPAAR

251 ISALNIVGDL LRVGALESK LASCRN**FM**YD** QSP**SRTSGPA** SGR**GTK**NRDG**

301 VDRRPGSTSV GDKGSGKRLE FGKPASEPAS PALPSAQGVV KLLL

Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence

1 - 19 2367.1699 2366.1626 2365.9644 0.1982 1 -.MEDSGKTFEEEEEETNYWR.D****

29 - 37 1089.5225 1088.5152 1088.5098 0.0054 0 R.AENTQEELR.E

29 - 44 1922.7892 1921.7819 1921.8766 -0.0946 1 R.AENTQEELREFQEGSR.E****

45 - 60 1949.8564 1948.8491 1948.9377 -0.0886 0 R.EYEALEAQLQIETR.N****

129 - 141 1595.7451 1594.7378 1594.7773 -0.0395 1 K.RATIMSLEDFEQR.L****

130 - 148 2280.0591 2279.0518 2279.1216 -0.0697 1 R.ATIMSLEDFEQLNQAIER.N**** Oxidation (M)

178 - 185 943.5264 942.5191 942.5134 0.0057 0 R.QELAVQK.Q****

186 - 200 1613.7577 1612.7504 1612.7991 -0.0487 1 K.QDKPRTPMPGSGQAK.R**** Oxidation (M)

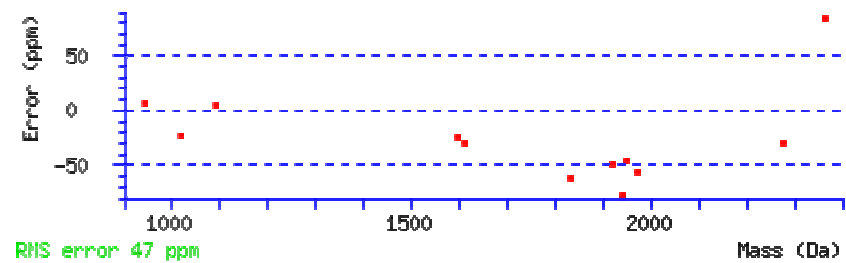
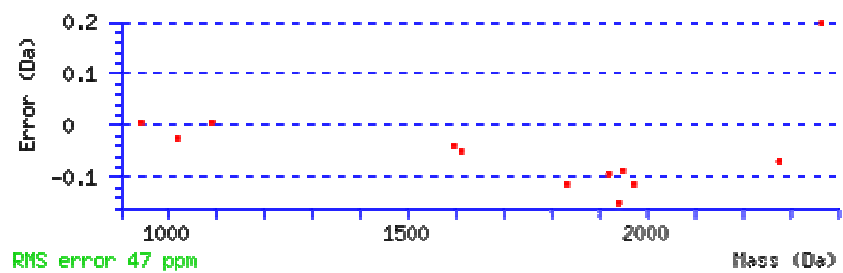
202 - 220 1940.7983 1939.7910 1939.9422 -0.1512 0 R.TDMAVQATGSVPSTPVAHR.G**** Oxidation (M)

271 - 285 1831.7089 1830.7016 1830.8141 -0.1125 1 K.LASCRNFM**YDQSP**SRT**.T**

276 - 293 1973.7650 1972.7577 1972.8697 -0.1120 1 R.NFMYDQSPSRTSGPASGR.G**** Oxidation (M)

286 - 296 1018.5042 1017.4969 1017.5203 -0.0234 1 R.TSGPASGRGK.N****

No match to: 905.6373, 909.0955, 915.5867, 922.6414, 925.6002, 931.5844, 937.4207, 950.6007, 953.3260, 959.5387, 966.5485, 968.5987, 975.4822, 982.6261, 985.5653, 996.6160, 1002.5701, 1028.1187, 1034.1261, 1044.0862, 1052.0951, 1058.5317, 1060.0507, 1066.0568, 1072.0615, 1075.5520, 1082.0081, 1088.0295, 1097.9819, 1103.9811, 1106.4950, 1119.5101, 1126.4972, 1135.5474, 1142.4967, 1151.6384, 1157.5088, 1162.4731, 1165.6495, 1179.5018, 1191.4890, 1218.4521, 1233.4529, 1239.9972, 1254.9518, 1261.9669, 1270.9199, 1276.9283, 1292.8920, 1300.3606, 1307.4904, 1316.4541, 1320.3954, 1329.5042, 1334.6627, 1339.5447, 1350.4692, 1354.4646, 1369.4629, 1377.4229, 1383.4705, 1406.5629, 1436.7889, 1469.8647, 1475.7852, 1487.8748, 1489.8916, 1498.0427, 1507.8630, 1515.7350, 1524.7726, 1531.8069, 1540.8894, 1549.8446, 1555.8352, 1562.7948, 1571.7882, 1578.8430, 1581.7450, 1588.6925, 1604.8394, 1622.7395, 1628.7584, 1638.7861, 1655.7479, 1670.2968, 1678.8091, 1699.7811, 1707.6793, 1716.7522, 1724.8387, 1742.7316, 1750.7052, 1760.7312, 1764.6462, 1766.6686, 1778.6855, 1780.6963, 1788.6838, 1791.6401, 1794.6986, 1802.7079, 1806.7583, 1813.7811, 1816.7009, 1826.6119, 1837.8350, 1851.8116, 1860.7385, 1871.8071, 1884.6288, 1897.7715, 1912.6924, 1965.9309, 1984.8228, 1993.8553, 2007.7238, 2015.8468, 2023.8359, 2031.8649, 2037.8372, 2050.9009, 2064.9116, 2082.8828, 2095.8892, 2106.7288, 2135.9851, 2149.9761, 2166.9866, 2184.0149, 2193.9829, 2207.9673, 2222.0286, 2225.0239, 2233.9998, 2239.0513, 2248.9856, 2263.0432, 2266.0483, 2298.1001, 2307.0608, 2322.0679, 2336.1018, 2349.1455, 2354.1206, 2383.9114, 2399.0269, 2418.1741, 2421.1829, 2434.1436, 2440.1172, 2446.1702, 2448.1616, 2458.1770, 2462.1541, 2477.0747, 2481.1750, 2487.1714, 2499.2290, 2502.2217, 2511.1855, 2525.1943, 2565.2957, 2584.2615, 2590.3147, 2609.3257, 2618.3706, 2637.3247, 2652.3301, 2664.4644, 2680.4490, 2692.4702, 2704.2983, 2707.5425, 2720.4434, 2749.5400, 2758.5981, 2771.6155, 2779.6313, 2814.5791, 2872.6655, 2884.6028, 2897.6401, 2902.6963, 2913.6414, 2932.8433, 3028.0457, 3053.0454



20 Annexin A4

Number of mass values searched: **75**

Number of mass values matched: **9**

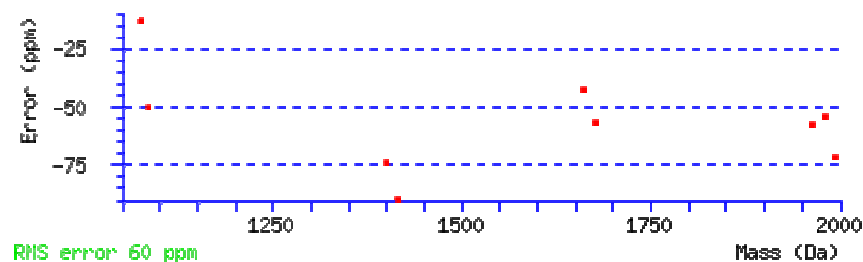
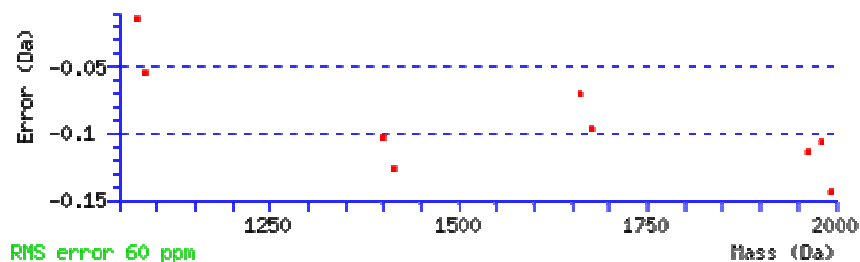
Sequence Coverage: **34%**

Matched peptides shown in **Bold Red**

1 MEAK**GGTVKA ASGFNATEDA QTLR**KAMKGL **GTDEDAIIGI LAYR**NTAQRQ
51 EIRSA**YKSTI** GRDLIEDLKS ELSSNFEQVI LGLMTP**TVLY DVQELRR**AMK
101 **GAGTDEGCLI EILASR**TPEE IRRINQTYQQ QYGR**SLEEDI CS**DT**SFMFQR**
151 VLVFLSAAGR **DEGNYLDDAL MK**QDAQELYE AGEKRWGTDE VKFLSILCSR
201 NR**NHLLHVFD EYKRISQ**KDI EQSIKSETSG SFEDALLAIV KCMR**SKPSYF**
251 **AERLYKSMKG** LGTDDNTLIR VMVSR**AEIDM LDIR**ASFKRL YGKSLYSFIK
301 GDTSGDYRKV LLILCGGDD

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
5 - 24	1993.8507	1992.8434	1992.9865	-0.1431	1	K.GGTVKAASGFNATEDAQTLR.K
29 - 44	1676.7900	1675.7827	1675.8781	-0.0954	0	K.GLGTDEDAIIGILAYR.N
101 - 116	1661.7462	1660.7389	1660.8090	-0.0701	0	K.GAGTDEGCLIEILASR.T
135 - 150	1964.7236	1963.7163	1963.8292	-0.1129	0	R.SLEEDICSDTSFMFQR.V
135 - 150	1980.7249	1979.7176	1979.8241	-0.1065	0	R.SLEEDICSDTSFMFQR.V Oxidation (M)
161 - 172	1399.5013	1398.4940	1398.5973	-0.1033	0	R.DEGNYLDDALMK.Q Oxidation (M)
203 - 213	1414.5846	1413.5773	1413.7041	-0.1268	0	R.NHLLHVDFEYK.R
245 - 253	1084.4880	1083.4807	1083.5349	-0.0542	0	R.SKPSYFAER.L
276 - 284	1075.5310	1074.5237	1074.5379	-0.0142	0	R.AEIDMLDIR.A

No match to: 909.0981, 915.0930, 924.4776, 932.3737, 941.4938, 948.4985, 954.5303, 960.3316, 996.6097, 1002.5620, 1034.1418, 1052.0997, 1058.5250, 1066.0594, 1090.5049, 1106.4828, 1179.4950, 1233.4436, 1247.5398, 1277.5452, 1307.4741, 1354.4323, 1436.7667, 1469.8391, 1475.7760, 1489.8767, 1507.8588, 1549.8378, 1555.8035, 1571.7837, 1578.8182, 1593.7509, 1638.7833, 1690.7921, 1699.7368, 1707.6826, 1716.7515, 1766.6605, 1779.6766, 1791.6576, 1794.6899, 1837.8162, 1851.7975, 1940.7950, 2094.9060, 2136.0002, 2149.9670, 2193.9385, 2225.0146, 2233.9968, 2248.9731, 2266.0332, 2298.0962, 2307.0591, 2322.0730, 2342.9834, 2383.9229, 2421.1760, 2448.1519, 2487.1748, 2501.2395, 2510.1714, 2705.3240, 2737.4905, 2780.1257, 2872.6599



27 Optineurin

Number of mass values searched: **200**

Number of mass values matched: **21**

Sequence Coverage: **37%**

Matched peptides shown in **Bold Red**

1 MSHQPLSCLT EKGDSPCETP GNGPSNMVHP SLDTFTPEEL LQQMKELLVI
51 NHQLK**EAMKL NNQAMKGR**FE ELSAWTEKQK EER**LLFEMQS KEVKER**LKAL
101 THENERLKEE LGKFKEKSEK PLEDLTGGYR YPR**ALEEEVE KLK**TQVEQEV****
151 **EHLKIQVMRL RAEKADLLGI VSELQLKLS GGSSSEDSFVE IR**MTEGETEG****
201 **AMKEMKNCPT PTRTDPISLS NCTEDAR**SCA EFEELTVSQL LLCLREGNQK
251 VERLEVALRE AKERISDFEK **KANGHSSTEK** QTARRADREK **EDKGQESVGS**
301 **EVETLSIQVT SLFK**ELQEAH TKLSEAELMK KRLQEKCQAL ERK**NSATPSE**
351 **LNEKQELVYS NKK**LELVES MRSEIKMEQA KTEEEKSRLA TLQATHNKLL
401 QEHNKALKTI EELTKQAEK VDK**MLLQELS EKLEAEQAL ASKQLQMD**EM
451 **KQTLAK**QEED LETMAVLRAQ MEVYCSDFHA ERAAREKIHE EK**EQLALQLA**
501 **ILLKENNDIE EGSRQSLME MQCRHGARTS DSDQQTILFQ RGAEDRSWQH**
551 GQQPRSIPIH SCPKCGEVLV DIDTLQIHVM DCII

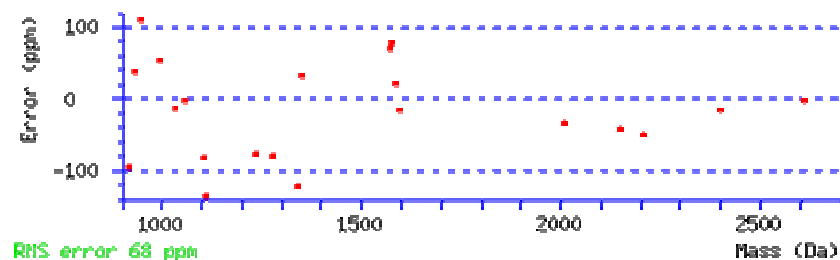
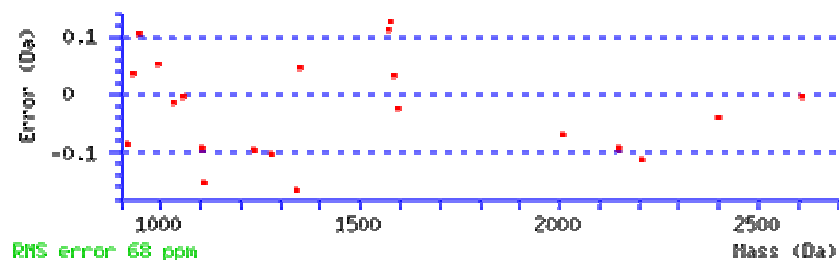
Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
56 - 66	1277.5313	1276.5240	1276.6267	-0.1027	1	K.EAMKLNNQAMK.G
60 - 68	1031.5277	1030.5204	1030.5342	-0.0137	1	K.LNNQAMKGR.F
84 - 91	995.5765	994.5692	994.5157	0.0535	0	R.LLFEMQSK.E
134 - 141	946.5777	945.5704	945.4655	0.1050	0	R.ALEEEVEK.L
144 - 154	1339.5195	1338.5122	1338.6779	-0.1657	0	K.TQVEQEVHLK.I
155 - 161	915.4681	914.4608	914.5484	-0.0875	1	K.IQVMRLR.A
155 - 161	931.5854	930.5781	930.5433	0.0348	1	K.IQVMRLR.A Oxidation (M)
193 - 206	1571.7861	1570.7788	1570.6677	0.1111	1	R.MTEGETEGAMKEMK.N
204 - 213	1233.4766	1232.4693	1232.5642	-0.0948	1	K.EMKNCPTPTR.T
214 - 227	1578.8303	1577.8230	1577.6991	0.1239	0	R.TDPISLSNCTEDAR.S
271 - 280	1058.5206	1057.5133	1057.5152	-0.0019	1	K.KANGHSSTEK.Q
291 - 314	2610.3098	2609.3025	2609.3072	-0.0047	1	K.EDKGQESVGSSEVETLSIQVTSLFK.E
344 - 362	2150.9641	2149.9568	2150.0491	-0.0923	1	K.NSATPSELNEKQELVYSNK.K
355 - 363	1108.4476	1107.4403	1107.5924	-0.1521	1	K.QELVYSNKK.L
424 - 432	1106.4839	1105.4766	1105.5689	-0.0923	0	K.MLLQELSEK.L Oxidation (M)
433 - 451	2207.9756	2206.9683	2207.0813	-0.1130	1	K.LELAEQALASKQLQMD EMK.Q 2 Oxidation (M)
444 - 456	1595.7528	1594.7455	1594.7695	-0.0239	1	K.QLQMD EMK QTLAK.Q 2 Oxidation (M)
493 - 504	1352.8967	1351.8894	1351.8438	0.0456	0	K.EQLALQLAILLK.E

505 - 524 2398.9629 2397.9556 2397.9947 -0.0391 1 K.ENNDIEEGGSRQSLMEMQCR.H Oxidation (M)

525 - 541 2009.8732 2008.8659 2008.9351 -0.0692 1 R.HGARTSDSDQQTLYLFQR.G

529 - 541 1588.7577 1587.7504 1587.7165 0.0339 0 R.TSDSDQQTLYLFQR.G

No match to: 905.5707, 909.0805, 921.5553, 927.5970, 937.3596, 940.6241, 948.5937, 951.6169, 958.5980, 966.4921, 971.6208, 982.4810, 985.5621, 1000.5552, 1002.5654, 1016.5394, 1028.1285, 1034.1306, 1044.0916, 1045.5579, 1052.0907, 1066.0525, 1072.0604, 1082.0201, 1088.0214, 1089.5052, 1095.5134, 1102.5315, 1118.4998, 1125.4321, 1128.4515, 1135.5459, 1141.4863, 1147.5325, 1158.5011, 1165.4845, 1173.5006, 1179.4980, 1191.4924, 1193.4980, 1201.4846, 1204.4799, 1218.4396, 1232.9685, 1254.9592, 1260.9625, 1265.4901, 1272.4257, 1276.9214, 1284.4333, 1292.8861, 1300.3650, 1307.4867, 1314.5107, 1320.3889, 1329.4707, 1336.4694, 1349.4595, 1354.4874, 1365.4272, 1379.4498, 1383.4741, 1390.5297, 1427.6563, 1434.7395, 1436.7767, 1450.8282, 1460.7836, 1469.8635, 1475.7855, 1487.8534, 1489.8929, 1496.7183, 1507.8619, 1517.7562, 1521.7742, 1524.7744, 1531.8385, 1544.0955, 1546.7988, 1549.8367, 1555.8242, 1562.8391, 1567.7212, 1593.7611, 1604.8420, 1630.7719, 1634.8572, 1638.7939, 1654.7887, 1657.7257, 1665.7529, 1669.7816, 1679.8275, 1695.7725, 1699.7306, 1707.6775, 1716.7540, 1724.7339, 1734.7012, 1741.6987, 1749.7036, 1762.7223, 1764.6439, 1766.6727, 1780.7083, 1791.6187, 1794.7073, 1804.7271, 1818.6827, 1832.7252, 1837.8167, 1851.8071, 1881.7748, 1890.8231, 1908.8248, 1932.8372, 1937.7863, 1940.8190, 1948.7841, 1959.7677, 1968.7468, 1979.8418, 1987.8240, 1993.8477, 2001.8467, 2019.8746, 2030.7764, 2050.8772, 2063.8840, 2082.8574, 2094.9287, 2135.9763, 2166.9639, 2184.0017, 2193.9695, 2221.0344, 2225.0249, 2233.9998, 2248.9900, 2263.0449, 2266.0327, 2280.0552, 2283.0945, 2296.1096, 2298.1040, 2307.0789, 2319.0457, 2342.9526, 2354.1489, 2367.1868, 2383.9124, 2420.1731, 2447.1462, 2458.1929, 2462.2109, 2480.2214, 2487.1929, 2503.1978, 2511.1895, 2525.1892, 2565.2463, 2584.2686, 2637.3157, 2648.4006, 2658.4504, 2663.4675, 2680.4475, 2690.4602, 2705.3086, 2737.4636, 2746.5803, 2756.5166, 2780.6328, 2814.6033, 2872.6624, 2902.7068, 2932.8232, 3053.0461



28 T-complex protein 1 subunit theta

Number of mass values searched: **100**

Number of mass values matched: **10**

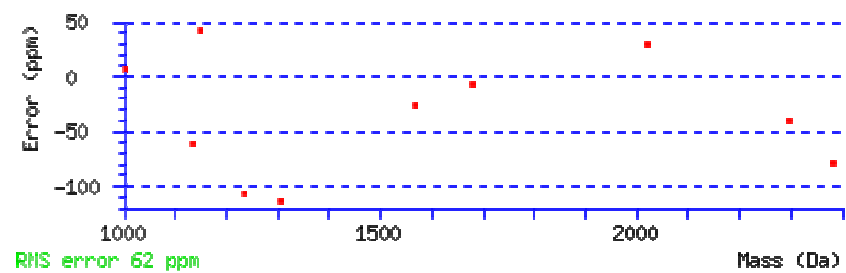
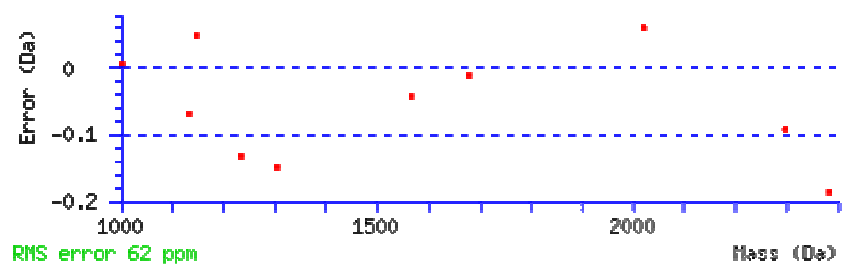
Sequence Coverage: **18%**

Matched peptides shown in **Bold Red**

1 MALHVPKAPG FAQMLK**DGAK HFSGLEEAVY RNIQACK**ELA QTTRTAYGPN
51 GMNK**MVINRL E**KLFVTNDAA TILRELEVQH PAAKMIVMAS HMQEQEVGDG
101 TNFVLVFAGA LLELAEELLR IGLSVSEVIS GYEIACKKAH EILPELVCCS
151 AKNLR**DVDEV S**LLRTSIMS KQYGSETFLA KLIAQACVSI FPDSGNFNVD
201 NIR**VCKILGS GIYSSSVLHG MVFK**KETEGD VTSVKDAKIA VYSCPFDGMI
251 TETKGTVLIK **TAEELMNFSK GEENLMDAQV K**AIAGTGANV IVTGGKVADI
301 ALHYANKYNI MLVRLNSKWD LRRLCKTVGA TALPKLTPPV QEEMGHCDVS
351 YLSEVGDTQV VVFK**HEKEDG AISTIVLR**GS TDNLMDDIER AVDDGVNTFK
401 VLTRDKRLVP GGGATEIELA KQITSYGETC PGLEQYAIKK FAEAFEAIPIR
451 ALAENSGVKA NEVISKLYSV HQEGNKNVGL DIEAEVPAVK DMLEASILDT
501 YLGKYWAIKL ATNAAVTVLR VDQIIMAKPA GGPKPPSGK **DWDDQND**

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
17 - 31	1678.8062	1677.7989	1677.8111	-0.0121	1	K.DGAKHFSGLEEAVYR.N
21 - 31	1307.4884	1306.4811	1306.6306	-0.1495	0	K.HFSGLEEAVYR.N
21 - 37	2022.0480	2021.0407	2020.9789	0.0619	1	K.HFSGLEEAVYRNIQACK.E
55 - 62	1002.5833	1001.5760	1001.5692	0.0069	1	K.MVINRLEK.L
156 - 165	1132.5157	1131.5084	1131.5772	-0.0687	0	R.DVDEVSSLLR.T
204 - 224	2298.1067	2297.0994	2297.1912	-0.0918	1	R.VCKILGSGIYSSSVLHGMVFK.K Oxidation (M)
261 - 281	2383.9243	2382.9170	2383.1035	-0.1865	1	K.TAEELMNFSKGEENLMDAQVK.A
271 - 281	1233.4465	1232.4392	1232.5707	-0.1315	0	K.GEENLMDAQVK.A
365 - 378	1567.8021	1566.7948	1566.8365	-0.0417	1	K.HEKEDGAISTIVLR.G
540 - 548	1150.4767	1149.4694	1149.4211	0.0484	1	K.KDWDDQND.-

No match to: 903.4845, 909.6007, 914.0999, 917.3636, 923.5176, 926.6054, 931.5978, 937.6195, 940.5468, 946.4162, 951.6740, 959.5707, 968.6669, 974.5239, 985.6049, 996.6190, 1018.2043, 1034.1799, 1045.5566, 1058.5337, 1083.6200, 1089.5247, 1106.4917, 1120.5242, 1142.5009, 1158.5245, 1165.5437, 1168.5566, 1175.5459, 1179.5264, 1191.5353, 1211.4087, 1228.5679, 1277.4966, 1314.5474, 1339.5243, 1353.9208, 1383.5035, 1398.5668, 1436.7914, 1475.8124, 1489.9166, 1492.9401, 1507.8480, 1514.5111, 1527.8988, 1530.7917, 1540.8794, 1549.8435, 1555.7957, 1572.7806, 1604.8276, 1638.7740, 1662.7578, 1670.7924, 1695.7520, 1707.7102, 1716.7864, 1747.6344, 1766.6891, 1779.6744, 1791.6260, 1794.7206, 1912.7236, 1939.8043, 1993.8506, 2050.0449, 2082.8477, 2094.9128, 2151.2603, 2192.9849, 2204.1514, 2222.2061, 2225.0278, 2265.0745, 2280.0725, 2283.0913, 2397.5723, 2421.1868, 2440.0955, 2446.1802, 2448.1743, 2456.7959, 2502.2224, 2637.3740, 2658.4514, 2688.3926, 2705.3130, 2746.5662, 2780.6248



29 T-complex protein 1 subunit theta

Number of mass values searched: **75**

Number of mass values matched: **10**

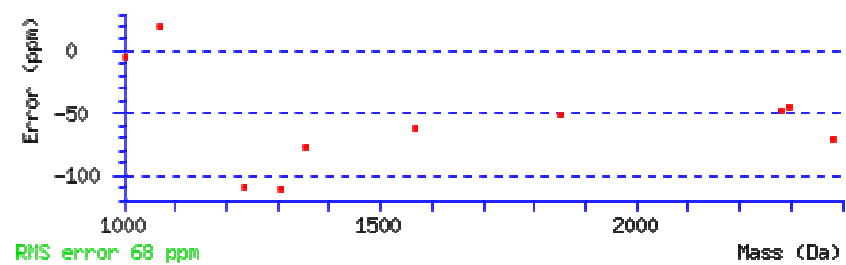
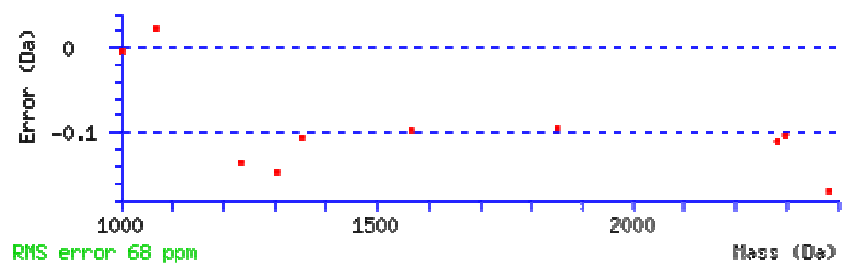
Sequence Coverage: **19%**

Matched peptides shown in **Bold Red**

1 MALHVPKAPG FAQMLKDGAK **HFSGLEEAVY RNIQACKELA QTTRTAYGPN**
51 **GMNKMVINRL E**KLFVTNDAA TILRELEVQH PAAKMIVMAS HMQEQEVGDG
101 TNFVLVFAGA LLELAEELLR IGLSVSEVIS GYEIACKKAH EILPELVCCS
151 AKNLRDDEV SLLRRTSIMS KQYGSETFLA KLIAQACVSI FPDGNGFNVD
201 NIR**VCKILGS GIYSSSVLHG MVFK**KETEGD VTSVKDAKIA VYSCPFDGMI
251 TETKGTVLIK **TAEELMNFSK GEENLMDAQV K**AIAGTGANV IVTGGKVADI
301 ALHYANKYNI MLVRLNSKWD LRRLCKTVGA TALPKLTPPV QEEMGHCDV
351 YLSEVGDQV VVFK**HEKEDG AISTIVLR**GS TDNLMDDIER AVDDGVNTFK
401 VLTRDKR**LVP GGGATEIELA K**QITSYGETC PGLEQYAIKK FAEAFEIPR
451 ALAENSGVKA NEVISKLYSV HQEGNKNVGL DIEAEVPAVK DMLEASILD
501 YLGKYWAIKL ATNAAVTVLR VDQIIMAKPA GGPKPPSGKK DWDDQND

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
21 - 31	1307.4912	1306.4839	1306.6306	-0.1467	0	K.HFSGLEEAVYR.N
38 - 54	1851.8079	1850.8006	1850.8945	-0.0938	1	K.ELAQTTRTAYGPNGMNK.M
45 - 54	1068.4998	1067.4925	1067.4706	0.0219	0	R.TAYGPNGMNK.M Oxidation (M)
55 - 62	1002.5713	1001.5640	1001.5692	-0.0051	1	K.MVINRLEK.L
204 - 224	2282.0938	2281.0865	2281.1963	-0.1098	1	R.VCKILGSGIYSSSVLHGMVFK.K
204 - 224	2298.0955	2297.0882	2297.1912	-0.1030	1	R.VCKILGSGIYSSSVLHGMVFK.K Oxidation (M)
261 - 281	2383.9404	2382.9331	2383.1035	-0.1704	1	K.TAEELMNFSKGEENLMDAQVK.A
271 - 281	1233.4418	1232.4345	1232.5707	-0.1362	0	K.GEENLMDAQVK.A
365 - 378	1567.7476	1566.7403	1566.8365	-0.0962	1	K.HEKEDGAISTIVLR.G
408 - 421	1354.6520	1353.6447	1353.7504	-0.1056	0	R.LVPGGGATEIELAK.Q

No match to: 907.5782, 916.5867, 928.5651, 940.3978, 950.5831, 960.5660, 967.4991, 985.5699, 996.6050, 1030.5259, 1034.1301, 1058.5345, 1066.0612, 1084.4938, 1089.5089, 1106.4717, 1108.4253, 1118.5027, 1141.4895, 1179.4961, 1190.4796, 1242.5585, 1277.5476, 1323.4613, 1339.5430, 1436.7833, 1475.7913, 1489.8870, 1507.8676, 1531.8503, 1549.8436, 1555.8381, 1571.7915, 1578.8353, 1595.7557, 1604.8418, 1638.8225, 1660.7957, 1707.6930, 1716.7474, 1750.7018, 1766.6682, 1780.6915, 1791.6464, 1794.6968, 1837.8099, 1880.8088, 1940.7992, 1993.8545, 2149.9670, 2192.9636, 2225.0176, 2233.9995, 2266.0496, 2284.0867, 2399.0337, 2421.1829, 2447.1570, 2487.1753, 2501.2361, 2510.1641, 2527.1545, 2636.3198, 2705.3054, 2780.1462



32 Tubulin alpha-1C chain

Number of mass values searched: **80**

Number of mass values matched: **11**

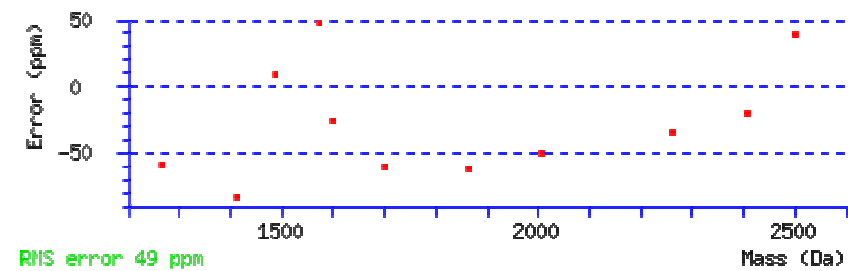
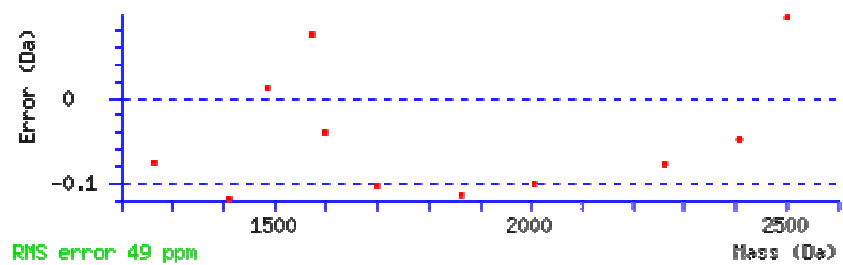
Sequence Coverage: **32%**

Matched peptides shown in **Bold Red**

1 MRECISIHVG QAGVQIGNAC WELYCLEHGI QPDGQMPSDK **TIGGGDDSF**
51 **TFFSETGAGK** HVPR**AVFVDL EPTVIDEVRT** GTYR**QLFHPE QLITGK**EDAA
101 NNYARGHYTI GKEIIDLVLDRIRKLADQCT GLQGFLVFHS FGGGTGSGFT
151 SLLMERLSVD YGKSKLEFS IYPAPQVSTA VPEPNSILT THTTLEHSDC
201 AFMVDNEAIY DICRRNLIDIE RPTYTNLNR**L ISQIVSSITA SLRFDGALNV**
251 **DLTEFQTNLV PYPRI**HFPLA TYAPVISA EK AYHEQLTVAE ITNACFEPAN
301 QMVKCDPR**HG KYMACCLLYR** GDVVPKDVNA AIATIKTKRT **IQFVDWCPTG**
351 **FKVGINYQPP** TVVPGDLAK **VQRAVCMLSN TTAIAEAWAR** LDHKFDLMYA
401 **KRAVHWYVG EGMEEGEFSE** AREDMAALEK DYEEVGADSA EGDDEGEEY

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
41 - 60	2007.7927	2006.7854	2006.8858	-0.1004	0	K.TIGGGDDSFNTFFSETGAGK.H
65 - 79	1701.8024	1700.7951	1700.8985	-0.1034	0	R.AVFVDLEPTVIDEVR.T
85 - 96	1410.6558	1409.6485	1409.7667	-0.1182	0	R.QLFHPEQLITGK.E
230 - 243	1487.8921	1486.8848	1486.8719	0.0130	0	R.LISQIVSSITASLR.F
244 - 264	2409.1606	2408.1533	2408.2012	-0.0479	0	R.FDGALNVDLTEFQTNLVYPYR.I
309 - 320	1571.8037	1570.7964	1570.7207	0.0758	1	R.HGKYMACCLLYR.G
312 - 320	1265.4728	1264.4655	1264.5403	-0.0747	0	K.YMACCLLYR.G Oxidation (M)
340 - 352	1598.7268	1597.7195	1597.7599	-0.0404	0	R.TIQFVDWCPTGFK.V
371 - 390	2264.0483	2263.0410	2263.1201	-0.0791	1	K.VQRAVCMLSN TTAIAEAWAR.L Oxidation (M)
374 - 390	1864.7892	1863.7819	1863.8971	-0.1152	0	R.AVCMLSN TTAIAEAWAR.L
402 - 422	2502.2117	2501.2044	2501.1070	0.0974	1	K.RAVHWYVVGEGMEEGEFSEAR.E Oxidation (M)

No match to: 908.5254, 918.5627, 924.5997, 985.5692, 1002.5760, 1031.5425, 1045.5627, 1058.5288, 1066.0055, 1082.0209, 1089.5013, 1106.4861, 1118.5035, 1141.4821, 1179.4958, 1233.4601, 1277.5382, 1300.3666, 1307.4841, 1320.4042, 1339.5182, 1354.3706, 1383.4714, 1393.5574, 1436.7714, 1475.7825, 1489.8914, 1507.8574, 1531.8452, 1549.8359, 1555.8304, 1578.8325, 1585.7266, 1604.8329, 1638.7928, 1657.7408, 1699.7365, 1716.7765, 1750.7057, 1763.6901, 1766.6666, 1780.6897, 1791.6418, 1794.6980, 1816.7054, 1837.8192, 1851.8066, 1940.7971, 1993.8508, 2149.9614, 2166.9902, 2193.9646, 2225.0181, 2236.0193, 2248.9897, 2281.0718, 2284.0845, 2298.0935, 2307.0745, 2342.9438, 2354.1311, 2368.1770, 2383.9070, 2399.0447, 2421.1721, 2448.1523, 2487.1663, 2510.1582, 2705.2986



33 Na(+)/H(+) exchange regulatory cofactor NHE-RF3

Number of mass values searched: **200**

Number of mass values matched: **14**

Sequence Coverage: **38%**

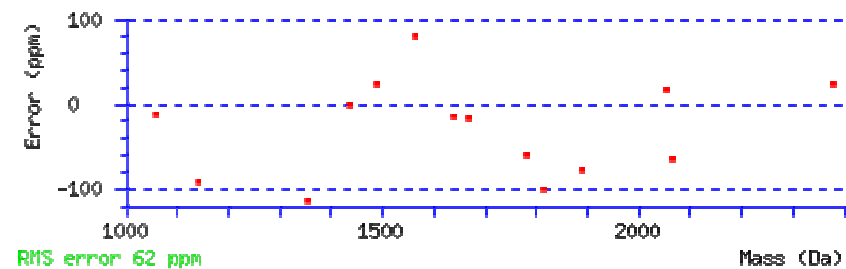
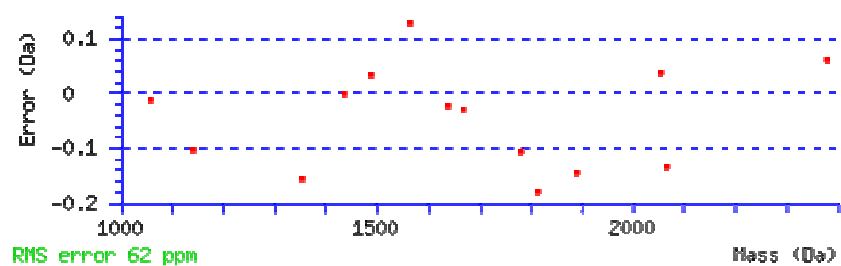
Matched peptides shown in **Bold Red**

1 MASTFNPREC KLSKQEGQNY GFFLRIEKDT DGHLR**VIEE GSPA**EKAGL
51 DGDRVLRING VFVDK**EEHAQ VVELVRK**SGN SVTLLVLDGD SYEKAVKNQV
101 DLKELDQSQR EAALNDK**KPG PGMNGAVEPC AQPR**LCYLVK EGNSFGFSLK
151 TIQGGK**GVYL TDIMPQGVAM** KAGVLADDHL IEVNGENVEN ASHEEVVEKV
201 TKSGSRIMFL LVDKETARCH SEQKTQFKR**E TASLKLPHQ PR**VVVIKKG
251 NGYGFYLRAG PEQKQGI**KD IEPGSPAEAA GLKNNDLVVA VNGKSVEALD**
301 **HDGVMIRK GGDQTTLLVL DKEAESIYSL ARFSPLLYCQ SQELPNGSVK**
351 EGPAPIPAPL EATGSEPTED AEGHKPKLCR **LLKEDDSYGF HLN**AIRGQPG
401 SFVKEVQQGG PADKAGLENE DVIIENVGEN VQEEPYDRVV ERIKSSGKHV
451 TLLVCGKMAY SYFQAKKIPI VSSMAEPLVA GPDEK**GETSA ESEHDAHPAK**
501 **DRTLSTASHS SSNSEDEM**

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
37 - 46	1058.5238	1057.5165	1057.5291	-0.0126	0	R.VIEEGSPA EK.A
66 - 77	1436.7830	1435.7757	1435.7783	-0.0026	1	K.EEHAQ VVELVRK.S
118 - 134	1781.7338	1780.7265	1780.8349	-0.1083	0	K.KPGPGMNGAVE PCAQPR.L Oxidation (M)
157 - 171	1638.8008	1637.7935	1637.8157	-0.0222	0	K.GVY LT DIMPQGV AMK.A Oxidation (M)
230 - 242	1489.8829	1488.8756	1488.8412	0.0344	1	R.ETAS LKLPHQPR.V
270 - 283	1354.5294	1353.5221	1353.6776	-0.1555	0	K.DIEPG SPAEAGLK.N
284 - 294	1142.5112	1141.5039	1141.6091	-0.1052	0	K.NNDLV AVNGK.S
295 - 309	1669.7921	1668.7848	1668.8141	-0.0293	0	K.SVEALD H GD VMIRK.K
295 - 310	1813.7297	1812.7224	1812.9040	-0.1816	1	K.SVEALD H GD VMIRK.G Oxidation (M)
311 - 332	2379.2996	2378.2923	2378.2329	0.0594	1	K.GGDQTTLLVLD K E AESIYSLAR.F
333 - 350	2066.8875	2065.8802	2066.0143	-0.1340	0	R.FSP LLYCQSQELPNGSVK.E
381 - 396	1890.8254	1889.8181	1889.9635	-0.1454	1	R.L L KEDDSYGF HLNAIR.G
486 - 500	1565.8098	1564.8025	1564.6754	0.1272	0	K.G ETSAE SE HDAHPAK.D
501 - 519	2054.8943	2053.8870	2053.8494	0.0376	1	K.D RTLSTASHSSNSEDEM.-

No match to: 901.1133, 908.5714, 911.6043, 914.6609, 917.3698, 924.6140, 927.6000, 931.5827, 937.6345, 940.5879, 948.5957, 951.5875, 959.5490, 968.5900, 973.5757, 982.6072, 985.5664, 993.5540, 996.6175, 1001.5570, 1016.5516, 1030.5267, 1034.1300, 1043.8966, 1045.5582, 1052.0945, 1066.0375, 1072.0677, 1082.0199, 1084.4696, 1088.5137, 1106.4690, 1112.4712, 1118.5055, 1126.4746, 1134.4730, 1148.5146, 1151.6165, 1159.4895, 1165.6309, 1174.4861, 1179.4952, 1189.4838, 1200.5272, 1211.4911, 1217.4574, 1233.4437, 1242.5450, 1254.9388, 1260.9667, 1276.9247, 1277.5347, 1287.5168, 1292.8881, 1302.5234, 1307.4839, 1314.5333, 1320.3954, 1329.4270, 1336.4691, 1339.5406, 1346.5065, 1363.4391, 1379.4639, 1383.4745, 1399.5435, 1410.6777, 1421.6036, 1434.7448, 1443.7487, 1458.7814, 1464.8152, 1469.8550, 1475.7842, 1487.8605, 1497.7684, 1501.7800, 1507.8585, 1515.7827, 1523.8030, 1529.8016, 1531.8464, 1546.8104, 1549.8423, 1562.8223, 1571.7916, 1578.8167, 1587.7784, 1593.7736, 1595.7474, 1604.8442, 1617.7399, 1634.8563, 1650.7681, 1656.8196, 1660.7979, 1676.8202, 1684.8226, 1696.7927, 1699.7695, 1708.6592, 1716.7589,

1724.8221, 1739.7468, 1747.8027, 1757.7690, 1765.6450, 1791.6324, 1794.7020, 1804.7986, 1821.7797, 1837.8213, 1845.8403, 1851.8081, 1859.7900, 1867.8126, 1875.8020, 1880.7917, 1904.9146, 1922.8225, 1940.8094, 1950.8409, 1963.8607, 1978.8130, 1986.9221, 1993.8553, 2007.8785, 2015.8541, 2022.8866, 2035.8585, 2038.8789, 2046.8862, 2082.8784, 2095.9011, 2111.9150, 2136.0010, 2149.9702, 2167.0027, 2170.9412, 2184.0090, 2193.9878, 2202.9524, 2208.9883, 2225.0256, 2234.0066, 2248.9976, 2263.0522, 2265.0510, 2276.0105, 2280.0706, 2283.0940, 2297.1086, 2299.0981, 2308.0706, 2314.0771, 2323.0923, 2343.0044, 2349.1423, 2365.2517, 2383.9211, 2400.1213, 2420.1860, 2447.1692, 2457.1440, 2462.2073, 2482.1704, 2487.1838, 2501.2422, 2509.1665, 2526.1855, 2538.2385, 2548.1907, 2565.2693, 2584.2773, 2609.3159, 2636.3223, 2652.3376, 2663.3923, 2680.4529, 2705.3123, 2720.4355, 2780.6343, 2807.5339, 2872.6697, 2902.7170, 2932.8469



35 ATP synthase subunit beta, mitochondrial

Number of mass values searched: 150

Number of mass values matched: 11

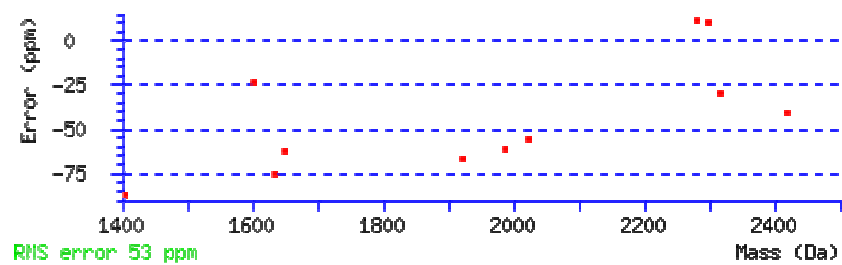
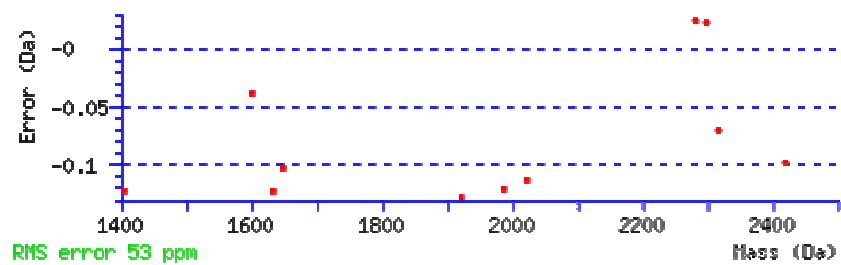
Sequence Coverage: 33%

Matched peptides shown in **Bold Red**

1 MLSLVGRVAS ASASGALR**GL SPSAALPQAQ LLLRAAPAGV** HPARDYAAQA
51 SAAPKAGTAT GRIVAVIGAV VDVQFDEGLP PILNALEVQG RDSR**LVLEVA**
101 **QHLGESTVRT** IAMDGTEGLV RGQKVLDSGA PIK**IPVGPET LGRIMNVIGE**
151 **PIDER**GPIKT KQFAPIHAEA PEFIEMSVEQ EILVTGIKVV DLLAPYAKGG
201 KIGLFGGAGV GKTVLIMELI NNVAK**AHGGY SVFAGVGERT REGNDLYHEM**
251 **IESGVINLKD** ATSK**VALVYG QMNEPPGARA** RVALTGLTVA EYFR**DQEGQD**
301 **VLLFIDNIFR** FTQAGSEVSA LLGR**IPSAVG YQPTLATDMG TMQER**ITTTK
351 KGSITSVQAI YVPADDLTDP APATTF AHL D ATT VLSR**AIA ELGIYPAVDP**
401 **LDSTSR**IMDP NIVGNEHYDV ARGVQKILQD YKSLQDIIAI LGMDELSEED
451 KLT VSRARKI QR**FLSQPFQV AEVFTGHMGK** LVPLKETIKG FQQILAGEYD
501 HLPEQAFYMV GPIEEAVAKA DKLAEEHGS

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
19 - 34	1634.8357	1633.8284	1633.9515	-0.1231	0	R.GLSPSAALPQAQLLLR.A
95 - 109	1650.8141	1649.8068	1649.9101	-0.1032	0	R.LVLEVAQHLGESTVR.T
134 - 155	2421.1833	2420.1760	2420.2733	-0.0973	1	K.IPVGPETLGRIMNVIGEPIDER.G Oxidation (M)
226 - 239	1406.5579	1405.5506	1405.6739	-0.1232	0	K.AHGGYSVFAGVGER.T
240 - 259	2318.0742	2317.0669	2317.1372	-0.0703	1	R.TREGNDLYHEMIESGVINLK.D
265 - 279	1601.7722	1600.7649	1600.8031	-0.0382	0	K.VALVYGMNEPPGAR.A
295 - 310	1921.8376	1920.8303	1920.9581	-0.1278	0	R.DQEGQDVLLFIDNIFR.F
325 - 345	2282.1040	2281.0967	2281.0719	0.0249	0	R.IPSAVGYQPTLATDMGMTQER.I Oxidation (M)
325 - 345	2298.0967	2297.0894	2297.0668	0.0226	0	R.IPSAVGYQPTLATDMGMTQER.I 2 Oxidation (M)
388 - 406	1987.9125	1986.9052	1987.0262	-0.1210	0	R.AIAELGIYPAVDPLDSTSR.I
463 - 480	2022.8986	2021.8913	2022.0033	-0.1120	0	R.FLSQPFQVAEVFTGHMGK.L

No match to: 905.5524, 909.0894, 915.1031, 925.5801, 931.5819, 939.5709, 948.4821, 954.6133, 960.6180, 973.5735, 985.5571, 996.6111, 1000.5480, 1002.5652, 1014.5712, 1029.5225, 1031.5259, 1034.1268, 1044.5376, 1052.0890, 1058.5208, 1066.0096, 1074.4983, 1082.0135, 1089.4995, 1106.4757, 1109.4434, 1118.4940, 1125.4548, 1132.4777, 1143.5135, 1165.4762, 1174.4806, 1179.4897, 1191.4697, 1200.5283, 1218.4364, 1233.4614, 1235.4031, 1242.5333, 1263.4973, 1277.5243, 1300.3578, 1307.4760, 1320.3859, 1328.4631, 1339.5280, 1350.4561, 1358.4130, 1365.4192, 1383.4673, 1391.5226, 1423.5934, 1434.7347, 1436.7789, 1450.7068, 1469.8627, 1475.7740, 1483.7499, 1487.8717, 1489.8762, 1497.7628, 1507.8621, 1523.7787, 1531.8411, 1545.8042, 1549.8362, 1555.8220, 1564.7980, 1571.7869, 1578.8306, 1584.6708, 1593.7664, 1604.8384, 1612.7389, 1620.7694, 1638.7903, 1660.7782, 1679.8124, 1699.7484, 1707.6727, 1716.7605, 1734.7041, 1741.6962, 1750.7225, 1765.6384, 1780.6930, 1791.6174, 1816.7386, 1837.8207, 1851.8060, 1867.7982, 1890.8240, 1929.7091, 1940.8241, 1948.7979, 1965.9093, 1978.8303, 1993.8577, 2050.8840, 2064.8962, 2082.8547, 2094.8911, 2104.9048, 2121.9126, 2135.9971, 2149.9783, 2166.9819, 2184.0085, 2193.9834, 2225.0364, 2234.0144, 2248.9980, 2265.0500, 2284.0964, 2307.0823, 2328.0933, 2342.9661, 2367.1956, 2383.9102, 2399.0439, 2446.1865, 2448.1697, 2477.0652, 2487.1860, 2501.2566, 2510.1638, 2525.1787, 2565.2822, 2584.2910, 2608.3103, 2637.3621, 2647.3782, 2705.3274, 2717.2468, 2746.5898, 2779.6494, 2872.6831, 2932.8726



36 Actin, cytoplasmic 2

Number of mass values searched: **100**

Number of mass values matched: **11**

Sequence Coverage: **35%**

Matched peptides shown in **Bold Red**

1 MEEEIALVI DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK

51 DSYVGDEAQS KRGILTLKYP IEHGIVTNWD DMEKI**IWHHTF YNELRVAPEE**

101 HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRRTTG

151 IVMDSGDGVT HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTER**GYSF**

201 TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEK**SY ELPDGGQVITI**

251 GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMK**CDVDIR** KDLYANTVLS

301 GGTTMYPGIA DRMQKEITAL APSTMKIKI**II APPERK**YSVW IGGASILASLS

351 TFQQMWISKQ EYDESGPSIV HRKCF

Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence

1 - 18 1966.9277 1965.9204 1965.8846 0.0359 0 -.MEEEIALVIDNNGSGMCK.A

2 - 18 1851.8008 1850.7935 1850.8390 -0.0455 0 M.EEEIALVIDNNGSGMCK.A Oxidation (M)

19 - 28 976.5035 975.4962 975.4410 0.0552 0 K.AGFAGDDAPR.A

29 - 50 2367.1882 2366.1809 2366.2464 -0.0655 1 R.AVFPSIVGRPRHQGVMVGMGQK.D Oxidation (M)

51 - 62 1354.4746 1353.4673 1353.6161 -0.1487 1 K.DSYVGDEAQSQR.G

85 - 95 1515.7522 1514.7449 1514.7419 0.0031 0 K.IWHHTFYNELR.V

96 - 113 1953.9238 1952.9165 1953.0571 -0.1406 0 R.VAPEEHPVLLTEAPLNPK.A

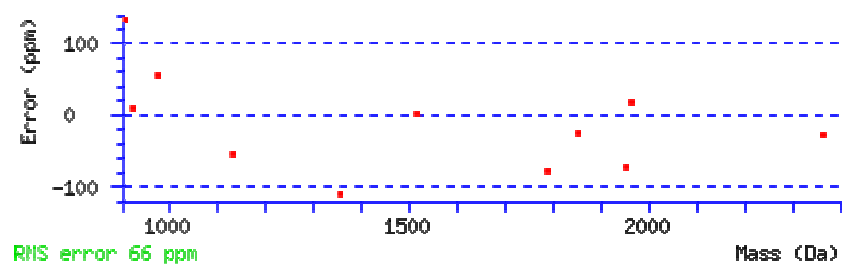
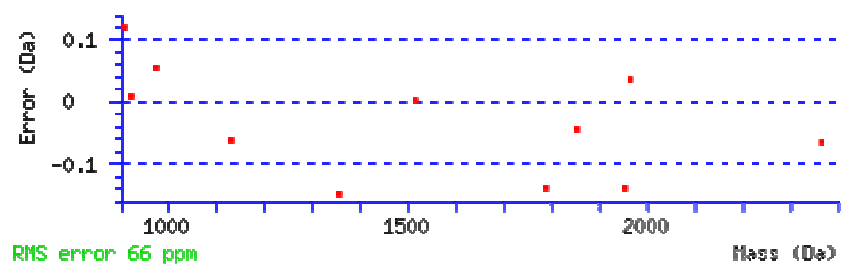
197 - 206 1132.4652 1131.4579 1131.5197 -0.0617 0 R.GYSFTTTAER.E

239 - 254 1790.7531 1789.7458 1789.8846 -0.1388 0 K.SYELPDGGQVITIGNER.F

285 - 291 905.5710 904.5637 904.4436 0.1201 1 K.CDVDIRK.D

329 - 336 923.5768 922.5695 922.5600 0.0096 1 K.IIAPPERK.Y

No match to: 917.3767, 931.5898, 945.6192, 985.5609, 1002.5698, 1031.5394, 1037.5315, 1058.5272, 1066.0588, 1074.5096, 1089.5066, 1106.4851, 1109.4447, 1118.4989, 1140.4943, 1146.4983, 1165.5144, 1179.4995, 1193.4938, 1233.4679, 1265.4828, 1277.5339, 1300.3643, 1307.4846, 1320.3923, 1339.5159, 1365.4257, 1383.4674, 1436.7675, 1458.7489, 1469.8444, 1475.7804, 1489.8773, 1499.7246, 1507.8542, 1530.7775, 1549.8347, 1555.8295, 1572.7610, 1585.7434, 1604.8217, 1638.7875, 1650.7477, 1657.7257, 1668.7687, 1699.7355, 1707.6758, 1716.7515, 1750.7168, 1765.6458, 1780.7003, 1804.7816, 1818.7646, 1837.8140, 1890.8258, 1940.8079, 1976.8044, 1993.8456, 2022.8876, 2046.9150, 2063.8982, 2082.8555, 2135.9780, 2149.9624, 2166.9753, 2170.9097, 2183.9902, 2193.9617, 2225.0110, 2239.0396, 2264.0432, 2282.0830, 2284.0752, 2298.0876, 2307.0574, 2329.0823, 2342.9634, 2353.1187, 2383.9272, 2399.0388, 2421.1665, 2448.1484, 2487.1716, 2501.2319, 2510.1465, 2565.2461, 2705.2925, 2872.6494, 2902.6919



37 Actin, cytoplasmic 2

Number of mass values searched: 100

Number of mass values matched: 13

Sequence Coverage: 45%

Matched peptides shown in **Bold Red**

1 MEEEIALVI DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK

51 DSYVGDEAQS KRGILTLKYP IEHGIVTNWD DMEKIWHHTF YNELRVAPEE

101 HPVLLTEAPL NPKANREKMT QIMFETFNTF AMYVAIQAVL SLYASGRRTG

151 IVMDSGDGVT HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF

201 TTTAEREIVR DIKEKLCYVA LDFAQEMATA ASSSSLEKSY ELPDQGVITI

251 GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIR KDLYANTVLS

301 GGTTMYPGIA DRMQKEITAL APSTMKIKII APPERKYSVW IGGSSILASLS

351 TFQMWISKQ EYDESGPSIV HRKCF

Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence

2 - 18 1851.8005 1850.7932 1850.8390 -0.0458 0 M.EEEEIALVIDNNGSGMCK.A Oxidation (M)

19 - 28 976.4955 975.4882 975.4410 0.0472 0 K.AGFAGDDAPR.A

29 - 50 2367.1956 2366.1883 2366.2464 -0.0581 1 R.AVFPSIVGRPRHQGVMVGMGQK.D Oxidation (M)

51 - 61 1198.5729 1197.5656 1197.5150 0.0507 0 K.DSYVGDEAQS.R

85 - 95 1515.7509 1514.7436 1514.7419 0.0018 0 K.IWHHTFYNELR.V

96 - 113 1953.9336 1952.9263 1953.0571 -0.1308 0 R.VAPEEHPVLLTEAPLNPK.A

197 - 206 1132.4548 1131.4475 1131.5197 -0.0721 0 R.GYSFTTTAER.E

197 - 210 1629.7585 1628.7512 1628.8158 -0.0646 1 R.GYSFTTTAEREIVR.D

239 - 254 1790.7743 1789.7670 1789.8846 -0.1176 0 K.SYELPDQGVITIGNER.F

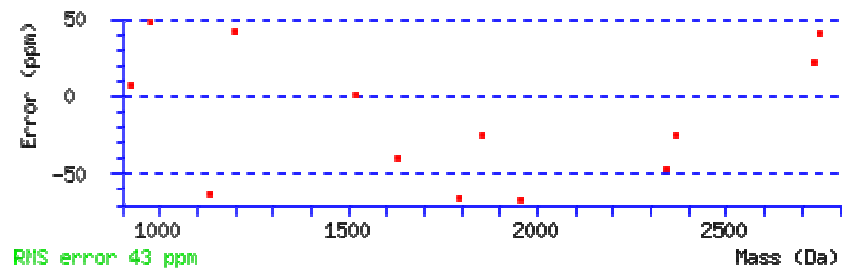
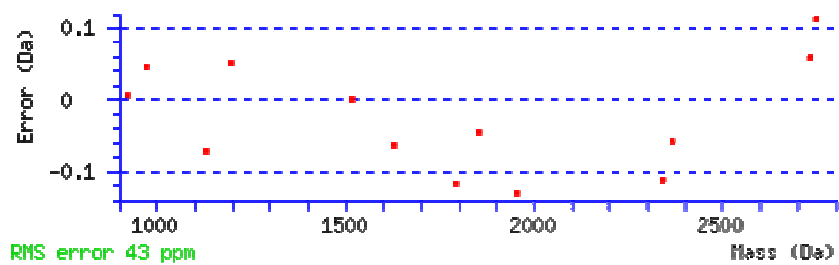
291 - 312 2343.0542 2342.0469 2342.1576 -0.1107 1 R.KDLYANTVLSGGTTMYPGIADR.M

329 - 336 923.5739 922.5666 922.5600 0.0067 1 K.IIAPPERK.Y

336 - 359 2730.4917 2729.4844 2729.4251 0.0593 1 R.KYSVWIGGSILASLSTFQMWISK.Q

336 - 359 2746.5398 2745.5325 2745.4200 0.1125 1 R.KYSVWIGGSILASLSTFQMWISK.Q Oxidation (M)

No match to: 917.3724, 939.5619, 945.6207, 985.5630, 1002.5779, 1031.5399, 1034.1315, 1052.0922, 1058.5299, 1066.0375, 1082.0219, 1089.5099, 1106.4863, 1118.5023, 1146.4673, 1173.4857, 1179.5001, 1191.4811, 1233.4624, 1277.5342, 1307.4811, 1339.5308, 1354.4152, 1383.4702, 1436.7849, 1469.8282, 1475.7855, 1489.8884, 1499.7125, 1507.8599, 1522.7866, 1530.7708, 1541.7664, 1549.8402, 1555.8234, 1567.7527, 1570.7733, 1572.7539, 1585.7472, 1593.7589, 1604.8262, 1638.7769, 1657.7314, 1667.7871, 1699.7456, 1707.6962, 1716.7518, 1750.7144, 1763.6980, 1766.6692, 1780.6940, 1798.7358, 1804.7903, 1818.7875, 1837.8248, 1940.8059, 1961.7987, 1976.7983, 1993.8580, 2010.9443, 2024.9524, 2063.9082, 2124.9839, 2166.9883, 2193.9822, 2211.0081, 2225.0281, 2233.9985, 2248.9839, 2258.0037, 2263.0542, 2281.0789, 2283.0979, 2297.1096, 2312.0527, 2336.1304, 2353.1643, 2383.9463, 2400.1440, 2421.1865, 2448.1748, 2487.1909, 2503.1958, 2510.1772, 2565.2488, 2705.3325, 2779.6531



38 Actin, cytoplasmic 2

Number of mass values searched: **250**

Number of mass values matched: **15**

Sequence Coverage: **46%**

Matched peptides shown in **Bold Red**

1 MEEEEIALVI DNGSGMCKAG FAGDDAPRAV FPSIVGRPRH QGVMVGMGQK

51 DSYVGDEAQS KRGILTLKYP IEHGIVTNWD DMEKIWHHTF YNELRVAPEE

101 HPVLLTEAPL NPKANREKMT QIMFETFNTP AMYVAIQAVL SLYASGRRTTG

151 IVMDSGDGVT HTVPIYEGYA LPHAILRLDL AGRDLTDYLM KILTERGYSF

201 TTTAEREIVR DIKEKLCYVA LDFEQEMATA ASSSSLEKSY ELPDQGVITI

251 GNERFRCPEA LFQPSFLGME SCGIHETTFN SIMKCDVDIRK KDLYANTVLS

301 GGTTMYPGIA DRMQKEITAL APSTMKIKII APPERKYSVW IGGSSILASLS

351 TFQQMWISKQ EYDESGPSIV HRKCF

Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence

2 - 18 1851.7750 1850.7677 1850.8390 -0.0713 0 M.EEEEIALVIDNNGSGMCK.A Oxidation (M)

19 - 28 976.5033 975.4960 975.4410 0.0550 0 K.AGFAGDDAPR.A

29 - 50 2367.1863 2366.1790 2366.2464 -0.0674 1 R.AVFPSIVGRPRHQGVMVGMGQK.D Oxidation (M)

40 - 50 1171.4414 1170.4341 1170.5638 -0.1297 0 R.HQGMVGMGQK.D

51 - 61 1198.5778 1197.5705 1197.5150 0.0556 0 K.DSYVGDEAQS.R

85 - 95 1515.7467 1514.7394 1514.7419 -0.0024 0 K.IWHHTFYNELR.V

96 - 113 1953.9526 1952.9453 1953.0571 -0.1118 0 R.VAPEEHPVLLTEAPLNPK.A

197 - 206 1132.4542 1131.4469 1131.5197 -0.0727 0 R.GYSFTTTAER.E

216 - 238 2566.2676 2565.2603 2565.1614 0.0989 0 K.LCYVALDFEQEMATAASSSSLEK.S Oxidation (M)

239 - 254 1790.7737 1789.7664 1789.8846 -0.1182 0 K.SYELPDQGVITIGNER.F

285 - 291 905.5814 904.5741 904.4436 0.1305 1 K.CDVDIRK.D

329 - 336 923.4128 922.4055 922.5600 -0.1544 1 K.IIAPPERK.Y

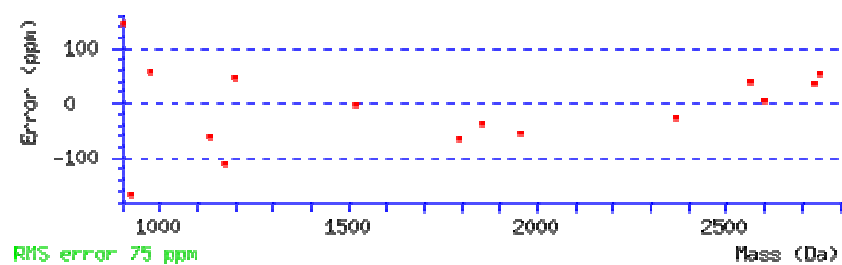
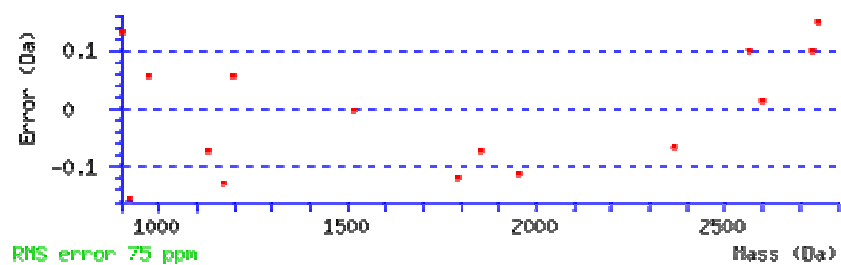
336 - 359 2730.5300 2729.5227 2729.4251 0.0976 1 R.KYSVWIGGSILASLSTFQQMWISK.Q

336 - 359 2746.5745 2745.5672 2745.4200 0.1472 1 R.KYSVWIGGSILASLSTFQQMWISK.Q Oxidation (M)

337 - 359 2602.3499 2601.3426 2601.3301 0.0125 0 K.YSVWIGGSILASLSTFQQMWISK.Q

No match to: 909.0821, 910.6542, 916.2701, 917.3735, 929.5222, 931.5948, 937.5298, 939.2963, 945.6109, 951.5923, 957.6073, 959.3074, 965.5639, 971.5142, 972.6075, 982.5092, 985.5591, 991.5764, 994.5756, 996.6179, 1001.5535, 1010.5839, 1016.5480, 1028.1166, 1031.5308, 1034.1249, 1044.0757, 1052.0887, 1058.5199, 1066.0531, 1072.0603, 1082.0171, 1087.5267, 1089.4939, 1097.9817, 1103.9908, 1108.4274, 1116.5415, 1118.4916, 1125.9559, 1126.4990, 1128.4121, 1140.5013, 1142.4966, 1146.4915, 1158.4742, 1163.4899, 1173.5012, 1179.4994, 1189.4633, 1207.5148, 1218.4438, 1228.5490, 1233.4381, 1239.9861, 1246.9977, 1253.4203, 1254.9530, 1260.9611, 1267.5177, 1272.5388, 1276.9276, 1283.5468, 1290.5457, 1292.8822, 1300.6512, 1301.5519, 1307.4801, 1314.6180, 1321.3818, 1329.4819, 1339.5326, 1346.6118, 1349.4121, 1353.6548, 1360.5272, 1365.4242, 1374.4862, 1382.4597, 1384.6104, 1391.5685, 1395.5759, 1404.6809, 1414.6301, 1421.7035, 1436.7958, 1443.7649, 1456.7340, 1470.8674, 1475.7909, 1482.8859, 1487.8823, 1489.8833, 1496.9457, 1499.7031, 1507.8585, 1514.7083, 1522.8020, 1528.7544, 1530.7850, 1541.8000, 1546.8113, 1549.8422, 1555.8303, 1562.8384, 1567.7527, 1571.7878, 1578.8257, 1585.7603, 1586.7407, 1593.7584, 1600.7808, 1604.8536, 1621.8190, 1625.8265, 1634.8451, 1638.7969, 1648.7847, 1655.7625, 1656.7556, 1660.7909, 1668.7802, 1678.0001, 1680.8325, 1692.9631, 1698.7975, 1707.6564, 1716.7670, 1725.0187, 1727.8434, 1735.6885, 1745.7808, 1748.7275, 1757.6740, 1762.7794, 1764.6646, 1766.6793, 1774.7275, 1780.7104, 1798.7155, 1804.7957, 1813.7621, 1818.7836, 1827.7788, 1833.7671, 1845.8954, 1861.8674, 1879.7516, 1881.6776, 1893.7699, 1902.9071, 1911.7754, 1920.8662,

1931.8037, 1940.7826, 1949.7595, 1961.8171, 1967.9729, 1975.8000, 1981.9543, 1990.8215, 1993.8535, 2005.8661, 2014.0667, 2022.9130, 2031.8695, 2046.8937, 2050.9282, 2059.9458, 2064.8601, 2073.9636, 2092.9763, 2106.9063, 2126.0027, 2141.9375, 2149.9966, 2168.0037, 2193.9941, 2206.0735, 2222.0403, 2225.0420, 2234.0034, 2245.0117, 2248.9875, 2258.0112, 2263.0417, 2265.0530, 2279.0862, 2282.0947, 2284.0986, 2298.1123, 2307.0996, 2319.0984, 2322.0830, 2336.1248, 2345.1277, 2354.1375, 2383.9250, 2394.1245, 2400.1650, 2418.1692, 2421.1926, 2431.1243, 2446.1794, 2448.1731, 2457.2617, 2461.0513, 2473.0151, 2481.1697, 2487.1907, 2503.1929, 2512.2229, 2524.2000, 2536.2559, 2545.2622, 2579.3738, 2583.2068, 2592.2300, 2607.2407, 2610.3372, 2626.3176, 2636.3357, 2652.3982, 2679.4387, 2689.4709, 2705.3220, 2720.4531, 2737.5232, 2772.5203, 2778.1143, 2780.6287, 2807.5474, 2871.6504, 2914.8303, 3033.9370



40 Homer protein homolog 1

Number of mass values searched: 200

Number of mass values matched: 11

Sequence Coverage: 31%

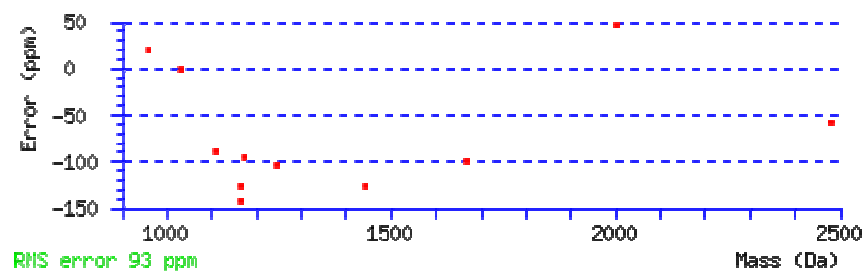
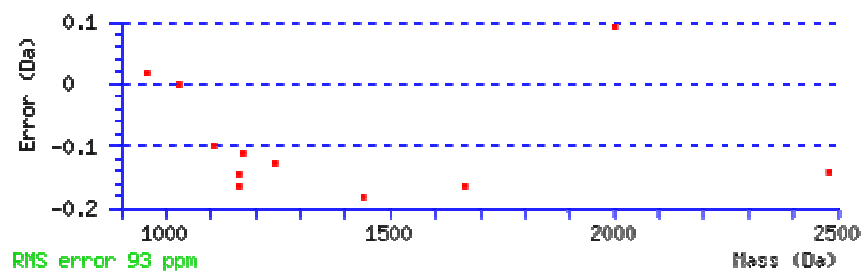
Matched peptides shown in **Bold Red**

1 MGEQPIFSTR AHVFQIDPNT **KKNWVPTSKH** AVTVSYFYDS TRNVYRIISI
51 DGSKAIINST ITPNMTFTKT SQKFGQWADS RANTVYGLGF SSEHLSKFA
101 EKQEFKEAA RLAKEKSQEK MELTSTPSQE SAGGDLQSPL TPESINGTDD
151 ERTPDVTQNS EPRAEPTQNA LPFPHSAGDR TQALSHASSA ISKHWEAELA
201 TLKGNNAKLT AALLESTANV KQWKQQLAAY QEEAERLHKR VTELECVSSQ
251 ANAVHSHKTE LNQTVQELEE TLKVKEEIE RLKQEIDNAR ELQEQRDSL
301 QKLQEVEIRN KDLEGQLSDL EQRLEK**SQNE QEAFRSNLKT LLEILDGKIF**
351 ELTELRDNLAKLLECS

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
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1 - 10	1165.4011	1164.3938	1164.5597	-0.1659	0	-.MGEQPIFSTR.A
22 - 29	959.5496	958.5423	958.5236	0.0187	1	K.KNWVPTSK.H
47 - 69	2481.1843	2480.1770	2480.3196	-0.1426	1	R.IISLDGSKAIINSTITPNMTFTK.T Oxidation (M)
55 - 69	1667.7024	1666.6951	1666.8600	-0.1649	0	K.AIINSTITPNMTFTK.T Oxidation (M)
99 - 107	1173.4816	1172.4743	1172.5866	-0.1123	1	K.FAEKFQEFK.E
153 - 163	1243.4626	1242.4553	1242.5840	-0.1287	0	R.TPDVTQNSEPR.A
259 - 275	2002.1631	2001.1558	2001.0630	0.0929	1	K.TELNQTVQELETLVK.E
274 - 281	1031.5356	1030.5283	1030.5294	-0.0011	1	K.VKEEIEER.L
327 - 335	1108.4028	1107.3955	1107.4945	-0.0990	0	K.SQNEQEAFR.S
336 - 348	1443.6589	1442.6516	1442.8344	-0.1828	1	R.SNLKTLLEILDGK.I
357 - 366	1162.4303	1161.4230	1161.5699	-0.1469	1	R.DNLAKLLECS.-

No match to: 906.4255, 909.6912, 914.5380, 915.4563, 917.3764, 923.4292, 929.4879, 935.4080, 937.4569, 943.4514, 945.4741, 951.6177, 953.4241, 961.4928, 965.4255, 971.4565, 973.4288, 979.4825, 981.3292, 983.3121, 985.5522, 991.5208, 998.5462, 1000.5458, 1002.5754, 1028.1401, 1029.4717, 1034.1382, 1044.5061, 1052.0936, 1058.5127, 1066.0704, 1072.0792, 1078.0973, 1082.0511, 1087.4760, 1089.5009, 1097.4445, 1103.4304, 1106.4036, 1115.3981, 1118.4731, 1124.6138, 1127.4144, 1133.7928, 1137.3867, 1143.4734, 1145.5040, 1151.3828, 1155.3872, 1170.3855, 1180.4641, 1188.4210, 1201.3770, 1211.5817, 1215.3864, 1227.6379, 1233.4476, 1241.3517, 1245.3722, 1252.0648, 1255.9707, 1259.3484, 1260.9761, 1269.3546, 1276.9535, 1283.9985, 1289.3931, 1298.5863, 1303.3835, 1310.1569, 1313.3763, 1320.3845, 1323.3357, 1331.3698, 1337.3959, 1339.5526, 1348.3033, 1352.3591, 1354.3707, 1361.3945, 1373.3365, 1396.3954, 1401.4586, 1417.5079, 1432.5869, 1436.7709, 1465.8981, 1475.7159, 1485.7115, 1487.8739, 1489.8846, 1496.7755, 1507.8544, 1522.8965, 1527.7855, 1531.8328, 1542.3137, 1546.7966, 1549.8424, 1555.8386, 1565.8577, 1571.7878, 1577.8152, 1589.6711, 1593.7634, 1594.7744, 1601.7302, 1604.8314, 1612.7251, 1624.7484, 1632.7386, 1634.8917, 1653.8625, 1659.7838, 1672.7273, 1688.7031, 1705.7791, 1722.9015, 1735.0825, 1744.9111, 1752.6837, 1754.4170, 1764.7042, 1766.6537, 1781.7202, 1790.7954, 1794.7095, 1812.6934, 1822.1083, 1837.0391, 1882.7268, 1900.5093, 1905.6818, 1922.7371, 1935.7794, 1945.9263, 1960.2281, 1962.7723, 1976.8082, 1987.2444, 1993.8463, 2011.8602, 2022.3103, 2058.8860, 2067.9390, 2086.1626, 2096.8123, 2112.8582, 2123.2378, 2144.6570, 2172.1929, 2194.6516, 2211.0249, 2225.0461, 2234.0349, 2243.9182, 2254.9937, 2267.0002, 2277.0537, 2283.1238, 2298.0876, 2308.0491, 2317.0415, 2320.9531, 2383.0847, 2421.1831, 2446.1741, 2448.1626, 2457.6357, 2461.3403, 2476.2759, 2487.2253, 2503.2405, 2509.2708, 2522.3359, 2526.1421, 2530.1609, 2592.2202, 2609.4373, 2636.3459, 2652.4016, 2707.4927, 2727.5007, 2738.5481, 2767.1729, 2777.5054, 2970.8933, 3009.3359



42 Guanine nucleotide-binding protein subunit alpha-11

Number of mass values searched: 100

Number of mass values matched: 8

Sequence Coverage: 30%

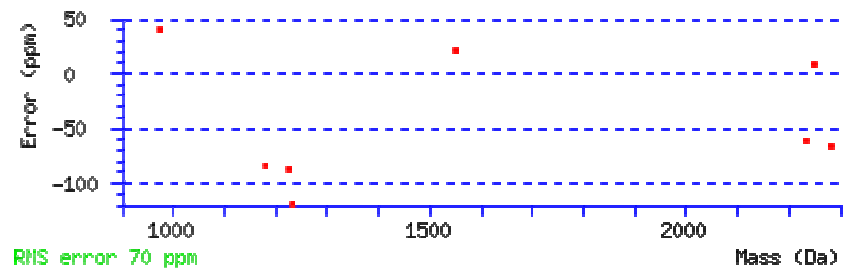
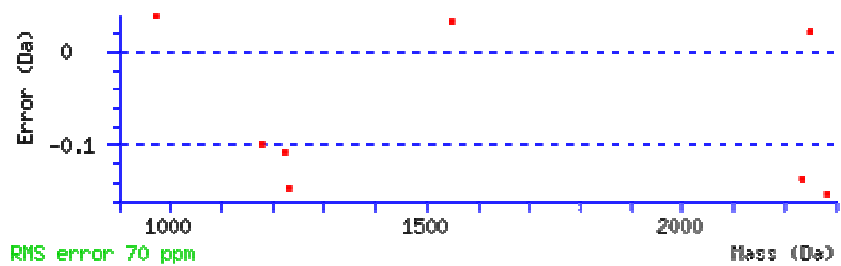
Matched peptides shown in **Bold Red**

1 MTLESMMACC LSDEVKESKR INAEIEKQLR RDKRDARREL KLLLLGTGE
51 GKSTFIKQMR IIHGAGYSEE DKRGFTKLVY QNIFTAMQAM VRAMETLKIL
101 **YK**YEQNKANA LLIREVDVEK **VTTFEHQYVN AIK**TLWSDPG VQECYDRRRE
151 **FQLSDSAKYY** LTDVDRIATV GYLPTQQDVL RVRVPTTGII EYPFLENII
201 FR**MVDVGGQR SER**RKWIHCF ENVTSIMFLV ALSEYDQVLV ESDNENRMEE
251 SKALFR**TIIT YPWFQNSSVI LFLNK**KDLLE DKILHSHLVD YPFEDGPQR
301 DAQAAREFIL KMFVDLNPDS DKIIYSHFTC ATDTENIRFV FAAVKDTILQ
351 LNLKEYNLV

Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence

1 - 19 2248.9844 2247.9771 2247.9554 0.0218 1 -.MTLESMMACCLSDEVKESK.R
20 - 27 972.5868 971.5795 971.5399 0.0396 1 K.RINAEIEK.Q
74 - 92 2234.0093 2233.0020 2233.1388 -0.1367 1 R.GFTKLVYQNIFTAMQAMVR.A Oxidation (M)
93 - 102 1225.5791 1224.5718 1224.6788 -0.1069 1 R.AMETLKILYK.Y Oxidation (M)
121 - 133 1549.8331 1548.8258 1548.7936 0.0322 0 K.VTTFEHQYVNAIK.T
149 - 158 1180.4968 1179.4895 1179.5884 -0.0989 1 R.REFQLSDSAK.Y
203 - 213 1233.4530 1232.4457 1232.5932 -0.1474 1 R.MVDVGGQRSER.R
257 - 275 2284.0840 2283.0767 2283.2303 -0.1536 0 R.TIITYPWFQNSSVILFLNK.K

No match to: 901.1002, 909.0784, 916.6199, 922.6417, 926.5854, 931.5918, 937.4409, 943.5621, 949.5701, 955.6136, 965.5972, 978.6183, 985.5634, 995.5604, 1001.5566, 1012.5805, 1028.1088, 1034.1279, 1044.0765, 1052.0913, 1058.5186, 1066.0464, 1075.2957, 1081.9929, 1089.4977, 1097.9810, 1106.4757, 1108.4092, 1118.4930, 1131.4819, 1144.5485, 1158.5426, 1165.5137, 1173.4984, 1192.4982, 1199.5544, 1210.4902, 1254.9458, 1263.5159, 1270.9077, 1276.9269, 1284.5320, 1292.9055, 1307.4971, 1320.3859, 1328.4491, 1339.5409, 1346.4941, 1354.4781, 1365.4222, 1383.4656, 1391.5281, 1436.7809, 1475.7814, 1487.8605, 1489.8837, 1496.8008, 1507.8557, 1515.7681, 1531.8473, 1545.8068, 1555.8254, 1562.8234, 1571.7817, 1578.8304, 1587.7695, 1595.7321, 1604.8431, 1634.8281, 1657.7109, 1676.8164, 1699.7513, 1707.6733, 1716.7643, 1766.6589, 1790.7538, 1794.6925, 1838.8010, 1993.8456, 2225.0176, 2298.0823, 2342.9465, 2367.1731, 2383.9233, 2398.9702, 2421.1741, 2447.1514, 2487.1721, 2503.1665, 2527.1326, 2565.1953, 2705.3037



43 Protein disulfide-isomerase A3

Number of mass values searched: **100**

Number of mass values matched: **12**

Sequence Coverage: **29%**

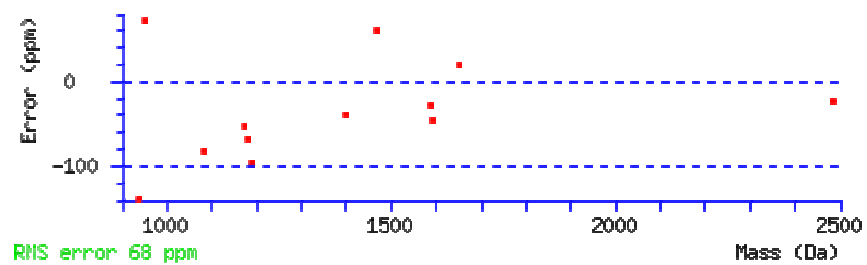
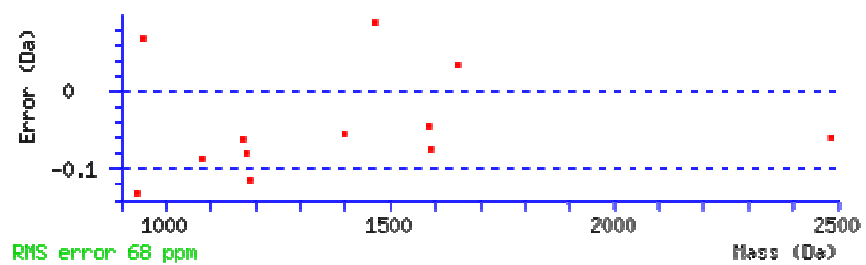
Matched peptides shown in **Bold Red**

1 MRFSC LALLP GVALLLASAR LAAASDVLEL TDENFESRVS DTGSAGLMLV
51 EFFAPWCGHC KRL**LAPEYEAA ATRLK**GIVPL AK**VDCTANTN TCNKYGV**SGY
101 **PTLKIFRDGE EAGAYDG**PRT ADGIVSHLKK QAGPASVPLR TEEEFKK**FIS**
151 **DKDASVVGFF RDLFSDGHSE** FLK**AASNLRD NYRFAHTNIE** SLVKEYDDNG
201 EGITIFRPLH LANKFED**KTV AYTEKK**MTSG KIKKFIQDSI FGLCPHMTED
251 NKDLIQGKDL LTAYYDV~~Y~~E KNAKGSNYWR **NRVMMVAK**KF LDAGHKLNFA
301 VASRKTFSHE LSDFGLESTT GEVPVVAIRT AKGEK**FVMQE EFSR**DGKALE
351 QFLQEYFDGN LKRYLKSEPI PESNEGPVKV VVAENFDDIV NEEDKDVLI**E**
401 FYAPWCGHCK NLEPKYKELG EKLSK**DPNIV IAKMDATAND VPSPYE**VKGF
451 **PTIYFSPANK K**LTPKKYEGG RELNDFISYL QR**EATNPPII QEEKPK**KKKI
501 AQEDL

Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence

63 - 73 1191.4858 1190.4785 1190.5931 -0.1146 0 R.LAPEYEAAATR.L
83 - 94 1397.5238 1396.5165 1396.5711 -0.0546 0 K.VDCTANTNTCNK.Y
95 - 104 1084.4795 1083.4722 1083.5601 -0.0878 0 K.YGVSGYPTLK.I
105 - 119 1652.7998 1651.7925 1651.7590 0.0335 1 K.IFRDGE EAGAYDGPR.T
148 - 161 1587.7723 1586.7650 1586.8093 -0.0443 1 K.FISDKDASVVGFFR.D
174 - 183 1179.5065 1178.4992 1178.5792 -0.0800 1 K.AASNLRDNYR.F
219 - 226 939.3835 938.3762 938.5073 -0.1311 1 K.TVAYTEKK.M
281 - 288 948.5799 947.5726 947.5045 0.0682 1 R.NRVMMVAK.K
336 - 344 1172.4781 1171.4708 1171.5332 -0.0624 0 K.FVMQEEFSR.D
426 - 448 2487.1831 2486.1758 2486.2363 -0.0604 1 K.DPNIVIAKMDATANDVPSPYEVK.G
449 - 461 1469.8680 1468.8607 1468.7714 0.0893 1 K.GFPTIYFSPANKK.L
483 - 496 1593.7750 1592.7677 1592.8409 -0.0732 0 R.EATNPPIIQEEKPK.K

No match to: 900.3538, 910.6797, 917.3655, 925.5876, 931.6033, 951.6017, 958.6134, 973.5739, 985.5682, 1000.5604, 1002.5692, 1018.5391, 1029.5436, 1031.5409, 1034.1349, 1052.0861, 1058.5259, 1066.0596, 1074.5114, 1082.0176, 1089.5016, 1106.4847, 1108.4194, 1118.4972, 1128.4359, 1142.5299, 1148.5250, 1157.5026, 1165.4969, 1201.5442, 1217.4568, 1233.4561, 1243.5573, 1254.5217, 1265.4882, 1277.5309, 1302.5074, 1307.4823, 1320.3926, 1339.5334, 1350.4648, 1354.4957, 1365.4077, 1379.4806, 1383.4912, 1436.7826, 1475.7843, 1489.8890, 1496.7322, 1507.8590, 1522.8070, 1531.8384, 1542.2322, 1549.8242, 1571.7852, 1578.8258, 1595.7375, 1604.8350, 1634.8448, 1638.7964, 1657.7048, 1669.7882, 1678.8024, 1699.7434, 1707.6891, 1716.7526, 1765.6536, 1780.7019, 1791.6233, 1813.7957, 1837.8231, 1851.8046, 1993.8466, 2046.9325, 2135.9915, 2149.9604, 2185.9792, 2225.0193, 2298.0918, 2383.9058, 2398.9917, 2420.1707, 2447.1414, 2501.2263, 2510.1567, 2643.3877, 2705.2896, 2932.8032



44 Baculoviral IAP repeat-containing protein 4

Number of mass values searched: **200**

Number of mass values matched: **16**

Sequence Coverage: **32%**

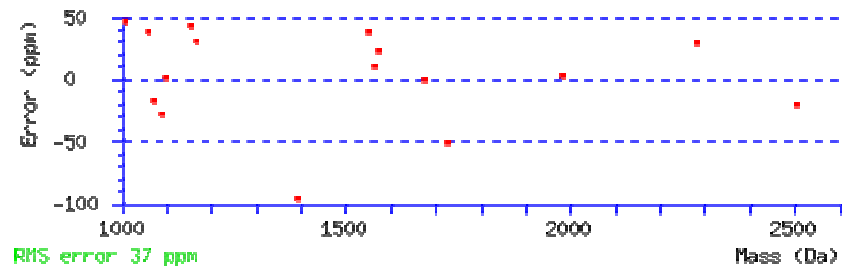
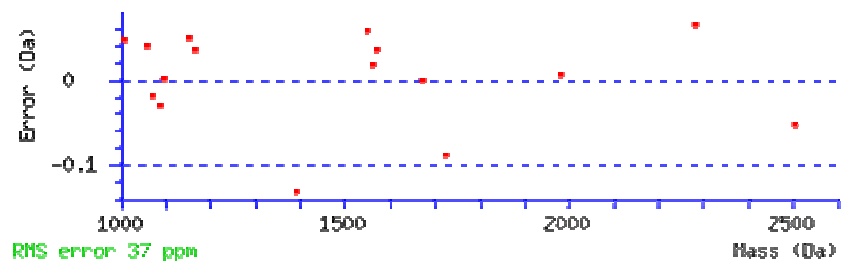
Matched peptides shown in **Bold Red**

1 **MTFNSFEGTR TFVLADTNK**D EEFVEEFNRL KTFANFPSSS PVSASTLAR
51 GFLYTGEGDT VQCFSCHAAI DRWQYGDSAV GRHRRISPNC RFINGFYFEN
101 GAAQSTNPGI QNGQYKSENC VGNRNPFPD RPPETHADYL LR**TGQVVDIS**
151 **DTIYPRNPAM CSEEAR**LKSF QNWPDYAHLT PRELASAGLY YTGADDQVQC
201 FCCGGK**LENW EPCDRAWSEH RRHFPNCFV LGRNVNVRSE** SGVSSDR**NFP**
251 **NSTNSPRNPA MAEYEAR**IVT FGTWTSSVNK **EQLARAGFYA LGE GDK**VKCF
301 HCGGGLTDWK PSEDPWEQHA **KWYPGCKYLL DEK**GQEYINN IHLTHSLEES
351 LGRTAEKTPS LTKKIDDIF QNPMVQEAIR **MGFSFKDIK** TMEEKIQTSG
401 SSYLSLEVL ADLVSQAKDN TEDESSQTS LKDISTEEQL RRLQEEK**LCK**
451 **ICMDRNIAIV FVPCGHLVTC** KQCAEAVDKC **PMCYTVITFK QK**IFMS

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
2 - 10	1058.5304	1057.5231	1057.4829	0.0402	0	M.TFNSFEGTR.T
11 - 19	1008.5826	1007.5753	1007.5288	0.0466	0	R.TFVLADTNK.D
143 - 156	1563.8184	1562.8111	1562.7941	0.0171	0	R.TGQVVDISDTIYPR.N
157 - 166	1164.5131	1163.5058	1163.4699	0.0359	0	R.NPAMCSEEAR.L
207 - 221	1984.8789	1983.8716	1983.8646	0.0071	1	K.LENW EPCDRAWSEHR.R
222 - 233	1549.8433	1548.8360	1548.7772	0.0588	1	R.RHFPNCFV LGR.N
223 - 233	1393.5503	1392.5430	1392.6761	-0.1331	0	R.HFPNCFV LGR.N
248 - 267	2282.0916	2281.0843	2281.0181	0.0662	1	R.NFPNSTNSPRNPAMAEYEAR.I Oxidation (M)
258 - 267	1151.5653	1150.5580	1150.5077	0.0504	0	R.NPAMAEYEAR.I
281 - 296	1724.7717	1723.7644	1723.8529	-0.0885	1	K.EQLARAGFYALGEGDK.V
322 - 333	1571.7914	1570.7841	1570.7490	0.0351	1	K.WYPGCKYLLDEK.G
381 - 389	1072.5317	1071.5244	1071.5423	-0.0179	1	R.MGFSFKDIK.K
381 - 389	1088.5139	1087.5066	1087.5372	-0.0306	1	R.MGFSFKDIK.K Oxidation (M)
448 - 455	1095.5114	1094.5041	1094.5035	0.0006	1	K.LCKICMDR.N
451 - 471	2503.1919	2502.1846	2502.2368	-0.0522	1	K.ICMDRNIAIVFVPCGHLVTC.K
480 - 492	1675.8009	1674.7936	1674.7932	0.0004	1	K.CPMCYTVITFKQK.I

No match to: 904.3263, 909.5662, 915.6188, 921.4772, 924.5657, 927.5797, 931.5951, 937.6382, 939.6525, 945.5093, 947.5278, 949.5990, 951.6136, 957.6036, 964.6121, 968.5801, 971.5947, 973.5872, 982.4763, 985.5765, 996.5970, 999.5604, 1001.5636, 1015.5763, 1023.5335, 1028.1222, 1031.5358, 1034.1337, 1044.0878, 1052.0961, 1066.0269, 1074.5181, 1080.4918, 1082.0267, 1098.0039, 1100.4803, 1106.4858, 1108.4309, 1116.5531, 1118.5065, 1125.4576, 1128.5056, 1135.5518, 1139.5087, 1141.5010, 1145.5497, 1158.5105, 1172.4753, 1179.4999, 1188.4872, 1191.4834, 1200.5409, 1207.4807, 1211.5203, 1217.4541, 1224.5023, 1233.4567, 1242.5189, 1254.9514, 1261.9658, 1265.4873, 1277.5387, 1284.4160, 1292.8944, 1300.3646, 1302.5160, 1307.4900, 1314.5300, 1320.4100, 1327.5083, 1329.4760, 1336.4734, 1339.5317, 1347.4897, 1353.5771, 1361.4825, 1365.4441, 1380.4783, 1383.4723, 1395.5166, 1398.5509, 1406.5264, 1410.6793, 1434.7604, 1436.7858,

1443.7382, 1451.7355, 1459.7939, 1469.8663, 1475.7886, 1487.8560, 1489.8907, 1498.7803, 1503.8452, 1507.8593, 1515.7739, 1525.8257, 1529.8276, 1531.8400, 1546.8070, 1555.8323, 1578.8298, 1585.7734, 1587.7689, 1595.7399, 1604.8457, 1612.7598, 1620.7849, 1630.8220, 1634.8528, 1638.8134, 1649.7533, 1652.7599, 1658.7222, 1660.8190, 1668.7605, 1678.8213, 1688.8577, 1699.7635, 1707.7053, 1716.7675, 1739.8201, 1747.6993, 1765.6547, 1780.6920, 1791.6354, 1794.7123, 1804.8129, 1814.7949, 1836.8486, 1838.8221, 1851.8048, 1866.8135, 1891.8108, 1942.8551, 1950.8467, 1965.9056, 1970.8645, 1978.8594, 1993.8556, 2007.8827, 2022.8680, 2035.8893, 2049.8584, 2064.8950, 2084.8994, 2129.9036, 2149.9727, 2170.9265, 2184.9946, 2193.9048, 2210.9990, 2225.0315, 2234.0139, 2239.0452, 2248.9790, 2265.0430, 2284.0830, 2299.0818, 2308.0510, 2316.0728, 2326.0798, 2342.9558, 2367.1670, 2383.9258, 2398.9939, 2421.1682, 2446.1707, 2448.1201, 2459.1838, 2462.1865, 2481.1643, 2487.1909, 2509.1641, 2527.1702, 2568.2312, 2592.3000, 2609.3145, 2637.3103, 2652.3186, 2664.3694, 2705.3059, 2872.6477, 2902.7173



45 Protein disulfide-isomerase A3

Number of mass values searched: **60**

Number of mass values matched: **14**

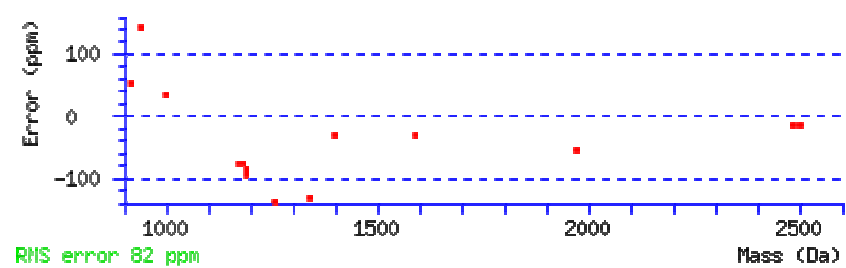
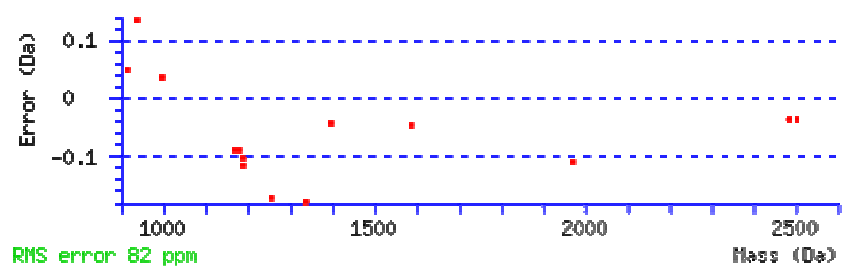
Sequence Coverage: **26%**

Matched peptides shown in **Bold Red**

1 MRFSCLLLP GVALLSAR LAAASDVLEL TDENFESRVS DTGSAGLMLV
51 EFFAPWCGHC KR**LAPEYEAA ATR**LKGIVPL AK**VDCTANTN TCNK**YGVSGY
101 PTLKIFRDGE EAGAYDGPRT ADGIVSHLKK QAGPASVPLR TEEEFKK**FIS**
151 **DKDASVVGFF** RDLFSDGHSE FLK**AASNLRD NYRFAHTNIE SLVK**EYDDNG
201 EGITIFRPLH LANKFEDK**TV AYTEKK**MTSG KIKKFIQDSI FGLCPHMTED
251 NKDLIQGKDL LTAYYDVVYE KNAKGSNYWR NRVMMVAK**KF LDAGHKL**NFA
301 VASRKTFSHE LSDFGLESTT GEVPVVAIRT AKGEK**FVMQE EFSRDGK****ALE**
351 **QFLQEYFDGN LK**RYLKSEPI PESNEGPVKV VVAENFDDIV NEEDKDVLI
401 FYAPWCGHCK NLEPKYKELG EKLSK**DPNIV IAKMDATAND VSPPYEVKGF**
451 **PTIYFSPANK** KLTPKKEGG RELNDFISYL QREATNPPII
QEEKPKKKKK
501 AQEDL

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
63 - 73	1191.4861	1190.4788	1190.5931	-0.1143	0	R.LAPEYEAA ATR .L
83 - 94	1397.5363	1396.5290	1396.5711	-0.0421	0	K.VDCTANT NTCNK .Y
148 - 161	1587.7706	1586.7633	1586.8093	-0.0460	1	K.FISDKDASVVG FFR .D
153 - 161	997.5461	996.5388	996.5029	0.0359	0	K.DASVVG FFR .D
174 - 183	1179.4966	1178.4893	1178.5792	-0.0899	1	K.AASNLRD NYR .F
184 - 194	1258.5056	1257.4983	1257.6717	-0.1734	0	R.FAHTN IESLVK .E
219 - 226	939.6486	938.6413	938.5073	0.1340	1	K.TVAY TEKK .M
289 - 296	915.5537	914.5464	914.4974	0.0490	1	K.KFLDAG HK .L
336 - 344	1172.4500	1171.4427	1171.5332	-0.0905	0	K.FVMQEE FSR .D
336 - 344	1188.4332	1187.4259	1187.5281	-0.1022	0	K.FVMQEE FSR .D Oxidation (M)
348 - 363	1970.8889	1969.8816	1969.9897	-0.1081	1	K.ALEQFLQEYFDGN LKR .Y
426 - 448	2487.2085	2486.2012	2486.2363	-0.0350	1	K.DPNIVIAKMDATAND VSPPYEVK .G
426 - 448	2503.2014	2502.1941	2502.2312	-0.0371	1	K.DPNIVIAKMDATAND VSPPYEVK .G Oxidation (M)
449 - 460	1341.5052	1340.4979	1340.6765	-0.1786	0	K.GFPTIY FSPANK .K

No match to: 905.5897, 909.1132, 922.5626, 926.6157, 931.5897, 949.5243, 960.6162, 978.5894, 985.5723, 1002.5583, 1031.5314, 1034.1403, 1052.1051, 1058.5223, 1066.0651, 1072.5240, 1082.0397, 1088.5018, 1108.4208, 1118.5063, 1203.4084, 1215.4387, 1233.4635, 1276.9346, 1354.5446, 1379.4626, 1436.7844, 1475.7886, 1489.8947, 1507.8578, 1531.8473, 1540.9160, 1549.8451, 1555.8401, 1571.7953, 1578.8348, 1595.7444, 1604.8545, 1653.7002, 1765.6614, 1794.7303, 1993.8694, 2211.0142, 2284.0896, 2303.0808, 2448.1509



47 Annexin A6

Number of mass values searched: 200

Number of mass values matched: 23

Sequence Coverage: 30%

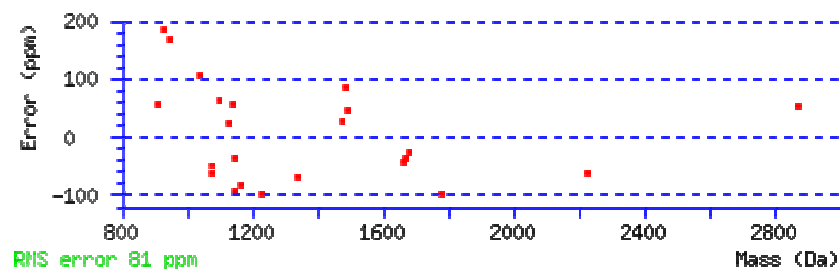
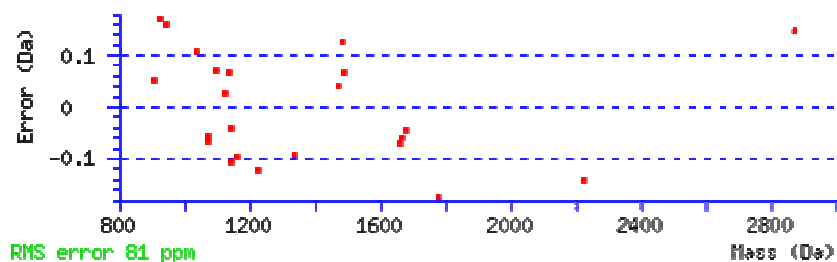
Matched peptides shown in **Bold Red**

1 **MAKIAQGAMY** RGSVHDFPEF DANQDAEALY TAMKGFSGDK **ESILELITSR**
51 **SNKQRQEICQ SYK**SLYGKDL IEDLKYELTG **KFERLIVNLM RPLAYCDAKE**
101 **IKDAISGIGT DEKCLIEILA SRT**NEQMHQL VAAVKDAYER **DLESDDIGDT**
151 **SGHFQKMLVV LLQG**TRENDV VVSEDLVQQD VQDLYEAGEL KWGTDEAQFI
201 YILGNRSKQH LRLVFDEYLK TTGKPIEASI RGELSGDFEK LMLAVVKCIR
251 **STPEYFAERL FK**AMKGLGTR DNTLIR**IMVS RSELDMLDIR** EIFRRTKYEKS
301 LYSMIK**NDTS GEYK**KALLKL CGGDDDDAAQ FFPEAAQVAY QMWELSAVSR
351 VELKGTVCAA NDFNPDADAK ALRKAMKGIG TDEATIIV THRSNAQRQQ
401 IRQTFKSHFG RDLMDL**SE ISGDLARLIL GLMMPPAHYD AKQLKAMEG**
451 **AGTDEK**TLIE ILATRTNAEI RAINEAYKED YHKSLEDALS SDTSGHFRR
501 LISLATGNRE EGGENRDQAQ EDAQVAEIL EIADTPSGDK TSLETR**FMTV**
551 **LCTRSYPHLR** RVFQEFIKKT NYDIEHVIKK EMSGDVKDAF VAIVQSVKKN
601 PLFFADKLYK SMKGAGTDEK TLTR**VMVSRSEIDLLNIRRE** FIEKYDKSLH
651 QAIEGDTSGD FMKALLALCG GED

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
2 - 11	1124.6144	1123.6071	1123.5808	0.0263	1	M.AKIAQGAMYR.G Oxidation (M)
4 - 11	909.5129	908.5056	908.4538	0.0518	0	K.IAQGAMYR.G
4 - 11	925.6273	924.6200	924.4487	0.1713	0	K.IAQGAMYR.G Oxidation (M)
41 - 50	1160.5565	1159.5492	1159.6448	-0.0956	0	K.ESILELITSR.S
41 - 53	1489.8904	1488.8831	1488.8147	0.0684	1	K.ESILELITSRSNK.Q
54 - 63	1339.5491	1338.5418	1338.6350	-0.0932	1	K.QRQEICQSYK.S
76 - 84	1142.5415	1141.5342	1141.5768	-0.0425	1	K.YELTGKFER.L
82 - 99	2225.0176	2224.0103	2224.1496	-0.1393	1	K.FERLIVNLMRPLAYCDAK.E Oxidation (M)
100 - 113	1475.7999	1474.7926	1474.7515	0.0411	1	K.EIKDAISGIGTDEK.C
114 - 122	1074.5299	1073.5226	1073.5903	-0.0677	0	K.CLIEILASR.T
141 - 166	2872.6357	2871.6284	2871.4801	0.1484	1	R.DLESDDIGDTSGHFQKMLVVLLQGTR.E
157 - 166	1145.5651	1144.5578	1144.6638	-0.1060	0	K.MLVVLLQGTR.E Oxidation (M)
251 - 259	1099.5760	1098.5687	1098.4982	0.0706	0	R.STPEYFAER.L
251 - 262	1487.8794	1486.8721	1486.7456	0.1265	1	R.STPEYFAERLFA.A
277 - 290	1677.8210	1676.8137	1676.8589	-0.0452	1	R.IMVSRSELDMLDIR.E
307 - 315	1041.5938	1040.5865	1040.4774	0.1091	1	K.NDTSGEYK.A

419 - 427 947.6392 946.6319 946.4720 0.1600 0 K.SEISGLAR.L
428 - 442 1669.8192 1668.8119 1668.8731 -0.0612 0 R.LILGLMPPAHYDAK.Q
446 - 456 1136.5907 1135.5834 1135.5179 0.0655 1 K.KAMEGAGTDEK.T
547 - 560 1780.7242 1779.7169 1779.8913 -0.1743 1 R.FMTVLCTRSYPHLR.R
625 - 638 1660.8337 1659.8264 1659.8978 -0.0713 1 R.VMVRSEIDLLNIR.R Oxidation (M)
630 - 638 1072.5457 1071.5384 1071.5924 -0.0540 0 R.SEIDLLNIR.R
630 - 639 1228.5779 1227.5706 1227.6935 -0.1229 1 R.SEIDLLNIRR.E

No match to: 902.3297, 912.6599, 917.3350, 923.3141, 927.5966, 933.3251, 938.3191, 941.6031, 949.6148, 951.6191, 957.6006, 961.2943, 968.6296, 971.6370, 978.6185, 982.6274, 985.5771, 996.6400, 1000.5736, 1002.5809, 1012.1840, 1014.1728, 1022.1454, 1028.1367, 1034.1469, 1044.1022, 1052.1079, 1058.5363, 1066.0697, 1082.0297, 1088.5269, 1089.5155, 1102.5433, 1106.4873, 1114.5593, 1118.5138, 1130.5554, 1151.6183, 1163.5468, 1173.5382, 1179.5200, 1186.5826, 1189.5122, 1191.4945, 1201.5642, 1209.5817, 1218.4683, 1233.4590, 1240.0066, 1247.5530, 1254.9637, 1261.9761, 1268.5665, 1270.9272, 1276.9459, 1283.5490, 1292.8998, 1299.5718, 1305.5212, 1313.5601, 1320.4060, 1327.5416, 1351.4868, 1353.9762, 1354.4916, 1361.5011, 1365.4480, 1377.5085, 1383.4939, 1392.6344, 1399.5668, 1410.6934, 1419.6572, 1427.7190, 1434.7925, 1436.7821, 1443.8463, 1453.8320, 1460.8423, 1463.8253, 1479.8291, 1496.8549, 1503.8484, 1507.8607, 1516.8154, 1523.8145, 1529.8428, 1531.8477, 1541.3281, 1543.1588, 1549.8425, 1555.8342, 1562.8307, 1567.7406, 1574.8114, 1577.8175, 1584.7854, 1587.7584, 1593.7805, 1604.8505, 1623.8389, 1630.8431, 1634.8752, 1639.8689, 1650.8175, 1675.8304, 1686.8999, 1695.8170, 1704.8293, 1707.6829, 1716.7665, 1722.7987, 1724.7706, 1732.5951, 1740.7520, 1748.6149, 1764.6416, 1766.6744, 1791.6312, 1794.7061, 1807.9426, 1837.8220, 1851.7914, 1880.7966, 1888.8207, 1894.8176, 1907.7899, 1921.8118, 1932.8064, 1940.8011, 1955.8087, 1960.8378, 1969.8264, 1978.8650, 1993.8558, 2002.9230, 2044.9052, 2075.9290, 2082.8723, 2094.9231, 2149.9631, 2192.9707, 2234.0093, 2248.9932, 2265.0369, 2283.0847, 2298.0950, 2308.0410, 2318.0674, 2336.0840, 2350.1064, 2367.1487, 2383.8972, 2400.0945, 2421.1663, 2434.1384, 2446.1611, 2448.1431, 2458.1665, 2462.1631, 2473.9619, 2481.1582, 2487.1614, 2503.1655, 2512.1646, 2525.1560, 2547.1470, 2566.2434, 2585.2244, 2593.2688, 2609.2954, 2636.2959, 2652.3203, 2705.2920, 2719.3877, 2737.5034, 2780.6074



48 RNA polymerase I-specific transcription initiation factor RRN3

Number of mass values searched: **70**

Number of mass values matched: **10**

Sequence Coverage: **21%**

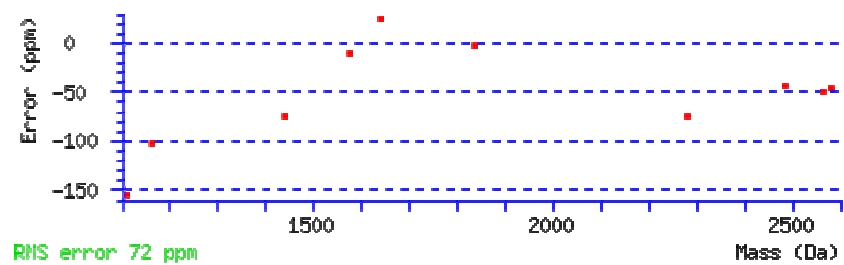
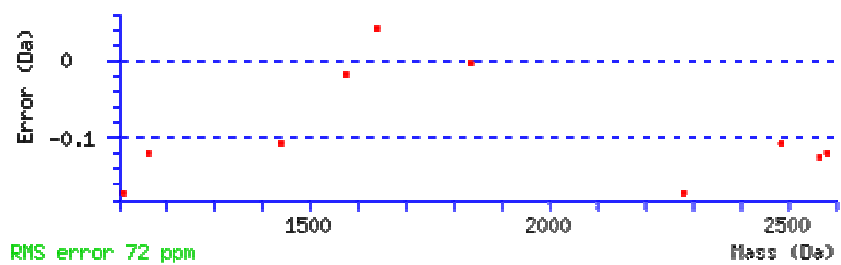
Matched peptides shown in **Bold Red**

1 MAAPLLHTRL SGDVTAAASA TLSASRTGLS DMLAESDFF NSPPKKTVERF
51 GGTVTEVLLK YKGETNDLE LLKNQLSDPD IK**DDQIINWL LEFRSSVMYL**
101 TKDFEQLINI ILRLPWLNRS QRVVEEYLAF LGNLVSAQTV FLRPCLSMIA
151 SHFVPPRVIV KEGGIDVSDS DEDDNLPAI FDTCHRALQI ITR**YVPSTPW**
201 FLMPILVEKF PFVRKSERTEC ECYVHLLRI **SLYFPTLRRE ILELVIEKLL**
251 KLDVSVSRQD IEDAEKAAQ TCGGDTTTEG LFNMDDEDTE DPEKK**ADQEQ**
301 PNQMAHPTAE RLDVLLCLLL SYIEDVCRVH GKIDNNKTKD LYRDLISIFD
351 KLLLPTHASC HVQFFMFFLC SFKLGFAEAF LEHLWKKLQD PNNPAIRQA
401 AANYIGSFLA RAKFIPLITV KTCLDLLVNW LHMYLTNQDS GTKAFCDVAL
451 HGPFYSACQA VFYTVVFRHK QLLSGNLKQG LQYLQSLNFE RIVLSQLNPL
501 KICLPQVVNF FAAITNK**YQL VFCYTIMER**N SRQMLPVIRS TAGGDSVQTC
551 TNPLDTFFPF DPCVLKRSKK FIDPIYQIWE DGSAAELQEF KKSTKKEVVE
601 DEDDDFLKGE VPQSDTVTGL TPSSFDTHFQ SPSSSVGSPP VLYIPGQSPL
651 LTRIYD

Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence

1 - 26 2584.2317 2583.2244 2583.3439 -0.1194 1 -.MAAPLLHTRLSDGVTAAASATLSASR.T Oxidation (M)
10 - 26 1577.7960 1576.7887 1576.8056 -0.0169 0 R.LSGDVTAAASATLSASR.T
50 - 60 1163.5471 1162.5398 1162.6598 -0.1200 0 R.FGGTVTEVLLK.Y
83 - 102 2487.1519 2486.1446 2486.2515 -0.1069 1 K.DDQIINWLLLEFRSSVMYLTK.D Oxidation (M)
95 - 113 2283.0703 2282.0630 2282.2344 -0.1714 1 R.SSVMYLTKDFEQLINIILR.L
194 - 214 2566.2681 2565.2608 2565.3858 -0.1250 1 R.YVPSTPWFLMPILVEKFPFVR.K
230 - 238 1109.4633 1108.4560 1108.6281 -0.1720 0 R.ISLYFPTLR.R
240 - 251 1439.8019 1438.7946 1438.9010 -0.1064 1 R.EILELVIEKLLK.L
296 - 311 1838.8049 1837.7976 1837.8013 -0.0037 0 K.ADQEQPNQMAHPTAER.L Oxidation (M)
518 - 529 1638.8075 1637.8002 1637.7582 0.0420 0 K.YQLVFCYTIMER.N Oxidation (M)

No match to: 905.1517, 911.3470, 921.3244, 927.5944, 996.6245, 1034.1428, 1052.1022, 1058.5378, 1068.5186, 1072.0670, 1078.0757, 1094.0360, 1179.5083, 1233.4739, 1320.4038, 1365.4346, 1383.4698, 1415.5986, 1435.7754, 1475.7936, 1479.8259, 1493.8191, 1501.7921, 1507.8530, 1523.7920, 1549.8290, 1555.8292, 1589.6996, 1707.6877, 1724.7415, 1740.7133, 1765.6522, 1794.7042, 1880.7908, 1888.7931, 1894.8065, 1907.7803, 1993.8428, 2022.9015, 2044.8958, 2095.9092, 2149.9534, 2192.9417, 2225.0107, 2233.9927, 2254.9629, 2267.0195, 2298.0657, 2307.0525, 2327.0771, 2342.9233, 2367.1711, 2383.8948, 2398.9758, 2419.1543, 2447.1350, 2501.2080, 2509.1458, 2705.2708, 2872.6084



49 Collagen type IV alpha-3-binding protein

Number of mass values searched: **50**

Number of mass values matched: **8**

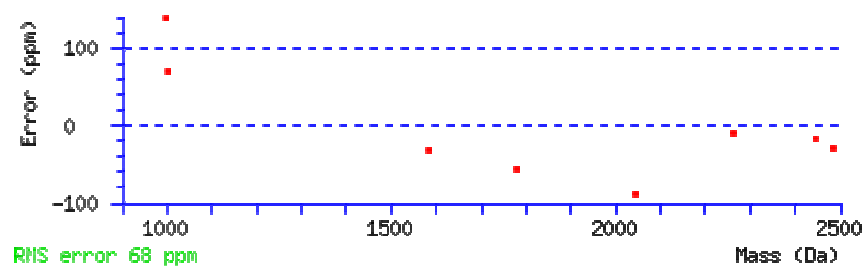
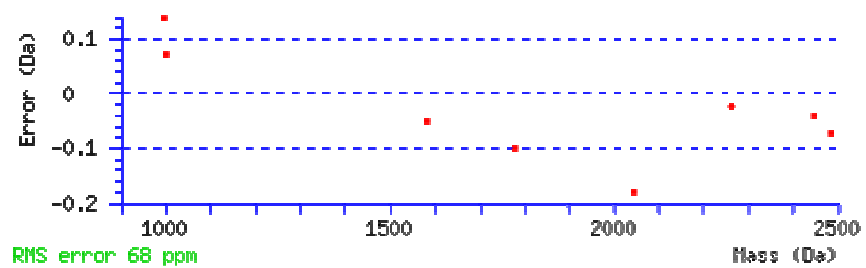
Sequence Coverage: **20%**

Matched peptides shown in **Bold Red**

1 MSDNQSWNSS GSEEDPETES GPPVERCGVL SKWTNYIHGW QDRWVVLKNN
51 TLSYYKSEDE TEYGCRGSIC LSKAVITPHD FDECR**FDISV NDSVWYLRAQ**
101 **DPEHR**QQWVD AIEQHKTESG YGSESSLRRH **GSMVSLVSGA SGYSATSTSS**
151 **FKKGHSLREK LAEMETFR**DI LCRQVDTLQK YFDVCADAVS KDELR**DKVV**
201 **EDDEDDFPTT** RSDGDFLHNT NGNKEKLFPH VTPKGINGID FKGEAITFKA
251 **TTAGILATLS HCIELMVK**RE ESWQKRHDRE VEKRRR**VEEA YKNVMEELK**K
301 KPRFGGPDYE EGPNSLINEE EFFDAVEAAL DRQDKIEEQS QSEKVRHLWHP
351 TSLPSGDTFS SVGTHRFVQK PYSRSSSMSS IDLVASDDV HRFSSQVEEM
401 VQNHMNYSLQ DVGGDANWQL VVEEGEMKVY RREVEENGIV LDPLKATHAV
451 KGVTGHEVCN YFWNVVDVRND WETTIENTFHV VETLADNAII VYQTHKRWWP
501 ASQRDVLYLS AIRKIPALTE NDPETWIVCN FSDVHDSAPL NNRCVRAK**IN**
551 **IAMICQTLVS PPEGDQEISR** DNILCKITYV ANVNPWWAP ASVLRAVAKR
601 EYPKFLKR**FT SYVQEK**TAGK PILF

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
86 - 105	2447.1326	2446.1253	2446.1666	-0.0412	1	R.FDISVNDSVWYLRAQDPEHR.Q
130 - 152	2264.0281	2263.0208	2263.0427	-0.0219	0	R.HGSMVSLVSGASGYSATSTSSFK.K Oxidation (M)
161 - 168	996.6193	995.6120	995.4746	0.1374	0	K.LAEMETFR.D
197 - 211	1780.6882	1779.6809	1779.7799	-0.0990	1	R.DKVVEDDEDDFPTTR.S
250 - 268	2044.8956	2043.8883	2044.0697	-0.1813	0	K.ATTAGILATLSHCIELMVK.R Oxidation (M)
287 - 299	1581.7310	1580.7237	1580.7756	-0.0518	1	R.VEEAYKNVMEELK.K
549 - 570	2487.1514	2486.1441	2486.2145	-0.0704	0	K.INIAMICQTLVSPPEGDQEISR.D Oxidation (M)
609 - 616	1001.5640	1000.5567	1000.4866	0.0702	0	R.FTSYVQEK.T

No match to: 900.3560, 917.3723, 927.5807, 941.5848, 985.5720, 1034.1315, 1058.5311, 1068.4988, 1089.5067, 1108.4294, 1118.5103, 1163.5398, 1233.4495, 1305.5083, 1339.5388, 1436.7826, 1439.7977, 1479.8204, 1489.8784, 1496.8501, 1507.8569, 1549.8376, 1555.8224, 1567.7225, 1577.8101, 1595.7365, 1604.8337, 1639.8464, 1724.7367, 1740.7216, 1749.6202, 1766.6689, 1794.6951, 1880.7917, 1894.7988, 1907.7747, 1993.8441, 2225.0081, 2233.9954, 2282.0747, 2284.0742, 2298.0830



50 Calpain-9

Number of mass values searched: **200**

Number of mass values matched: **13**

Sequence Coverage: **26%**

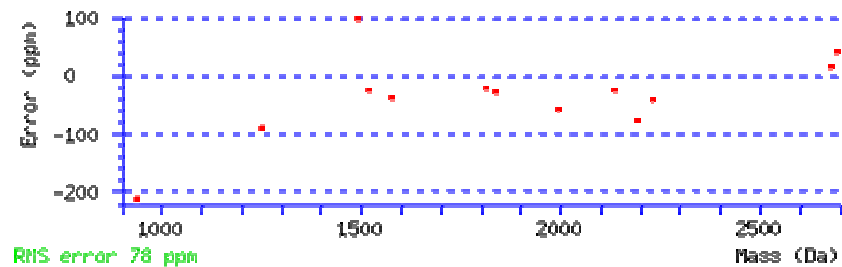
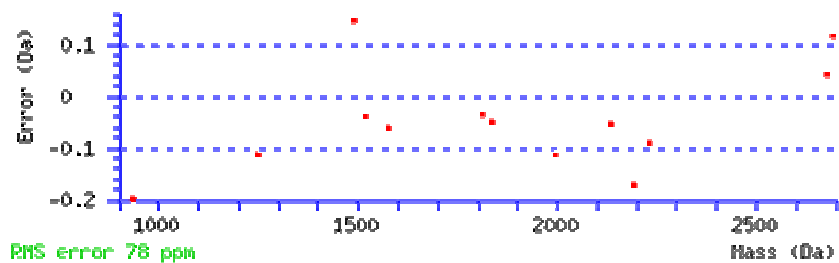
Matched peptides shown in **Bold Red**

1 MPYLHR**SLRP QPQPVPGDAR TIHSSGQSFE QLR**QGCLQSG TLFEDADFP
51 SNVSLFYSER PQVPFVWKR GEIVEKPEFI LGGATRTDIC QGELGDCWLL
101 AAIALSLTLNQ KALTRVVPQD QGFGSGYAGI FHFQFWQHSE WLDVVIDDRL
151 PTFKDRLVFL HSADHNEFWS ALLEKAYAKL NGSYEALEGG SAIEAMEDFT
201 GGVAENFQIR EAPEDFFEIL EKALK**RGSLL GCSIDTLNAS ESEARTSLGL**
251 **IKGHAYTVTG LDQVNFHGQR IKLIRVRNPW GQVEWNGPWS DSSPEWRSVD**
301 LEEQK**RLGHT ALDDGEFWMA FK**DFKIHFDK VEICNLTPDA LEDSAHRWE
351 VTIHQGSWVR GSTAGGCRNF LDTFWTNPQI KLSLTER**DEG QEGCTFLAAL**
401 **MQKDRRRLKR FGANMLTIGY AIYQCPDKDG HLSRDFFR**YH ASLARSKTFI
451 NLREVSERFQ LPPGDYILIP STFEPHQEAD FCLRIFSEKR AVTRDLDENI
501 DIDLPELKP TPQEEETEEE QQFRALFQRV **AGEDMEVSAE ELEYVNAVL**
551 **QKKTALKFKR LSLSCRNI SLMDTSGNGK** LEFEEFR**VFW DKLKH**WMDLF
601 LQFDVDKSGT MSSYELRTAL KAAGFQLGGH LLQLVLRYA DEDLQLDFDD
651 YLNCLVRL**LEN ASRVFQSLSV** KNKDFIHLNI NEFISLTMNI

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
7 - 20	1517.7799	1516.7726	1516.8110	-0.0384	0	R.SLRPQPQPVPGDAR.T
21 - 33	1489.8881	1488.8808	1488.7321	0.1487	0	R.TIHSSGQSFEQLR.Q
226 - 245	2135.9812	2134.9739	2135.0277	-0.0537	1	K.RGSLLGCSIDTLNASESEAR.T
227 - 252	2692.4995	2691.4922	2691.3749	0.1173	1	R.GSLLGCSIDTLNASESEARTSLGLIK.G
306 - 322	1993.8455	1992.8382	1992.9516	-0.1134	1	K.RLGHTALDDGEFWMAFK.D
307 - 322	1837.8071	1836.7998	1836.8505	-0.0507	0	R.LGHTALDDGEFWMAFK.D
388 - 403	1813.7733	1812.7660	1812.8022	-0.0362	0	R.DEGQEGCTFLAALMQK.D Oxidation (M)
410 - 428	2233.9817	2232.9744	2233.0660	-0.0916	1	K.RFGANMLTIGYAIYQCPDK.D Oxidation (M)
429 - 438	1249.4950	1248.4877	1248.6000	-0.1123	1	K.DGHLSRDFFR.Y
530 - 553	2680.3801	2679.3728	2679.3313	0.0416	1	R.VAGEDMEVSAEELEYVNAVLQKK.T Oxidation (M)
561 - 580	2194.9448	2193.9375	2194.1086	-0.1710	1	R.LSLSCRNIISLMDTSGNGK.L Oxidation (M)
588 - 594	935.3381	934.3308	934.5276	-0.1968	1	R.VFWDKLLK.H
658 - 671	1577.8038	1576.7965	1576.8573	-0.0608	1	R.LENASRVFQSLSVK.N

No match to: 905.3300, 909.1039, 916.3305, 922.3142, 927.5897, 933.3311, 938.3033, 941.5869, 948.3018, 951.3071, 958.3135, 964.2993, 968.2548, 977.2985, 985.5811, 996.6151, 1002.5854, 1012.1665, 1022.1423, 1028.1289, 1034.1373, 1044.0934, 1052.0983, 1058.5376, 1060.0601, 1066.0592, 1072.0742, 1082.0270, 1088.0360, 1097.9929, 1103.9977, 1110.4823, 1118.5260, 1142.5225, 1151.6027, 1163.5565, 1179.5166, 1193.5009, 1218.4747, 1223.0303, 1233.4574, 1238.9926, 1254.9559, 1261.9673, 1270.9175, 1276.9293, 1283.5374, 1291.5000, 1292.8967, 1306.5088, 1313.5675, 1320.4485, 1334.4587, 1339.5229, 1350.4932, 1357.4855, 1365.4561, 1383.4686, 1399.5476, 1415.6119, 1436.7765, 1439.7968, 1446.7717, 1450.1492, 1453.8231, 1462.7925, 1466.1490, 1475.7952,

1479.8246, 1486.8202, 1493.8304, 1501.7882, 1507.8538, 1523.7709, 1531.8394, 1549.8363, 1555.8293, 1567.7198, 1574.8036, 1581.7418, 1589.7075, 1596.7417, 1604.8148, 1612.7150, 1624.7590, 1630.8070, 1638.8091, 1649.7606, 1657.7340, 1665.7599, 1669.7847, 1677.7629, 1690.7710, 1694.7604, 1707.7018, 1715.7562, 1724.7472, 1732.7189, 1740.7324, 1749.7350, 1754.7177, 1763.6917, 1766.6866, 1781.7284, 1791.6514, 1794.7183, 1803.7739, 1821.7622, 1851.8158, 1867.7748, 1880.7999, 1888.7974, 1894.8097, 1902.7983, 1907.7975, 1915.7743, 1921.7960, 1930.7806, 1940.8037, 1949.8121, 1964.8499, 1978.8367, 1986.8525, 2002.8846, 2015.8427, 2022.8669, 2029.8842, 2037.8561, 2044.8960, 2058.9016, 2066.8943, 2076.9033, 2085.8708, 2095.8984, 2101.9185, 2115.9199, 2149.9512, 2170.9143, 2185.9570, 2206.9805, 2210.9900, 2225.0081, 2248.9900, 2264.0132, 2279.0559, 2283.0662, 2296.0632, 2299.0474, 2308.0488, 2319.0691, 2342.9780, 2349.1167, 2358.0381, 2372.0625, 2383.8970, 2399.0220, 2403.1580, 2416.1289, 2419.1428, 2429.1023, 2446.1433, 2448.1357, 2458.1501, 2482.1492, 2487.1460, 2501.2063, 2510.1462, 2525.1604, 2541.1853, 2554.2046, 2564.3054, 2584.2332, 2594.2590, 2602.2693, 2612.2781, 2626.2852, 2637.2834, 2651.3340, 2661.3315, 2705.2568, 2736.4053, 2746.4963, 2780.5745, 2872.5935, 2902.6458, 2932.7639, 3052.9626



51 Heat shock cognate 71 kDa protein

Number of mass values searched: **50**

Number of mass values matched: **13**

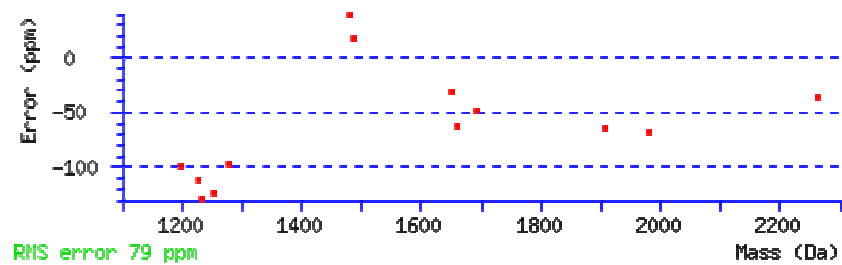
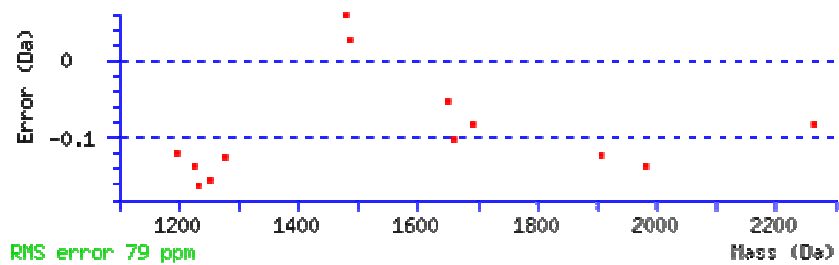
Sequence Coverage: **26%**

Matched peptides shown in **Bold Red**

1 MSK**GPAVGID LGTTYSCVGV FQH GKVEIIA NDQGNRTTPS YVAFTDTER**
51 IGDAAK**NQVA MNPTNTVFDA** KRLIGRRFDD AVVQSDMKHW PFMVVNDAGR
101 PKVQVEYKGE TK**SFYPEEVS SMVLTKMKEI** AEAYLGK**TVT NAVVTVPAYF**
151 **NDSQR**QATKD **AGTIAGLNVL RIINEPTAAA IAYGLDKKVG** AERNVLIFDL
201 GGGTFDVSIL TIEDGIFEVK **STAGDTHLGG EDFDNRMVNH FIAEFK**RKHK
251 KDISENKRAV RRLRTACERA KRTLSSSTQA SIEIDSLYEG IDFYTSITRA
301 **RFEELNADLF** RGTLPVEKA LRDAKLDKSQ IHDIVLVGGS TRIPKIQKLL
351 QDFFNKELN KSINPDEAVA YGAAVQAAIL SGDKSENVQD LLLLDVTPLS
401 LGIETAGGVM TVLIKRNTTI PTKQTQFTT YSDNQPGVLI QVYEGERAMT
451 KDNLLGKFE LTGIPPAPRG VPQIEVTFDI DANGILNVSA VDKSTGKENK
501 ITITNDKGR LSKEDIERMVQ EAEKYKAED EQRDKVSSKN SLESYAFNMK
551 ATVEDEKLQG KINDEKQKI LDK**CNEIISW LDK**NQTAEKE EFEHQKKELE
601 KVCNPIITKL YQSAGGMPGG MPGGFPGGGA PPSGGASSGP TIEEVD

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
4 - 25	2263.0352	2262.0279	2262.1104	-0.0824	0	K.GPAVGIDLGGTTYSCVGVFQHGK.V
26 - 36	1228.4901	1227.4828	1227.6207	-0.1379	0	K.VEIIANDQGNR.T
37 - 49	1487.7269	1486.7196	1486.6940	0.0256	0	R.TTPSYVAFTDTER.L
57 - 71	1649.7430	1648.7357	1648.7879	-0.0522	0	K.NQVAMNPTNTVFDK.R
113 - 128	1907.7919	1906.7846	1906.9056	-0.1210	1	K.SFYPEEVSSMVLTKMK.E 2 Oxidation (M)
138 - 155	1981.8618	1980.8545	1980.9905	-0.1360	0	K.TVTNAVVTVPAYFNDSQR.Q
160 - 171	1199.5560	1198.5487	1198.6670	-0.1183	0	K.DAGTIAGLNVLR.I
172 - 187	1659.7927	1658.7854	1658.8879	-0.1025	0	R.IINEPTAAAIAAYGLDK.K
221 - 236	1691.6429	1690.6356	1690.7183	-0.0827	0	K.STAGDTHLGGEDFDNR.M
237 - 246	1235.4639	1234.4566	1234.6169	-0.1602	0	R.MVNHFAEFK.R
300 - 311	1480.8118	1479.8045	1479.7470	0.0575	1	R.ARFEELNADLFR.G
302 - 311	1253.4620	1252.4547	1252.6088	-0.1541	0	R.FEELNADLFR.G
574 - 583	1277.4952	1276.4879	1276.6122	-0.1242	0	K.CNEIISWLDK.N

No match to: 927.5770, 941.5832, 1002.5743, 1058.5294, 1066.0536, 1082.5155, 1089.4877, 1108.4257, 1163.5367, 1179.5006, 1211.5510, 1267.4670, 1292.4679, 1307.4840, 1415.6079, 1439.7983, 1457.7843, 1479.8204, 1494.8153, 1501.7424, 1508.8452, 1555.8235, 1567.7205, 1595.7357, 1639.8617, 1668.7748, 1705.6669, 1724.7461, 1746.6854, 1766.6730, 1794.7031, 1880.7963, 1993.8529, 2225.0266, 2284.0864, 2447.1526, 2775.4980



52 Cytochrome P450 2D11

Number of mass values searched: **250**

Number of mass values matched: **16**

Sequence Coverage: **43%**

Matched peptides shown in **Bold Red**

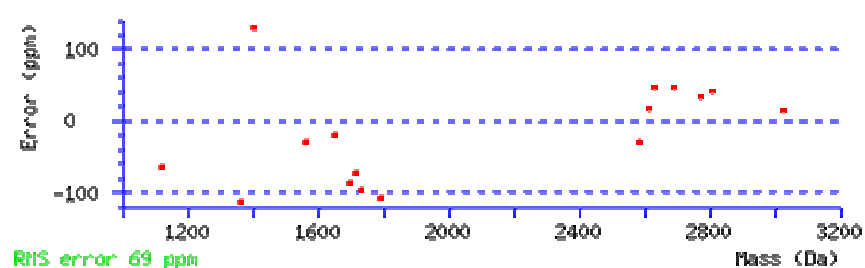
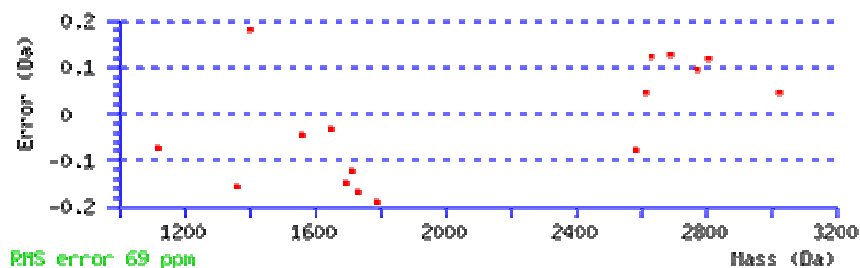
1 **MELLTGAGLW SVAIFTVIFI LLVDMHR**HQ HWTSRCPGPG VPWPVLGNL
51 QVDLDNMPYS LYKLQNR**YGD VFSLQMAWKP MVVINGLKAM** KEMLLTCGED
101 TADRPPVPIF EYLGVKPGSQ GVVLPAPYGP WREQRRFSVS TLRNFGLG**K**
151 **SLEEWVTKEA RHLCDAF**TAQ AGQPINPNM LNKSTCNVIA SLIFARRFEY
201 **EDPFLIRMLK** MLK**ECFTEIS GFIPGVLNEF PIFLRIPGLA DMVFQGGKSF**
251 **MAILDNLLTE NR**TTWDPDQP PR**NLDAFLA EIEKAK**GNAE SSFNENLRM
301 VVLDLFTAGM VTTSTTLSWA LLLMILHPDV QRR**VQQEIDA VIGVQHP**EM
351 **ADQAR**MPYTN AVIHEVQRFGL TLLHCLCHAS QVVFTFTQVQD FLVTKGSTLI
401 PNLSSVLKGE TWWEKPLRFH PEHFLDAQGH FVKPEAFMPF SAGHR**SCLGE**
451 **ALARMELFLF FTCLLQRFSI SVPDGGQP**PS NYR**VHAI**PVA PFPYQLCAVM
501 HEQGH

Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence

2 - 28 **3027.7537 3026.7464 3026.7031 0.0433 0 M.ELLTGAGLWSVAIFTVIFILLVDMHR.H**
68 - 91 **2774.5020 2773.4947 2773.4005 0.0942 1 R.YGDVFSLQMAWKPMVVINGLKAMK.E** 3 Oxidation (M)
150 - 158 **1119.5321 1118.5248 1118.5972 -0.0723 1 K.KSLEEWVTK.E**
159 - 183 **2809.4688 2808.4615 2808.3435 0.1180 1 K.EARHLCDAF**TAQAGQPINPNMLNK.S Oxidation (M)
198 - 210 **1700.7227 1699.7154 1699.8643 -0.1489 1 R.FEYEDPFLIRMLK.M**
214 - 235 **2585.2305 2584.2232 2584.3036 -0.0804 0 K.ECFTEISGFIPGVLNEFPIFLR.I**
236 - 248 **1403.9181 1402.9108 1402.7279 0.1829 0 R.IPGLADMVFQGGK.S**
249 - 262 **1652.7998 1651.7925 1651.8239 -0.0314 0 K.SFMAILDNLLTENR.T** Oxidation (M)
273 - 284 **1363.5548 1362.5475 1362.7031 -0.1555 0 R.NLDAFLAEIEK.A**
273 - 286 **1562.7958 1561.7885 1561.8351 -0.0466 1 R.NLDAFLAEIEKAK.G**
333 - 355 **2618.3564 2617.3491 2617.3031 0.0461 1 R.RVQQEIDAVIGVQHP**EMADQAR.M
333 - 355 **2634.4277 2633.4204 2633.2980 0.1224 1 R.RVQQEIDAVIGVQHP**EMADQAR.M Oxidation (M)
446 - 467 **2691.4734 2690.4661 2690.3383 0.1279 1 R.SCLGEALARMELFLFF**TCLLQR.F Oxidation (M)
455 - 467 **1717.7565 1716.7492 1716.8732 -0.1239 0 R.MELFLFF**TCLLQR.F
455 - 467 **1733.7054 1732.6981 1732.8681 -0.1699 0 R.MELFLFF**TCLLQR.F Oxidation (M)
468 - 483 **1791.6750 1790.6677 1790.8588 -0.1910 0 R.FSISVPDGGQP**PSNYR.V

No match to: 907.5479, 909.0749, 915.0704, 920.9401, 921.5902, 923.2885, 926.6112, 928.3618, 931.5953, 937.6088, 938.5287, 941.3238, 947.3952, 953.0029, 953.5353, 955.2898, 959.1671, 965.2753, 967.0538, 969.4506, 975.3014, 982.6368, 990.4473, 996.6091, 1001.5267, 1002.5798, 1012.5142, 1018.3087, 1031.5204, 1034.1117, 1045.1688, 1058.5436, 1066.0367, 1081.9880, 1087.9943, 1101.9690, 1104.9484, 1106.4941, 1113.8204, 1125.5520, 1131.8561, 1132.6453, 1139.5007, 1144.5502, 1147.8733, 1155.4973, 1161.5563, 1164.6033, 1173.8469, 1175.4525, 1179.4915, 1188.4099, 1191.4976, 1201.4767, 1219.5328, 1227.2256, 1232.9282, 1233.4408, 1240.5316, 1244.9423, 1253.1119, 1260.6532, 1262.5392, 1265.4634, 1272.4235, 1277.5248, 1292.8252, 1300.4434,

1302.4131, 1307.8585, 1316.5564, 1320.3784, 1337.6829, 1345.4811, 1350.4739, 1358.4442, 1365.4645, 1378.7483, 1384.4556, 1423.7473, 1430.6393, 1434.8232, 1436.7800, 1456.7441, 1461.8280, 1475.7792, 1482.7140, 1485.8179, 1489.8563, 1491.8064, 1498.7263, 1507.8450, 1519.9243, 1527.8856, 1529.8103, 1540.9769, 1549.8546, 1555.8088, 1571.7567, 1578.8210, 1585.8214, 1594.7250, 1604.8951, 1614.7170, 1623.9727, 1630.8551, 1633.8103, 1641.7511, 1649.8939, 1658.7173, 1662.6328, 1675.8419, 1690.0814, 1696.7715, 1707.6700, 1715.7556, 1726.6863, 1730.6455, 1745.7834, 1748.6393, 1752.7344, 1760.8108, 1765.6421, 1766.6444, 1774.9370, 1777.6445, 1780.7063, 1794.6869, 1809.6211, 1838.7883, 1851.8027, 1862.8790, 1890.9158, 1898.7002, 1914.7412, 1922.8712, 1931.8335, 1940.8231, 1948.8146, 1965.7617, 1974.1514, 1979.7971, 1987.5942, 1993.8386, 2002.0570, 2005.3762, 2008.8153, 2017.9470, 2025.8297, 2034.3954, 2038.7740, 2050.8701, 2064.8669, 2081.9338, 2092.2397, 2096.9187, 2105.9019, 2121.9187, 2132.7913, 2135.9861, 2149.9612, 2163.9392, 2166.9558, 2190.0339, 2193.9280, 2201.9492, 2207.9683, 2221.0078, 2225.0061, 2232.9810, 2249.9648, 2263.0054, 2265.0557, 2276.0059, 2280.1675, 2282.0830, 2284.0618, 2298.0662, 2307.0347, 2320.0122, 2342.8975, 2359.1025, 2367.1211, 2381.0784, 2383.8794, 2397.5146, 2398.9719, 2419.1719, 2435.1367, 2446.1436, 2448.1238, 2457.2017, 2475.0093, 2482.1299, 2487.1348, 2500.2129, 2503.1689, 2525.1509, 2541.1997, 2565.2629, 2582.2622, 2606.2097, 2611.2839, 2637.2563, 2648.4082, 2652.3657, 2666.4287, 2670.2876, 2681.8223, 2701.3420, 2704.2839, 2707.5042, 2717.2385, 2746.5510, 2757.5396, 2765.5500, 2780.5847, 2791.4546, 2806.5076, 2831.3921, 2872.6267, 2889.6570, 2898.7937, 2921.8127, 2924.6589, 2931.7559, 2949.6580, 2961.9478, 2975.7747, 2989.8079, 2999.9150, 3005.9878, 3039.5500, 3052.9690



53 Pyruvate kinase isozymes M1/M2

Number of mass values searched: **200**

Number of mass values matched: **15**

Sequence Coverage: **38%**

Matched peptides shown in **Bold Red**

1 MPKPHSEAGT AFIQTQQLHA AMADTFLEHM CRLDIDSAPI
TARNTGICT

51 IGPASR**SVEM LKEMIKSGMN VAR**LNFSHGT HEYHAETIKN VREATESFAS

101 DPILYRPVAV ALDTKGPEIR TGLIK**GSGTA EVELKK**GATL KITLDNAYME

151 KCDENILWLD YKNICKVVEV GSKIYVDDGL ISLQVKEK**GA DFLVTEVENG**

201 **GSLGSK****GVN LPGAAVDLPA VSEKDIQDLK FGVEQDVMV FASFIR**KAAD

251 VHEVRKVLGE KGKNIKISK IENHEGVR**RF DEILEASDGI MVAR**GDLGIE

301 IPAQKVFLLAQ KMMIGR**CNRA GKPVICATQM LESMIK**KPRP TR**AEGSDVAN**

351 **AVLDGADCIM LSGETAKGDY PLEAVR**MQHL IAREAEAAIY HLQLFEELRR

401 LAPITSDPTE AA**AVGAVEAS FKCCSGAIV LTKSGRSAHQ VARYRPR**API

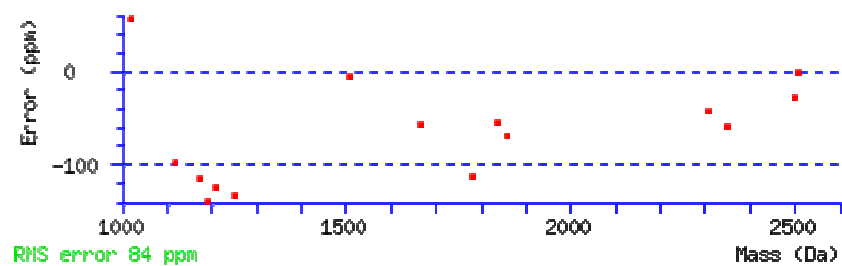
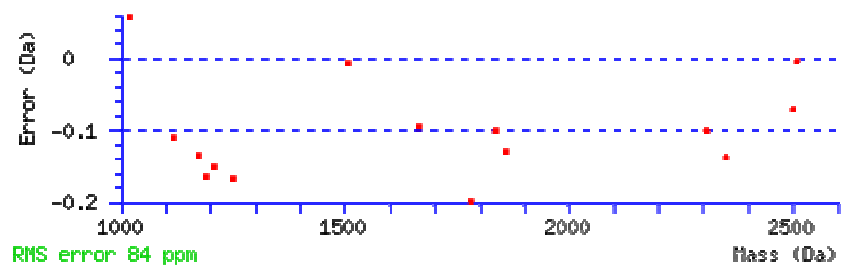
451 **IAVTRNPQTA RQAHLR****GIF PVLCKDAVLN AWAEDVDLRV NLAMDVGKAR**

501 GFFKKGDVVI VLTGWRPGSG FTNTMRVVPV P

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
57 - 66	1207.4923	1206.4850	1206.6352	-0.1502	1	R.SVEMLKEMIK.S
63 - 73	1251.4513	1250.4440	1250.6111	-0.1671	1	K.EMIKSGMNVAR.L Oxidation (M)
126 - 136	1118.4961	1117.4888	1117.5979	-0.1091	1	K.GSGTAEVELKK.G
189 - 206	1779.6770	1778.6697	1778.8687	-0.1989	0	K.GADFLVTEVENGGSLGSK.K
208 - 230	2349.1299	2348.1226	2348.2587	-0.1361	1	K.GVNLPGAAVDLPAVSEKDIQDLK.F
231 - 246	1859.7708	1858.7635	1858.8924	-0.1289	0	K.FGVEQDVMVFASFIR.K
279 - 294	1837.8109	1836.8036	1836.9040	-0.1004	1	R.RFDEILEASDGIMVAR.G Oxidation (M)
280 - 294	1665.7219	1664.7146	1664.8080	-0.0933	0	R.FDEILEASDGIMVAR.G
317 - 336	2307.0449	2306.0376	2306.1367	-0.0991	1	R.CNRAGKPVICATQMLESMIK.K
343 - 367	2510.1353	2509.1280	2509.1312	-0.0032	0	R.AEGSDVANAVLDGADCIMLSGETAK.G Oxidation (M)
368 - 376	1019.5742	1018.5669	1018.5083	0.0586	0	K.GDYPLEAVR.M
448 - 461	1507.8638	1506.8565	1506.8630	-0.0065	1	R.APIIAVTRNPQTA.R
468 - 489	2501.2148	2500.2075	2500.2784	-0.0709	1	R.GIFPVLCKDAVLNAWAEDVDLR.V
490 - 500	1173.5060	1172.4987	1172.6336	-0.1348	1	R.VNLAMDVGKAR.G
490 - 500	1189.4707	1188.4634	1188.6285	-0.1651	1	R.VNLAMDVGKAR.G Oxidation (M)

No match to: 905.5579, 912.3720, 915.3774, 921.3270, 927.5601, 931.5862, 939.3342, 948.5007, 951.5801, 958.5265, 963.5306, 969.5731, 973.5755, 982.4802, 985.5502, 995.5942, 1001.5516, 1002.5639, 1029.5256, 1031.5265, 1034.1091, 1045.5581, 1053.0784, 1058.5199, 1065.9911, 1072.0366, 1074.5012, 1081.9922, 1088.0109, 1089.5045, 1103.9604, 1106.4758, 1108.4277, 1125.4558, 1132.4861, 1140.4948, 1146.5088, 1153.4963, 1164.4838, 1179.4923, 1193.4980, 1201.5090, 1218.4343, 1232.4546, 1233.4484, 1245.4670, 1260.9374, 1276.9020, 1277.5348, 1285.3883, 1292.8615, 1302.5051, 1309.4600, 1316.5068, 1320.3971, 1329.4380, 1339.5127, 1350.4636, 1359.4396, 1365.4244, 1372.4495, 1379.4745, 1383.4628, 1393.5258, 1410.6227, 1421.6055, 1425.6672, 1434.7424,

1436.7808, 1443.6707, 1452.7322, 1459.7655, 1469.8582, 1475.7764, 1487.8125, 1489.8527, 1517.7849, 1524.7772, 1531.8401, 1540.8643, 1547.7740, 1549.8524, 1555.8168, 1562.8162, 1571.7753, 1578.8185, 1587.7440, 1593.7454, 1595.7518, 1604.8330, 1614.7545, 1633.7821, 1638.7836, 1651.7461, 1657.7185, 1675.7900, 1678.7869, 1686.8693, 1695.7687, 1699.7267, 1707.6636, 1716.7412, 1731.7173, 1735.7056, 1743.7732, 1750.6868, 1762.6942, 1765.6320, 1791.6216, 1794.6859, 1807.7894, 1813.7638, 1821.6932, 1842.5758, 1851.7924, 1867.7698, 1877.7422, 1884.6360, 1911.7510, 1927.7721, 1939.7808, 1949.8105, 1965.8982, 1979.8060, 1986.7889, 1993.8228, 2007.8472, 2017.8093, 2022.8611, 2030.8441, 2037.8341, 2045.8777, 2050.8418, 2064.8618, 2073.8149, 2081.8416, 2095.9038, 2104.8564, 2121.9177, 2135.9751, 2149.9385, 2158.8411, 2167.9253, 2185.9480, 2195.9453, 2220.9941, 2225.0017, 2233.9705, 2239.0244, 2248.9866, 2257.9551, 2264.0085, 2277.0325, 2282.0659, 2284.0566, 2298.0757, 2319.0613, 2329.0649, 2339.9595, 2367.1631, 2399.0083, 2418.0999, 2421.1333, 2446.1428, 2448.1279, 2457.1838, 2481.1335, 2487.1240, 2527.1389, 2564.3049, 2584.2148, 2627.3506, 2642.2517, 2652.3274, 2662.3464, 2691.4868, 2705.2676, 2717.2334, 2733.2673, 2780.5774, 2808.4836, 2823.5737, 2872.6226, 2895.6538, 2932.7971



56 Ornithine aminotransferase, mitochondrial

Number of mass values searched: **75**

Number of mass values matched: **8**

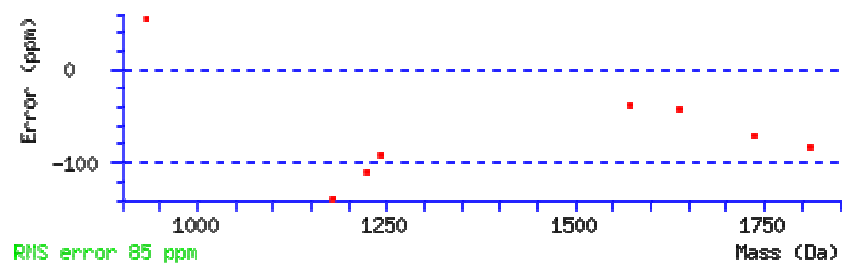
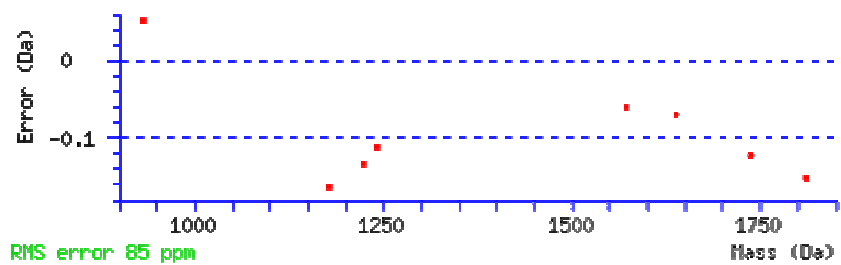
Sequence Coverage: **20%**

Matched peptides shown in **Bold Red**

1 MLSKLASLQT IAALRR**GVHT SVASATSVAT KKTEQGPPSS EYIFER**ESK'
51 **GAHNYHPLPV ALER**GKGIYM **WDVEGR**QYFD FLSAYGAVSQ GHCHPKIIDA
101 MKSQVDKLTLSRAFYNNVL GEYEEYITKL FNYNKVLPMM TGVEAGETAC
151 KLARR**WGYTV KGIQK**YKAKI VFADGNFWGR TLSAISSSTD PTSYDGFPGPF
201 MPGFETIPYN DLPALERALQ DPNVAAFMVE PIQGEAGVIV PDPGYLTGVR
251 ELCTR**HQVLF IADEIQTGLA RT**GRWLAVDH ENVRPDMVLL GKALSGGLYP
301 VSAVLCDDDEI MLTIKPGEHG STYGGNPLGC RIAIAALEVL EEENLAENAD
351 KMGAILRKEL MKLPSDVVTS VRGKGLLNAI VIRETKDCDA WKVCLRLRDN
401 GLLAKPTHGD IIRLAPPLVI KEDEIR**ESVE IINK**TILSF

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
16 - 31	1571.7911	1570.7838	1570.8427	-0.0589	1	R.RGVHTSVASATSVATK.K
33 - 46	1639.6893	1638.6820	1638.7525	-0.0705	0	K.TEQGPPSSEYIFER.E
50 - 64	1736.7644	1735.7571	1735.8794	-0.1223	0	K.YGAHNYHPLPVALER.G
67 - 76	1225.4320	1224.4247	1224.5597	-0.1350	0	K.GIYMWDVEGR.Q
67 - 76	1241.4495	1240.4422	1240.5547	-0.1124	0	K.GIYMWDVEGR.Q Oxidation (M)
156 - 165	1179.4891	1178.4818	1178.6448	-0.1630	1	R.WGYTVKGIQK.Y
256 - 271	1810.8285	1809.8212	1809.9737	-0.1525	0	R.HQVLFIADEIQTGLAR.T
427 - 434	931.5608	930.5535	930.5022	0.0513	0	R.ESVEIINK.T

No match to: 911.0968, 917.4144, 921.4565, 937.4077, 945.5325, 948.4932, 957.3528, 965.4413, 973.6011, 985.5302, 1000.5397, 1002.5543, 1031.5203, 1034.1448, 1052.0988, 1058.5143, 1066.0681, 1082.0474, 1084.0359, 1089.5038, 1106.4462, 1108.4297, 1118.4799, 1141.4503, 1147.5315, 1193.5107, 1201.4023, 1217.3750, 1233.4469, 1265.4945, 1277.5334, 1300.3544, 1307.4767, 1320.3701, 1329.4852, 1339.5122, 1353.6067, 1365.4185, 1383.4868, 1436.7731, 1475.7871, 1489.8932, 1507.8639, 1549.8484, 1555.8401, 1578.8240, 1585.6797, 1595.7689, 1604.8741, 1653.7413, 1699.7673, 1707.6947, 1716.7740, 1766.6769, 1791.6146, 1837.8477, 1993.8596, 2171.9204, 2225.0740, 2283.0945, 2297.0774, 2383.9084, 2448.1599, 2487.2109, 2510.1868, 2642.2224, 2705.3167



57 Transcobalamin-2

Number of mass values searched: **80**

Number of mass values matched: **11**

Sequence Coverage: **36%**

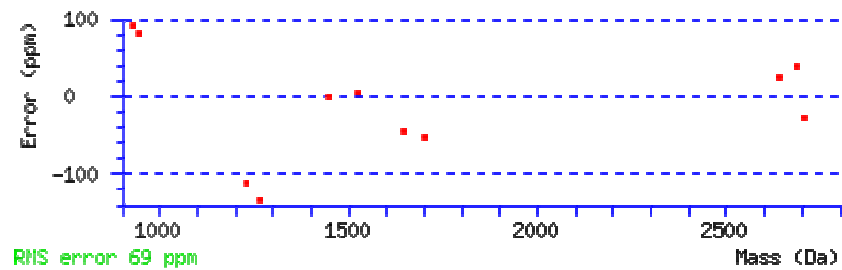
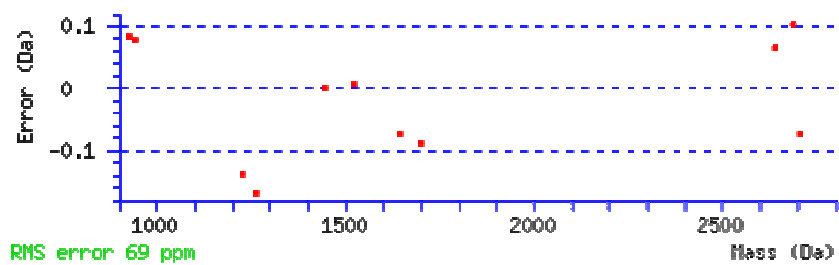
Matched peptides shown in **Bold Red**

1 MELLKALLLL SGVFGALAEF CVIPRIDSQL VEKLGQRLLP **WMDRLSSEIQI**
51 **NPSVFGVGLR**L SSMQAGTKED LYLHSLK**IHY QQCLLR**STSS DDNSSCQPKL
101 **SGGSLALYLL ALR**ANCEFFG SRKGDRLISQ LKWFLDEDEK AIGHNHEGHP
151 NTNYYQYGLS ILALCVHQKR LHDSVVGKLL YAVEHDYFTY QGHVSVDETEA
201 MAGLALTCLE **RFNFN**SDLRP **RIT**MAIETVR EKILKSQAPE GYFGNIYSTP
251 LALQMLMTSP ASGVGLGTAC IKAGTSLLLS LQDGAQFNPL MISQLLPILN
301 **HKTYLDLIFP DCQASR**VMLV PAVEDPVHIS EVISVTLK**VA SALS**PYEQTF
351 **FVFAGSSLED VLKLAQDGGG** FTYGTQASLS GPYLTSVLGK DAGDREYWQL
401 **LRAPDTPLLQ GIADYKPDG** ETIELRLVLRW

Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence

38 - 44 930.5723 929.5650 929.4793 0.0857 0 R.LLPWMDR.L
38 - 44 946.5587 945.5514 945.4742 0.0772 0 R.LLPWMDR.L Oxidation (M)
45 - 59 1645.8160 1644.8087 1644.8835 -0.0748 0 R.LSSEQLNPSVFGVGLR.L
78 - 86 1230.5042 1229.4969 1229.6339 -0.1370 0 K.IHYQQCLLR.S
100 - 113 1446.8682 1445.8609 1445.8606 0.0004 0 K.LSGGSLALYLLALR.A
212 - 221 1265.4708 1264.4635 1264.6313 -0.1677 0 R.FNFNSDLRPR.I
303 - 316 1698.7258 1697.7185 1697.8083 -0.0898 0 K.TYLDLIFPDCQASR.V
339 - 363 2705.2981 2704.2908 2704.3636 -0.0728 0 K.VASALSPYEQTFFVFAGSSLEDVLK.L
364 - 390 2688.4548 2687.4475 2687.3443 0.1032 0 K.LAQDGGGFTYGTQASLSGPYLTSVLGK.D
391 - 402 1521.7526 1520.7453 1520.7372 0.0082 1 K.DAGDREYWQLLR.A
403 - 426 2640.4170 2639.4097 2639.3442 0.0655 0 R.APDTPLLQGIADYKPDGETIELR.L

No match to: 902.5616, 913.5627, 919.5359, 959.5403, 985.5684, 989.5574, 1002.5692, 1034.1327, 1058.5283, 1066.0511, 1089.4982, 1106.4886, 1118.5043, 1142.5051, 1179.4955, 1233.4517, 1307.4865, 1339.5345, 1354.5142, 1383.4689, 1431.6575, 1436.7794, 1475.7841, 1489.8790, 1507.8561, 1531.8314, 1549.8329, 1555.8179, 1571.7671, 1577.8094, 1595.7369, 1604.8289, 1609.7465, 1634.8208, 1659.8148, 1669.7787, 1707.6808, 1716.7548, 1750.7217, 1766.6665, 1780.6917, 1794.6960, 1837.8201, 1890.8369, 1940.8048, 1993.8467, 2063.9385, 2149.9648, 2170.9146, 2192.9651, 2225.0156, 2233.9978, 2239.0391, 2265.0437, 2298.0967, 2310.0710, 2336.0947, 2353.1321, 2367.1621, 2383.9133, 2399.0950, 2421.1677, 2432.1284, 2446.1660, 2448.1528, 2487.1626, 2510.1555, 2654.4265, 2902.6877



58 WNT1-inducible-signaling pathway protein 1

Number of mass values searched: **70**

Number of mass values matched: **6**

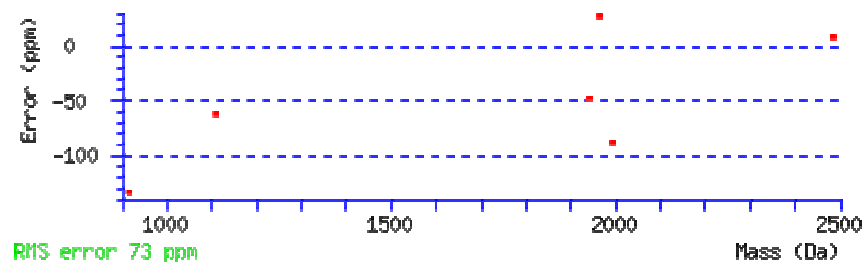
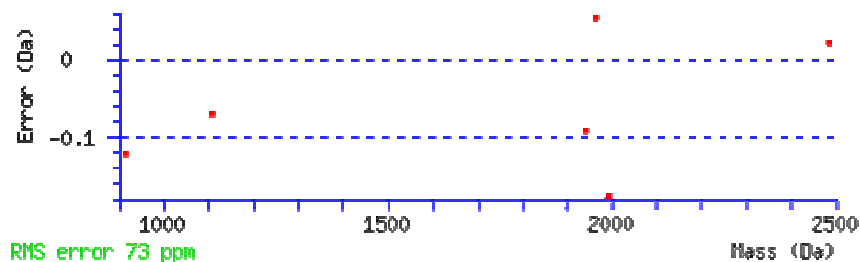
Sequence Coverage: **23%**

Matched peptides shown in **Bold Red**

1 MRWLLPWTLA AVAVLRVGNL LATALSPTPT TMTFTPAPLE ETTTRPEFCI
51 WPCECPQSPP RCPLGVSLIT DGCECKICA QQLGDNCTEA AICDPHRGLY
101 CDYSGDRPRY AIGVCAQVVG VGCVLDGVRY TNGESFPNC RYNCTCIDGT
151 VGCTPLCLSP RPPRLWCRQP RHVRVPGQCC EQWVCDDAR RPR**QTALLDT**
201 **RAFAASGAVE QRY**ENCIAYT SPWSPCSTTC GLGISTRISN VNARCWPEQE
251 SRLCNLRPCD **VDIQLHIK**AG KK**CLAVYQPE EATNFTLAGC VSTR**TYRPKY
301 **CGVCTDNRCC IPYK**SKTISV DFQCPEPGPF SR**QVLWINAC FCNLSCR**NPN
351 DIFADLESYP DFEIIAN

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
194 - 201	917.3826	916.3753	916.4978	-0.1225	0	R.QTALLDTR.A
202 - 212	1106.4894	1105.4821	1105.5516	-0.0695	0	R.AFAASGAVEQR.Y
253 - 268	1993.8558	1992.8485	1993.0237	-0.1752	0	R.LCNLRPCD VDIQLHIK .A
273 - 294	2487.1865	2486.1792	2486.1570	0.0222	0	K.CLAVYQPE EATNFTLAGCVSTR .T
300 - 314	1965.8605	1964.8532	1964.8002	0.0531	1	K.YCGVCTDN RCCIPYK .S
333 - 347	1940.8007	1939.7934	1939.8855	-0.0921	0	R.QVLWINAC FCNLSCR .N

No match to: 985.5701, 1002.5750, 1031.5382, 1034.1294, 1045.5593, 1052.0906, 1058.5236, 1066.0559, 1082.0194, 1089.4966, 1118.4982, 1142.5094, 1179.5035, 1233.4658, 1253.4647, 1267.4690, 1320.3988, 1354.4862, 1436.7767, 1475.7854, 1487.7528, 1501.7434, 1507.8561, 1549.8363, 1555.8276, 1571.7867, 1578.8269, 1604.8339, 1638.7898, 1659.7822, 1691.6597, 1699.7361, 1707.6852, 1716.7626, 1750.7133, 1764.6616, 1766.6750, 1780.6949, 1791.6422, 1794.7053, 1804.7192, 1816.6921, 1838.8135, 1851.8094, 1981.8654, 2150.9614, 2167.0063, 2193.9807, 2225.0305, 2234.0144, 2248.9973, 2263.0479, 2281.0757, 2298.1108, 2307.0684, 2320.0820, 2354.1523, 2383.9324, 2399.0229, 2421.1880, 2448.1738, 2502.2192, 2565.2803, 2705.3118



60 Alpha-enolase

Number of mass values searched: **75**

Number of mass values matched: **13**

Sequence Coverage: **38%**

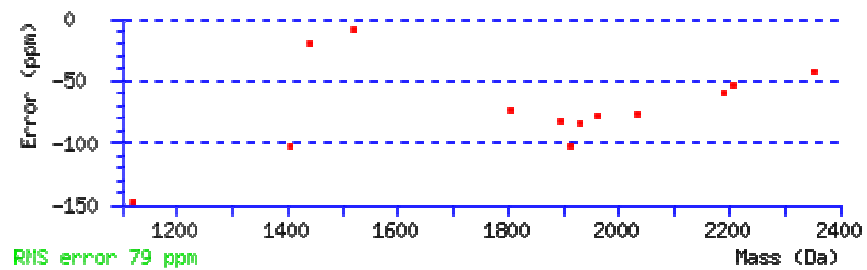
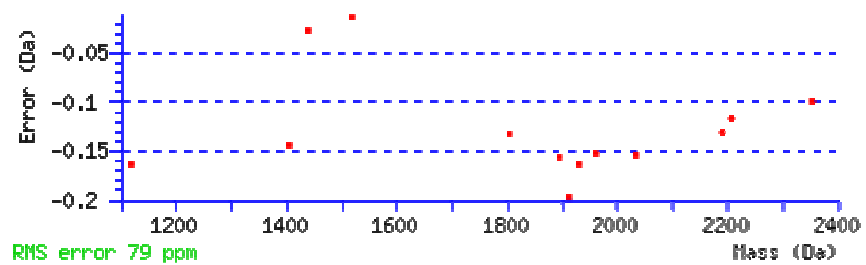
Matched peptides shown in **Bold Red**

1 MSILRIHARE IFDSR**GNPTV EVDLYTAK**GL FR**AAVPSGAS TGIYEAL**ELR
51 DNDKTRFMGK GVSQAVEHIN KTIAPALVSK KVNVEQEKI DKLMIEMDGT
101 ENKSK**FGANA ILGVSLAVCK** AGAVEKGVPL YRHIADLAGN PEVILPVPAP
151 NVINGGSHAG NKL**LAMQEFMI LPVGASSFRE** AMRIGAEVYH NLKNVIKEKY
201 GK**DATNVGDE GGFAPNILEN** KEALELLKTA IAK**AGYTDQV VIGMDVAASE**
251 **FYR**SGKYDLD FKSPDDPSRY **ITPDQLADLY** KSFVQNYPPV SIEDPFDQDD
301 WGAWQK**FTAS AGIQVVGDDL TVTNPK**RIAK AASEKSCNCL LLKVNQIGSV
351 TESLQACKLA QSNWGWGMVS HRS**GETEDTF IADLVVGLCT GQIK**TGAPCR
401 SER**LAKYNQI LR**IEEELGSK AKFAGRSFRN PLAK

Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence

16 - 28 1406.5726 1405.5653 1405.7089 -0.1436 0 R.GNPTVEVDLYTAK.G
33 - 50 1804.8112 1803.8039 1803.9366 -0.1327 0 R.AAVPSGASTGIYEALELR.D
106 - 120 1519.8181 1518.8108 1518.8228 -0.0120 0 K.FGANAILGVSLAVCK.A
163 - 179 1896.8151 1895.8078 1895.9637 -0.1559 0 K.LAMQEFMILPVGASSFR.E
163 - 179 1912.7683 1911.7610 1911.9587 -0.1976 0 K.LAMQEFMILPVGASSFR.E Oxidation (M)
163 - 179 1928.7972 1927.7899 1927.9536 -0.1637 0 K.LAMQEFMILPVGASSFR.E 2 Oxidation (M)
203 - 221 1960.7731 1959.7658 1959.9174 -0.1516 0 K.DATNVGDEGGFAPNILENK.E
234 - 253 2191.9026 2190.8953 2191.0256 -0.1303 0 K.AGYTDQVVIGMDVAASEFYR.S
234 - 253 2207.9109 2206.9036 2207.0205 -0.1169 0 K.AGYTDQVVIGMDVAASEFYR.S Oxidation (M)
270 - 281 1439.7141 1438.7068 1438.7344 -0.0276 0 R.YITPDQLADLYK.S
307 - 326 2032.9005 2031.8932 2032.0477 -0.1545 0 K.FTASAGIQVVGDDLTVTNPK.R
373 - 394 2353.0608 2352.0535 2352.1519 -0.0984 0 R.SGETEDTFIADLVVGLCTGQIK.T
404 - 412 1118.5034 1117.4961 1117.6607 -0.1646 1 R.LAKYNQILR.I

No match to: 909.0877, 917.3311, 931.5867, 985.5668, 996.6185, 1002.5718, 1028.1228, 1031.5374, 1034.1271, 1052.0852, 1058.5265, 1066.0487, 1084.4711, 1089.5051, 1106.4932, 1142.5096, 1165.6324, 1179.4968, 1191.4871, 1233.4519, 1260.9470, 1276.9103, 1307.4811, 1320.3915, 1339.5269, 1354.4679, 1383.4606, 1425.6575, 1436.7729, 1475.7726, 1489.8774, 1507.8507, 1531.8170, 1542.7340, 1549.8320, 1555.8085, 1571.7721, 1578.8134, 1585.7230, 1593.7428, 1604.8236, 1634.7675, 1707.7039, 1716.7488, 1766.6521, 1791.6200, 1794.6837, 1818.8224, 1838.7930, 1940.7949, 1993.8386, 2224.9866, 2233.9607, 2248.9570, 2266.9888, 2298.0635, 2326.0564, 2383.8772, 2447.1123, 2487.1255, 2503.1255, 2705.2502



5 Rab GTPase-binding effector protein 2

Number of mass values searched: **100**

Number of mass values matched: **14**

Sequence Coverage: **19%**

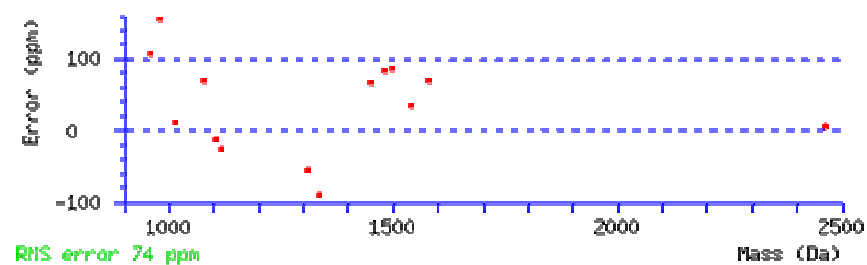
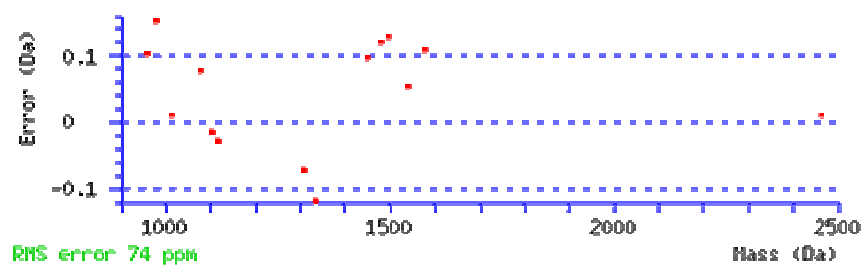
Matched peptides shown in **Bold Red**

1 MAAAPATLAL DPQPQEK**QKD ASESSELSRL RAELAGALAE METMKAVAEV**
51 **SESTK**AEAVA AVQRQCQEEV ASLQAILKDS ISSYETQIAA LKQER**QQQQQ**
101 **DFEEKDRE**ELG HLKQLLAR**AH PLDSLEKQME** KAHEDSEKLR EIVLPMEQEI
151 TELKQKLRQA EELIQEIQR PRQPASLHGS TELLPLSRNP SPPLPLEEP
201 SGDAGPAAEA FAHNCDDSAS ISSFSLGGAA GSASLRGPQG LSPEQEETAS
251 LVSTGTLVPE GIFLPPGYQ LVPDSQWEQL QVEGRQLQK**E LESVSRERDE**
301 **LQEGLRRSNE DCAK**QMQVLL AQVQNSEQLL RTLQGTVSQA QERVQLQMAE
351 LATSHKCLSQ EVKRLNEENQ GLRAEQLPSS ALQGSEQRED QDEALPSSIQ
401 ELHLLVQNTR QQAR**ARQQAQ EHEAER**LRIE IVKLREALDE ETAAKASLER
451 QLRVQREETD VLEASLCSLR IETERVQEQ RKAQLTDLLS EQRAKTLRLQ
501 AELETSEQVQ RDFVRLSQAL QVRLERIRQA ETLQQVRS**SIL DEAPLR**DIRD
551 IKDS

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
18 - 29	1336.5142	1335.5069	1335.6266	-0.1197	1	K.QKDASESSELSR.L
20 - 29	1080.5571	1079.5498	1079.4731	0.0768	0	K.DASESSELSR.L
32 - 45	1480.8241	1479.8168	1479.6949	0.1220	0	R.AELAGALAEMETMK.A Oxidation (M)
32 - 45	1496.8279	1495.8206	1495.6898	0.1308	0	R.AELAGALAEMETMK.A 2 Oxidation (M)
32 - 55	2466.2217	2465.2144	2465.2029	0.0115	1	R.AELAGALAEMETMKAVAEVSESTK.A
96 - 105	1307.5134	1306.5061	1306.5789	-0.0728	0	R.QQQQDFEEK.D
96 - 107	1578.8236	1577.8163	1577.7070	0.1093	1	R.QQQQDFEEKDR.E
119 - 131	1541.8164	1540.8091	1540.7555	0.0536	1	R.AHPLDSLEKQMEK.A Oxidation (M)
290 - 298	1104.5511	1103.5438	1103.5571	-0.0132	1	K.ELESVSRER.D
299 - 306	959.5834	958.5761	958.4720	0.1042	0	R.DELQEGLR.R
299 - 307	1115.5522	1114.5449	1114.5731	-0.0281	1	R.DELQEGLRR.S
307 - 314	979.5790	978.5717	978.4189	0.1529	1	R.RSNEDCAK.Q
415 - 426	1452.7908	1451.7835	1451.6865	0.0970	1	R.ARQQAQEHEAER.L
538 - 546	1013.5736	1012.5663	1012.5553	0.0110	0	R.SILDEAPLR.D

No match to: 901.6014, 908.5963, 911.6083, 913.5970, 916.5970, 923.5925, 926.5950, 929.5991, 935.5974, 939.5944, 941.5908, 943.5884, 949.5951, 953.5880, 956.5874, 971.5907, 973.5805, 982.5854, 985.5803, 987.5812, 996.6010, 1000.5738, 1002.5769, 1010.5771, 1016.5707, 1022.5733, 1028.5712, 1031.5640, 1041.5675, 1044.5680, 1055.5697, 1058.5509, 1064.5608, 1071.5552, 1074.5560, 1086.5542, 1089.5458, 1101.5529, 1118.5486, 1124.5465, 1133.5497, 1144.5464, 1147.5463, 1158.5385, 1161.5376, 1167.5532, 1175.5359, 1179.5181, 1191.5311, 1203.5331, 1206.5354, 1219.5264, 1233.4867, 1246.5271, 1249.5193, 1263.5223, 1274.5203, 1278.5248, 1293.5208, 1322.5081, 1350.5068, 1365.5078, 1379.5233, 1394.5763, 1409.6504, 1423.7136, 1436.7640, 1468.8094,

1489.8556, 1507.8525, 1523.8334, 1549.8412, 1555.8278, 1571.7988, 1597.8123, 1604.8240, 1612.8202, 1626.8202, 1655.8142, 1670.8220, 1724.8314, 1794.7355, 2211.0173, 2421.1880, 2448.1516, 2464.2212



9 SPARC

Number of mass values searched: **100**

Number of mass values matched: **13**

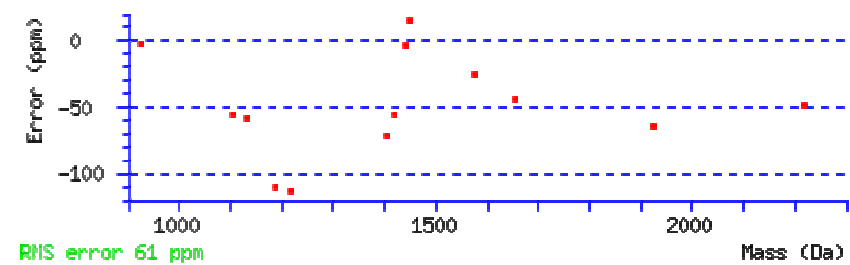
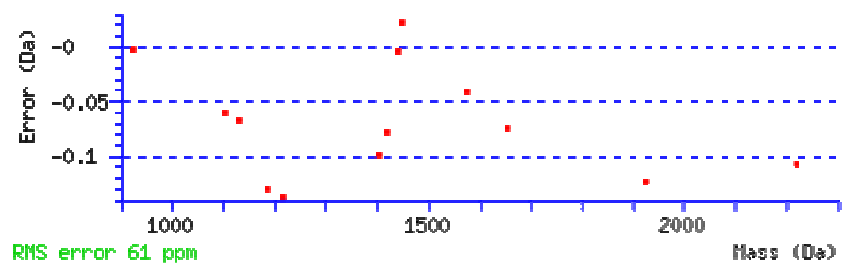
Sequence Coverage: **41%**

Matched peptides shown in **Bold Red**

1 MRAWIFFLLC LAGRALAAPQ QTEVAEEIVE EETVVEETGV PVGANPVQVE
51 MGEFEDGAE TVEEVVADNP CQNHCKHGK VCELDENPT MCVCQDPTSC
101 PAPIGEFEKV CSNDNK**TFDS SCHFFATK**CT LEGTKKGHL **HLDYIGPKY**
151 **IAPCLDSELT EFPLRMRDWL KNLVTLYER DEGNLLTEK** QKLRVKKIHE
201 **NEKRLEAGDH PVELLARDFE** KNYNMYIFPV HWQFGQLDQH PIDGYLSHTE
251 LAPLR**APLIP MEHCTTRFE TCDLNDKYI ALEEWAGCFG IKEQDINKDL**
301 **VI**

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
117 - 128	1447.6532	1446.6459	1446.6238	0.0221	0	K.TFDSSCHFFATK.C
140 - 149	1215.4812	1214.4739	1214.6118	-0.1378	0	K.LHLDYIGPK.Y
150 - 165	1923.8287	1922.8214	1922.9448	-0.1234	0	K.YIAPCLDSELTFFPLR.M
172 - 180	1106.5593	1105.5520	1105.6131	-0.0611	0	K.NLVTLYER.D
172 - 190	2220.0437	2219.0364	2219.1433	-0.1069	1	K.NLVTLYERDEGNLLTEK.Q
181 - 190	1132.4810	1131.4737	1131.5408	-0.0670	0	R.DEGNLLTEK.Q
198 - 204	925.4833	924.4760	924.4777	-0.0017	1	K.IHENEKR.L
204 - 217	1575.8199	1574.8126	1574.8529	-0.0402	1	K.RLEAGDHPVELLAR.D
205 - 217	1419.6805	1418.6732	1418.7518	-0.0785	0	R.LEAGDHPVELLAR.D
256 - 267	1441.6879	1440.6806	1440.6853	-0.0047	0	R.APLIPMEHCTTR.F Oxidation (M)
268 - 278	1403.4789	1402.4716	1402.5711	-0.0995	0	R.FFETCDLNDK.Y
279 - 292	1656.7356	1655.7283	1655.8017	-0.0734	0	K.YIALEEWAGCFGIK.E
293 - 302	1186.5004	1185.4931	1185.6241	-0.1310	1	K.EQDINKDLVI.-

No match to: 910.3611, 919.5107, 931.5536, 937.4913, 945.5878, 985.5529, 1002.5766, 1030.5149, 1033.5212, 1045.5642, 1058.5269, 1060.0568, 1066.0675, 1074.4982, 1082.0333, 1089.5042, 1120.5604, 1140.4960, 1157.5037, 1165.4940, 1179.5021, 1193.4934, 1200.4890, 1233.4744, 1235.4205, 1265.4823, 1270.9232, 1277.5182, 1293.4486, 1307.4767, 1320.4026, 1339.5132, 1350.4679, 1354.4539, 1365.4092, 1377.4629, 1393.5410, 1426.6539, 1433.7394, 1469.8413, 1475.7811, 1489.8552, 1493.7582, 1507.8538, 1523.7972, 1531.8514, 1549.8488, 1556.8557, 1571.7903, 1589.8060, 1604.8239, 1638.7949, 1670.7362, 1681.7800, 1699.7418, 1707.6860, 1716.7609, 1740.6824, 1760.7761, 1766.6753, 1778.7019, 1791.6323, 1808.7672, 1837.8093, 1851.8047, 1867.7996, 1880.8021, 1937.8408, 1951.8499, 1965.8962, 1993.8539, 2022.9325, 2136.0127, 2149.9685, 2184.9819, 2193.9216, 2201.9749, 2225.0303, 2284.0920, 2298.0957, 2383.9104, 2399.0095, 2421.1680, 2448.1448, 2501.2595, 2705.3171, 2717.2563



25 T-complex protein 1 subunit theta

Number of mass values searched: **100**

Number of mass values matched: **11**

Sequence Coverage: **27%**

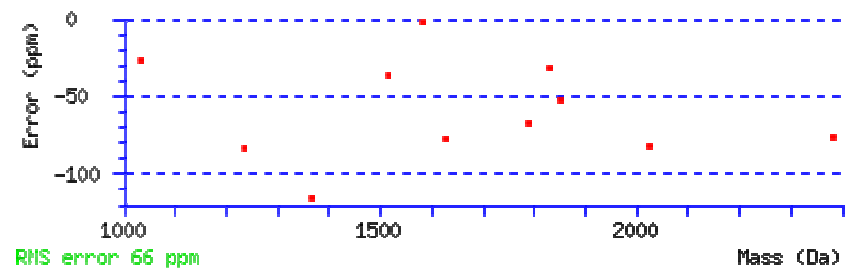
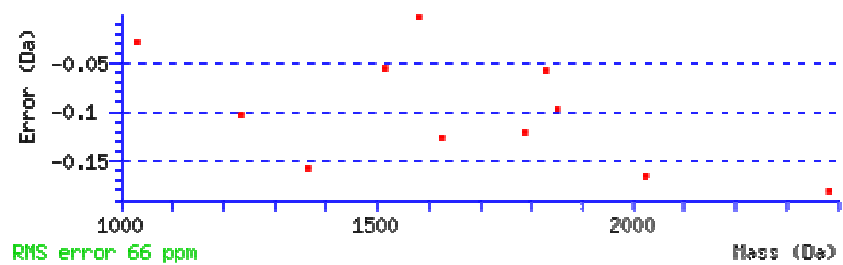
Matched peptides shown in **Bold Red**

1 MALHVPKAPG FAQMLKDGAK HFSGLEEAVY RNIQACK**ELA QTTRTAYGPN**
51 **GMNK**MVINRL EKLFVTNDAA TILRELEVQH PAAKMIVMAS HMQEQEVGDG
101 TNFVLVFAGA LLELAEELLR IGLSVSEVIS GYEIACKKAH EILPELVCCS
151 AK**NLRDVDEV SLLR**TSIMS **KQYGSETFLA** KLIAQACVSI FPDSGNFNVD
201 NIRVCK**ILGS GIYSSSVLHG MVFKK**ETEGD VTSVKDAK**IA VYSCPF**DGMI
251 **TETK**GTVLIK **TAEELMNFSK** **GEENLMDAQV** KAIAGTGANV IVTGGKVADI
301 ALHYANKYNI MLVRL**LNSKWD LR**RLCKTVGA TALPKLTPPV QEEMGHCDSDV
351 YLSEVGDTQV VVFKHEKEDG AISTIVLR**GS TDNL**MDDIER AVDDGVTNFK
401 VLTRDKRLVP GGGATEIELA KQITSYGETC PGLEQYAIKK FAEAFEAIPIR
451 **ALAENSGVKA NEVISK**LYSV HQEGNKNVGL DIEAEVPAVK **DMLEASILD**T
501 **YLGK**YWAIKL ATNAAVTVLR VDQIIMAKPA GGPKPPSGKK DWDDDDQND

Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence

38 - 54 1851.8053 1850.7980 1850.8945 -0.0964 1 K.ELAQTTRTAYGPNGMNK.M
153 - 165 1515.7573 1514.7500 1514.8053 -0.0552 1 K.NLRDVDEVSSLLR.T
166 - 181 1790.7792 1789.7719 1789.8920 -0.1201 1 R.TSIMSKQYGSETFLAK.L
207 - 225 2022.9390 2021.9317 2022.0972 -0.1655 1 K.ILGSGIYSSSVLHGMVFKK.E
239 - 254 1831.8030 1830.7957 1830.8532 -0.0575 0 K.IAVYSCPFDMITETK.G
261 - 281 2383.9302 2382.9229 2383.1035 -0.1806 1 K.TAEELMNFSKGEENLMDAQVK.A
271 - 281 1233.4745 1232.4672 1232.5707 -0.1035 0 K.GEENLMDAQVK.A
315 - 322 1031.5358 1030.5285 1030.5560 -0.0274 1 R.LNSKWDLR.R
379 - 390 1365.4368 1364.4295 1364.5878 -0.1583 0 R.GSTDNLMDIER.A
451 - 466 1629.7538 1628.7465 1628.8733 -0.1268 1 R.ALAENSGVKANEVISK.L
491 - 504 1584.7797 1583.7724 1583.7753 -0.0028 0 K.DMLEASILDYLGK.Y Oxidation (M)

No match to: 1003.5593, 1036.5321, 1058.5240, 1070.5293, 1082.5464, 1093.4967, 1107.4875, 1141.5061, 1165.4985, 1179.4943, 1198.5786, 1218.4856, 1241.4500, 1251.4650, 1262.4463, 1300.4155, 1320.4197, 1340.4816, 1357.4745, 1379.4812, 1393.5352, 1410.5914, 1425.6392, 1434.7352, 1438.6882, 1460.7524, 1469.8580, 1481.8358, 1493.7595, 1500.7714, 1507.8469, 1523.7810, 1541.7574, 1549.6768, 1556.7968, 1571.7633, 1598.7333, 1605.7795, 1620.7744, 1638.7886, 1652.8346, 1657.7218, 1667.7076, 1676.7419, 1693.7611, 1707.6902, 1716.7665, 1729.7339, 1742.7738, 1757.7921, 1765.6438, 1774.7615, 1798.8903, 1813.7894, 1843.8252, 1886.8040, 1897.7865, 1905.8560, 1914.8129, 1943.8248, 1953.9305, 1996.8591, 2012.8267, 2039.9054, 2048.9353, 2086.8979, 2095.9363, 2109.0286, 2119.9297, 2136.0205, 2149.9866, 2165.9561, 2181.9910, 2225.0349, 2286.0657, 2297.1021, 2309.0308, 2324.0754, 2342.9497, 2352.0767, 2359.1016, 2418.1216, 2448.1802, 2501.2839, 2565.2673, 2584.2903, 2602.3523, 2643.4299, 2661.4395



30 RuvB-like 2

Number of mass values searched: **200**

Number of mass values matched: **16**

Sequence Coverage: **40%**

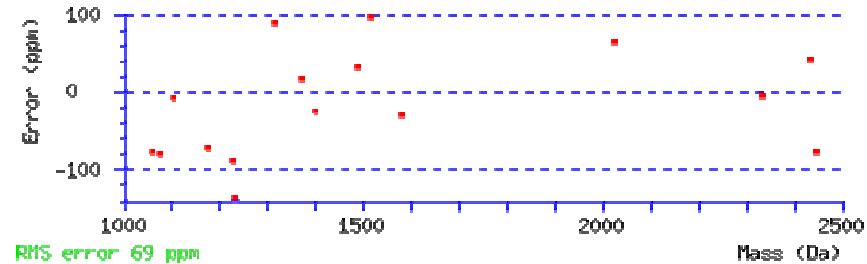
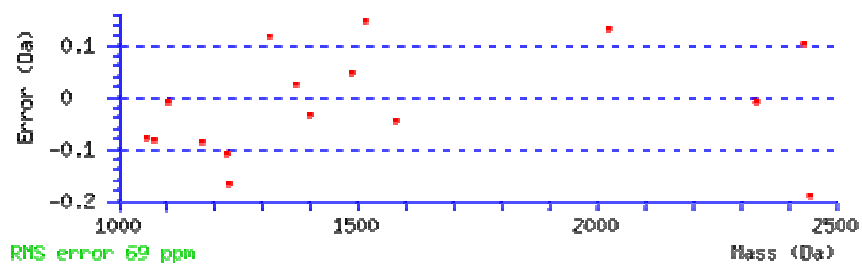
Matched peptides shown in **Bold Red**

1 MATVAATTKV PEIRDVTRIE RIGAHSHIRG LGLDDALEPR QASQGMVGG
51 AARRAAGVVL EMIREGKIAG RAVLIAGQPG TGKTAIAMGM AQALGPDTPF
101 TAIAGSEIFS LEMSKTEALT QAFRRSIGVR IKEETEIEEG EVVEIQIDRP
151 ATGTGSKVGK LTLK**TTEMET IYDLGTKMIE SLTKDKVQAG DVITIDKATG**
201 KISKLGRSFT RAR**DYDAMGS QTKFVQCPDG ELQKRKEVVH TVSLHEIDVI**
251 NSRTQGFLAL FSGDTGEIKS EVREQINAKV AEWREEGKAE IIPGVLFIDE
301 VHMLDIESFS FLNRALES DM APVLIMATNR GITRIRGTSY QSPHGIPIDL
351 LDRLLIVSTS PYSEKDTKQI LRIRCEEDV EMSEDAYTVL TRIGLETSLR
401 YAIQLITAAS LVCR**KRGTE VQVDDIKRVY SLFLDES**RST QYMKEYQDAF
451 LFNELKGETM DTS

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss Sequence
1 - 14	1487.8733	1486.8660	1486.8177	0.0483	1 -.MATVAATTKVPEIR.D
22 - 40	2027.2102	2026.2029	2026.0708	0.1321	1 R.IGAHSHIRGLGLDDALEPR.Q
41 - 53	1316.7916	1315.7843	1315.6667	0.1177	0 R.QASQGMVQQLAAR.R
55 - 64	1058.5217	1057.5144	1057.5954	-0.0810	0 R.AAGVVLEMIR.E
55 - 64	1074.5133	1073.5060	1073.5903	-0.0843	0 R.AAGVVLEMIR.E Oxidation (M)
55 - 67	1372.7850	1371.7777	1371.7544	0.0233	1 R.AAGVVLEMIREGK.I
165 - 184	2336.1150	2335.1077	2335.1175	-0.0097	1 K.TTEMETIYDLGTKMIESLTK.D 2 Oxidation (M)
185 - 197	1401.7236	1400.7163	1400.7511	-0.0348	1 K.DKVQAGDVITIDK.A
214 - 234	2433.1726	2432.1653	2432.0624	0.1029	1 R.DYDAMGSQTKFVQCPDGELQK.R Oxidation (M)
270 - 279	1173.5367	1172.5294	1172.6149	-0.0855	1 K.SEVREQINAK.V
280 - 288	1103.5406	1102.5333	1102.5407	-0.0074	1 K.VAEWREEGK.A
393 - 414	2448.1731	2447.1658	2447.3570	-0.1912	1 R.IGLETSLRYAIQLITAASLVCR.K
401 - 414	1578.8206	1577.8133	1577.8599	-0.0466	0 R.YAIQLITAASLVCR.K
417 - 427	1231.4846	1230.4773	1230.6456	-0.1683	1 R.KGTEVQVDDIK.R
429 - 438	1228.5110	1227.5037	1227.6135	-0.1098	0 R.VYSLFLDES.R
445 - 456	1516.8774	1515.8701	1515.7245	0.1456	0 K.EYQDAFLFNEK.G

No match to: 906.6078, 909.0865, 914.6265, 916.2983, 922.4907, 925.7141, 931.5969, 937.7024, 940.2978, 946.6080, 949.5988, 951.6268, 957.5974, 964.6725, 969.6749, 971.5829, 977.6147, 983.6754, 985.5594, 996.6179, 1000.5553, 1002.5667, 1016.5475, 1023.1134, 1029.5355, 1031.5231, 1039.0201, 1042.5504, 1044.0773, 1052.6248, 1060.0349, 1066.0449, 1072.0481, 1082.0051, 1088.0314, 1089.5044, 1097.9063, 1106.4188, 1108.4142, 1118.5020, 1124.5782, 1130.5314, 1134.5586, 1141.7251, 1143.5433, 1145.5457, 1152.5195, 1160.5410, 1165.5787, 1174.4579, 1183.5583, 1185.6056, 1189.4918, 1191.5027, 1199.5656, 1209.5385, 1216.4760, 1218.4178, 1233.4385, 1240.5624, 1248.9293, 1255.9584, 1263.6346, 1266.4967, 1270.9019, 1277.9191, 1286.8668, 1292.8718, 1300.5640, 1308.8262, 1322.4458, 1324.8478, 1326.5060, 1337.5200, 1339.5353, 1346.4879, 1353.6975, 1354.5151, 1361.9357, 1363.5455, 1377.4705, 1393.6086, 1411.6547, 1436.7815, 1443.6606,

1452.8087, 1462.8309, 1476.1062, 1489.8798, 1498.1039, 1505.8400, 1507.8555, 1523.8444, 1528.8021, 1531.8513, 1543.1514, 1545.8031, 1549.8446, 1555.8162, 1564.8383, 1571.7719, 1585.7661, 1587.7634, 1594.7642, 1595.7594, 1604.8541, 1618.7174, 1630.8315, 1635.9016, 1649.8280, 1660.8005, 1668.9049, 1676.8124, 1686.9857, 1700.9528, 1704.8070, 1714.7572, 1722.8068, 1742.6992, 1753.5959, 1760.8240, 1766.6642, 1779.9872, 1792.6488, 1801.7775, 1810.9568, 1821.9559, 1833.0458, 1842.9225, 1867.8054, 1873.0009, 1899.1342, 1916.0328, 1931.0531, 1933.8684, 1945.8347, 1953.0615, 1959.8303, 1984.0380, 1988.8518, 1992.1462, 2003.9077, 2012.0997, 2036.9370, 2047.8525, 2065.9192, 2076.8596, 2104.2017, 2122.1345, 2178.0132, 2211.9885, 2246.5503, 2266.0986, 2270.3748, 2279.2241, 2303.5464, 2309.0530, 2317.0740, 2326.2961, 2397.9998, 2418.1851, 2421.1924, 2431.1611, 2446.1821, 2457.0073, 2462.1951, 2473.9895, 2487.1892, 2503.1812, 2519.1753, 2526.1699, 2541.1553, 2563.2354, 2579.3271, 2593.2920, 2609.3350, 2624.2305, 2637.3303, 2652.3350, 2705.4009, 2720.5696, 2749.5464, 2762.0242, 2784.5305



41 Activator of 90 kDa heat shock protein ATPase homolog 1

Number of mass values searched: **150**

Number of mass values matched: **12**

Sequence Coverage: **37%**

Matched peptides shown in **Bold Red**

1 MAKWGEDPR WIVEERADAT NVNNWHWTER **DASNWSTEKL KTLFLAVRVE**

51 NEEGKCEVTE VNKLDGEASI NNRKGLIFF YEWTIKLNWT **GTSKSGVQYK**

101 GHVEIPNLS ENSVDEVEIS VSLAKDEPDT NLVALMK**EDG VKLLREAVGI**

151 YISTLKTEFT QGMILPTVNG ESDVPVGPQA LKTETCKAKS APSK**SQAKPV**

201 GVKIPTCKIT LKETFLTSPE ELYRVFTTQE LVQAFTHAPA ALEADRGGKF

251 HMVDGNTGE FTDLVPEK**HI AMKWR**FK**SWP EGHFATITLT FIDK**NGETEL

301 CMEGR**GIPAP EEERTRQG**WQ RYYFEGIKQT FGYGARLF

Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence

2 - 10 1015.5742 1014.5669 1014.4883 0.0786 1 M.AKWGEDPR.W

31 - 41 1278.5273 1277.5200 1277.6252 -0.1051 1 R.DASNWSTEKLK.T

42 - 55 1604.8334 1603.8261 1603.8569 -0.0308 1 K.TLFLAVRVNEEGK.C

56 - 73 2047.9399 2046.9326 2046.9640 -0.0314 1 K.CEVTEVKNLDGEASINNR.K

87 - 94 906.5762 905.5689 905.4607 0.1082 0 K.LNWTGTSK.S

138 - 145 929.5983 928.5910 928.5342 0.0569 1 K.EDGVKLLR.E

146 - 156 1193.5236 1192.5163 1192.6703 -0.1540 0 R.EAVGIYISTLK.T

195 - 203 913.6227 912.6154 912.5393 0.0762 0 K.SQAKPVGVK.I

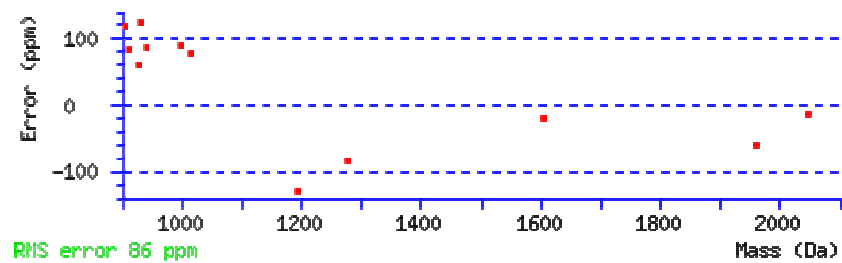
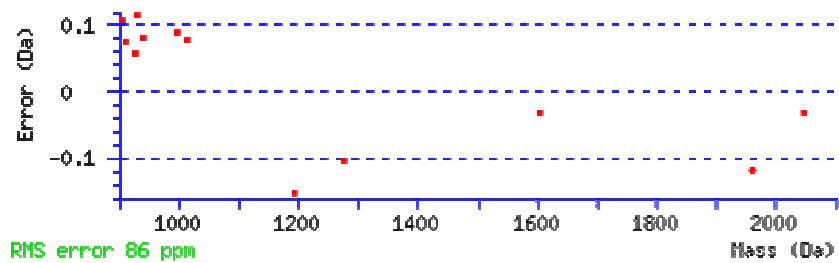
269 - 275 941.5952 940.5879 940.5065 0.0814 1 K.HIAMKWR.F

278 - 294 1962.8792 1961.8719 1961.9887 -0.1168 0 K.SWPEGHFATITLTFIDK.N

306 - 314 997.5838 996.5765 996.4876 0.0889 0 R.GIPAPEER.T

315 - 321 931.6021 930.5948 930.4784 0.1164 1 R.TRQGWQR.Y

No match to: 909.5907, 916.5938, 922.6000, 924.6220, 926.6013, 939.5987, 943.5815, 949.5967, 955.6043, 958.5857, 968.6101, 971.5885, 973.5708, 982.5974, 985.5799, 991.5703, 1000.5719, 1002.5784, 1017.5687, 1028.5643, 1031.5570, 1040.5642, 1044.1021, 1052.5680, 1058.5320, 1060.0594, 1066.0696, 1072.5457, 1076.5586, 1082.0332, 1089.5261, 1097.9902, 1104.5459, 1113.5393, 1118.5254, 1128.5336, 1131.5486, 1134.5365, 1145.5571, 1151.5649, 1157.5358, 1160.5452, 1163.5437, 1172.5432, 1175.5276, 1179.5143, 1190.5442, 1201.5153, 1206.5188, 1217.5035, 1221.5360, 1228.5348, 1232.9664, 1233.4756, 1242.5465, 1249.5150, 1256.5280, 1263.4977, 1270.9340, 1286.8984, 1293.5099, 1307.5140, 1322.5100, 1333.5323, 1336.5167, 1339.5321, 1347.5084, 1350.4958, 1353.5195, 1363.5104, 1366.4803, 1377.5381, 1380.5173, 1387.5684, 1393.5811, 1409.6619, 1424.7141, 1436.7832, 1450.8054, 1466.8123, 1476.1346, 1483.8320, 1489.8726, 1496.8254, 1507.8528, 1515.8165, 1523.8359, 1527.8489, 1531.8423, 1541.8180, 1549.8345, 1555.8285, 1564.8086, 1571.7985, 1578.8400, 1587.7819, 1594.8068, 1597.7902, 1615.8030, 1624.7996, 1629.8317, 1638.8127, 1642.7970, 1653.8173, 1661.7976, 1670.8141, 1685.8176, 1698.8105, 1703.8243, 1714.8191, 1726.8649, 1741.8221, 1757.8575, 1773.8569, 1782.8796, 1791.6200, 1800.8601, 1860.8956, 1918.8994, 1932.8867, 1945.9227, 1974.9600, 1991.9756, 2005.9644, 2030.9885, 2094.0022, 2146.0334, 2383.9502, 2398.6130, 2421.2217, 2435.2407, 2446.2107, 2448.1802, 2457.3198, 2462.3325, 2487.2295, 2503.2251, 2636.3940



54 5-azacytidine-induced protein 2

Number of mass values searched: **120**

Number of mass values matched: **8**

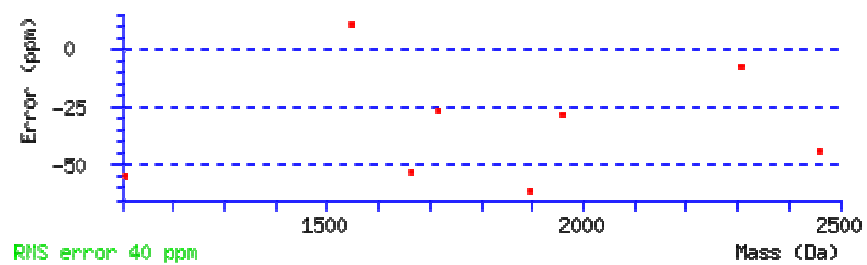
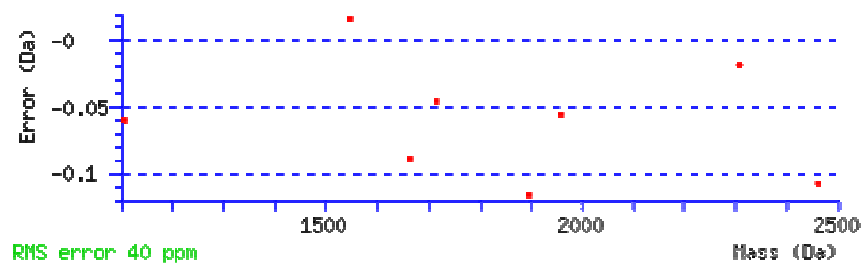
Sequence Coverage: **24%**

Matched peptides shown in **Bold Red**

1 MDTLVEDDIC ILNHEKAHRR EAVTPLSAYP GDESVASHFA LVTAYEDIK
51 RLKDSEKENS FLKKRIRALE ERLVGARADE ETSSVGREQV NKAYHAYREV
101 CIDRDNLKNQ LEKINKDNSE SLKMLNEQLQ SKEVELLQLR TEVETQQVMR
151 NLNPPSSSWE VEKLSCDLKI HGLEQELGLL RKECSDLRTE LQKARQTGPP
201 QEDILQGRDV IRPSSLREEH VPHQGLHHSD NMQHAYWELK REMSNLHLVT
251 QVQAELLRKL KTSAAVKKAC TPVGCVEDLG RDSTKLHLTN FTATYKRHPS
301 LSPNGKAPCY APSSPLPGDR KVFSDKAVLQ SWTDNERLVP NDGADFPEHS
351 SYGRNSLEDN SWVFPSPPKS SETAFGENKS KILPLSNLPP LHYLDQQNQ
401 CLYKS

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
1 - 16	1960.8439	1959.8366	1959.8918	-0.0551	0	-.MDTLVEDDICILNHEK.A Oxidation (M)
1 - 19	2309.0833	2308.0760	2308.0940	-0.0180	1	-.MDTLVEDDICILNHEKAHR.R
73 - 87	1546.7980	1545.7907	1545.7747	0.0160	1	R.LVGARADEETSSVGR.E
124 - 132	1106.4907	1105.4834	1105.5437	-0.0603	0	K.MLNEQLQSK.E Oxidation (M)
194 - 208	1665.7782	1664.7709	1664.8594	-0.0885	1	K.ARQTGPPQEDILQGR.D
196 - 217	2462.2026	2461.1953	2461.3037	-0.1084	1	R.QTGPPQEDILQGRDVIRPSSLR.E
322 - 337	1894.8136	1893.8063	1893.9221	-0.1158	1	K.VFSDKAVLQSWTDNER.L
355 - 369	1716.7764	1715.7691	1715.8155	-0.0464	0	R.NSLEDNSWVFPSPPK.S

No match to: 905.5685, 909.1025, 915.5192, 921.5958, 927.6274, 931.6047, 937.6160, 940.6747, 946.5799, 951.6473, 958.5972, 965.5654, 969.6224, 975.5670, 985.5731, 996.6290, 1000.5619, 1002.5694, 1029.5447, 1031.5398, 1037.5236, 1045.5701, 1052.6335, 1058.5339, 1072.0676, 1088.0281, 1089.5162, 1097.9795, 1104.0037, 1118.5121, 1127.4846, 1134.5118, 1141.4954, 1145.5497, 1151.5867, 1165.6465, 1179.5137, 1192.5044, 1200.5295, 1218.4714, 1232.9515, 1233.4534, 1245.4694, 1254.5023, 1265.5143, 1273.4655, 1276.9247, 1286.4921, 1292.8901, 1299.4949, 1307.4885, 1320.4276, 1330.4550, 1339.5416, 1354.4745, 1365.4519, 1383.4897, 1436.7856, 1443.7440, 1451.7626, 1460.7914, 1467.8162, 1475.8049, 1489.8815, 1507.8650, 1523.8110, 1531.8479, 1549.8390, 1555.8281, 1562.8237, 1571.7974, 1577.8153, 1587.7538, 1595.7953, 1604.8348, 1626.8129, 1639.8247, 1660.8040, 1679.8074, 1699.7394, 1707.7084, 1724.7858, 1765.6505, 1791.6285, 1807.7592, 1822.7374, 1838.8208, 1880.8030, 1910.7770, 1923.8010, 1940.8031, 2007.8514, 2050.8972, 2149.9780, 2193.9604, 2235.0896, 2249.0273, 2268.0583, 2298.1189, 2327.1343, 2340.1387, 2383.9480, 2399.0703, 2421.2078, 2434.1934, 2446.2012, 2448.1616, 2457.0439, 2487.1924, 2503.2190, 2637.3521, 2705.3567



62 Cytosolic 5'-nucleotidase 3

Number of mass values searched: **150**

Number of mass values matched: **11**

Sequence Coverage: **46%**

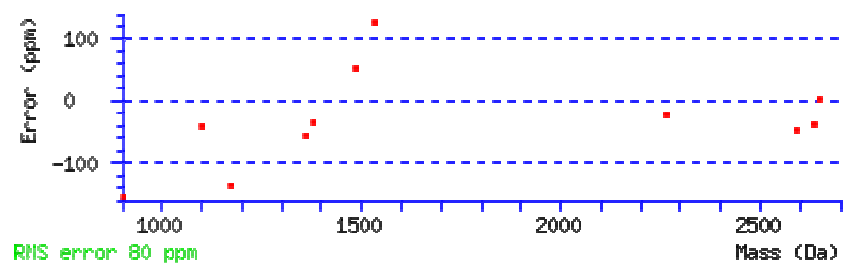
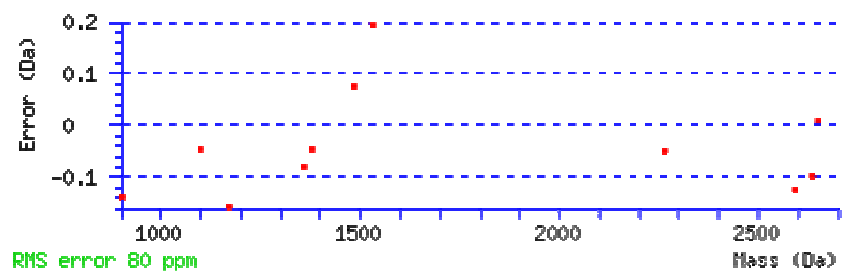
Matched peptides shown in **Bold Red**

1 MDRAAVARVG AVASASVCAV VAGVVLAQYI FTLKRKTGRK TKIEMMPEF
51 QKSSVRIKNP TRVEEIIICGL IKGGAALKQI ITDFDMLSR FSYNGKRCPT
101 CHNIIDNCKL VTDECRRKLL QLKEQYYAIE VDPVLTVEEK FPYMVEWYTK
151 SHGLLIEQGI PKAKLKEIVA DSDVMLKEGY ENFFGK LQQH GIPVFIFSAG
201 IGDVLEEVI R QAGVYHSNVK VVS NFMDFDE NGVLKGFKE LIHVF NKHGD
251 ALKNTDYFSQ LKDNSNIILL GDSQGDLRMA DGVANVEHIL KIGYLNDRVD
301 ELLEKYMDSY DIVLVKEESL EVVNSILQKT L

Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence

1 - 8 905.3221 904.3148 904.4549 -0.1400 1 -.MDRAAVAR.V Oxidation (M)
9 - 34 2593.3169 2592.3096 2592.4350 -0.1253 0 R.VGAVASASVCAVVAGVVLAQYIFTLK.R
63 - 72 1173.4960 1172.4887 1172.6475 -0.1588 0 R.VEEIIICGLIK.G
78 - 96 2265.0718 2264.0645 2264.1147 -0.0502 1 K.LQIITDFDMLSRFSYNGK.R Oxidation (M)
98 - 109 1531.8385 1530.8312 1530.6378 0.1935 0 R.CPTCHNIIDNCK.L
141 - 150 1379.5863 1378.5790 1378.6268 -0.0477 0 K.FPYMVEWYTK.S Oxidation (M)
141 - 162 2652.3601 2651.3528 2651.3458 0.0071 1 K.FPYMVEWYTKSHGLLIEQGIPK.A Oxidation (M)
187 - 210 2637.3420 2636.3347 2636.4326 -0.0979 0 K.LQQHGIPVFIFSAGIGDVLEEVI R.Q
211 - 220 1102.5175 1101.5102 1101.5567 -0.0465 0 R.QAGVYHSNVK.V
306 - 316 1361.5873 1360.5800 1360.6584 -0.0784 0 K.YMDSYDIVLVK.E Oxidation (M)
317 - 329 1487.8701 1486.8628 1486.7879 0.0750 0 K.EESLEVVNSILQK.T

No match to: 910.6569, 914.6152, 921.3055, 926.6487, 931.6012, 937.6183, 941.6133, 947.6183, 949.6013, 951.6110, 958.6157, 965.6014, 971.6024, 977.6060, 985.5652, 1000.5585, 1002.5733, 1014.5770, 1023.5338, 1028.5618, 1029.5317, 1031.5350, 1040.5641, 1044.0803, 1045.5541, 1052.6189, 1058.5233, 1066.0505, 1068.4962, 1074.5104, 1082.0181, 1084.4634, 1089.5032, 1099.5684, 1106.4373, 1118.5054, 1124.6328, 1130.5234, 1136.5962, 1143.5432, 1145.5492, 1153.5892, 1156.4626, 1165.5660, 1183.5497, 1189.4800, 1191.4746, 1200.5592, 1211.5387, 1217.4608, 1218.4336, 1228.5278, 1233.4402, 1240.5394, 1242.5477, 1252.4435, 1263.4727, 1270.9048, 1278.5884, 1296.5659, 1308.4772, 1318.5958, 1326.4785, 1337.5385, 1339.5377, 1354.1279, 1368.5187, 1375.5876, 1393.6302, 1401.6970, 1410.6907, 1418.7887, 1427.6935, 1434.7721, 1436.7792, 1443.7762, 1458.8014, 1462.8335, 1464.8300, 1472.7897, 1481.8629, 1489.8849, 1496.8627, 1504.8650, 1507.8541, 1516.8601, 1523.8676, 1529.8477, 1541.2827, 1548.7563, 1549.8314, 1555.8164, 1562.8278, 1571.7764, 1578.8318, 1587.7443, 1593.7600, 1604.8413, 1613.7449, 1630.8374, 1634.8781, 1649.8413, 1660.8263, 1675.8431, 1678.8407, 1686.9164, 1697.9585, 1704.8074, 1714.7539, 1722.8053, 1742.7396, 1759.7506, 1791.6226, 1822.0074, 1960.8090, 2300.0583, 2309.0386, 2318.0950, 2336.1047, 2368.1030, 2394.1345, 2404.1567, 2419.1870, 2421.1987, 2431.1626, 2434.1794, 2446.1924, 2448.1824, 2457.2708, 2462.1990, 2474.0125, 2487.1855, 2503.1846, 2525.1797, 2541.1687, 2564.2595, 2567.2939, 2609.3357, 2619.3313



63 Ankyrin repeat domain-containing protein 16

Number of mass values searched: **100**

Number of mass values matched: **8**

Sequence Coverage: **28%**

Matched peptides shown in **Bold Red**

1 MALPGDPRRL CRLVQEGRLR **DLQEELAVAR** GCRGPAGDTL LHCAARHGRQ
51 DILAYLVEAW SMDIEATNRD YKRPLHEAAS MGHR**DCVRYL LGR**GAVVDSL
101 KKADWTPLMM ACTRKNLDVI QDLVEHGANP LLK**NKDGWNS FHIASREGHP**
151 VILRYLLTVC PDAWKTESNI RRTPLHTAAM HGCLEAVQVL LERCHYEPDC
201 RDNCGVTPFM DAIQCGHVSI AKLLLEQHKC CSSAADSMGA QALHRAAVTG
251 QDEAIRFLVC GLGIDVDVRA KSSQLTALHY AAKE**EGQNTV QTLLSLGADI**
301 NSTDERNRSV LHLACAGQHV ACTRLLQSG LKDS EDTGT LAQQLTRSVD
351 ILQDFDHVK S

Start - End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
1 - 9	1028.5734	1027.5661	1027.5233	0.0428	1	-.MALPGDPRR.L Oxidation (M)
21 - 30	1143.5366	1142.5293	1142.5931	-0.0638	0	R.DLQEELAVAR.G
85 - 93	1151.6040	1150.5967	1150.5917	0.0050	1	R.DCVRYLLGR.G
134 - 146	1531.8419	1530.8346	1530.7328	0.1019	1	K.NKDGWNSFHIASR.E
147 - 154	920.6356	919.6283	919.5239	0.1044	0	R.EGHPVILR.Y
202 - 222	2336.1223	2335.1150	2335.0396	0.0755	0	R.DNCGVTPFMDAIQCGHVSIAK.L Oxidation (M)
246 - 256	1130.5251	1129.5178	1129.5727	-0.0549	0	R.AAVTGQDEAIR.F
284 - 306	2462.2209	2461.2136	2461.1932	0.0204	0	K.EGQNTVQTLLSLGADINSTDER.N

No match to: 911.6223, 914.6027, 927.6432, 931.5934, 937.6636, 940.6704, 946.6240, 949.6241, 951.6068, 957.6459, 963.6786, 972.6182, 979.6112, 985.5679, 1000.5555, 1002.5706, 1029.5400, 1031.5341, 1044.0980, 1054.1857, 1058.5243, 1066.0598, 1068.4938, 1074.5115, 1082.0245, 1084.4581, 1089.5046, 1100.5228, 1106.4253, 1113.5217, 1118.5028, 1145.5676, 1161.5538, 1174.4911, 1183.5504, 1189.4716, 1191.4727, 1199.5543, 1211.5293, 1218.4331, 1233.4454, 1242.5487, 1252.4446, 1270.9248, 1286.8950, 1321.5922, 1326.4918, 1339.5453, 1346.5165, 1354.0055, 1410.6913, 1436.7808, 1464.8275, 1476.1320, 1487.8744, 1489.8868, 1507.8590, 1541.3051, 1549.8403, 1556.8319, 1571.7910, 1578.8484, 1587.7592, 1604.8480, 1630.8473, 1649.8582, 1660.8396, 1678.8617, 1687.0063, 1704.8337, 1714.7697, 1722.8170, 1960.8308, 2318.1125, 2368.1257, 2394.1563, 2419.2085, 2421.2229, 2434.2156, 2446.2119, 2448.2080, 2457.6631, 2474.0449, 2487.1917, 2503.2051, 2525.1968, 2540.1013, 2562.2842, 2593.3416, 2609.3730, 2636.3589, 2652.3804

