

Supplemental Material

S1.

The following section contains the sequences of proteins identified from AD and MCI hippocampus and IPL. The primary sequences were obtained from the NCBI database with sequences in **bold red** representing portions of the protein that correspond to tryptic peptides obtained from spots isolated from 2D gels, digested with trypsin, and subjected to MALDI-TOF mass spectrometry. Mass peak values for the peaks are listed below the NCBI sequence with **red mass values** representing peptides that were matched to the primary sequence. The amino acid sequences with any oxidative modifications that correspond to **red-labeled** MS peaks and MOWSE score probability graphs are also included for each protein.

Match to: **S68209** Score: **68** Expect: **0.023**
sds22 protein homolog – human

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: **23**

Number of mass values matched: **7**

Sequence Coverage: **26%**

Mached peptides shown in **Bold Red** in the primary sequence obtained from the NCBI database

1 MAAERGAGQQ QSQEMMEVDR RVESEESGDE EGKKHSSGIVADLSEQSLKD
51 GEERGEEDPE EEHELPVDME TINLDRDAED VDLNHYRIGK IEGFEVLKKV
101 KTLCLRQNLK CIENLEELQ SLRELDLYDN QIKKIENLEA LTELEILDIS
151 FNLLRNIEGV DKLTRLKCLF LVNNKISKIE NLSNLHQLQM LELGSNRIRA
201 IENIDTLTNL ESLFLGKNKI TKLQNLDAIT NLTVLMSQSNRLTKIEGLQN
251 LVNLRELYLS HNGIEVIEGL ENNNKLTMLD IASNRICKIE NISHLTELQE
301 FWMNDNLLES WSDLDELKGA **RSLETVYLER** NPLQKDPQYR RKMVLMALPSV
351 RQIDATFVRF

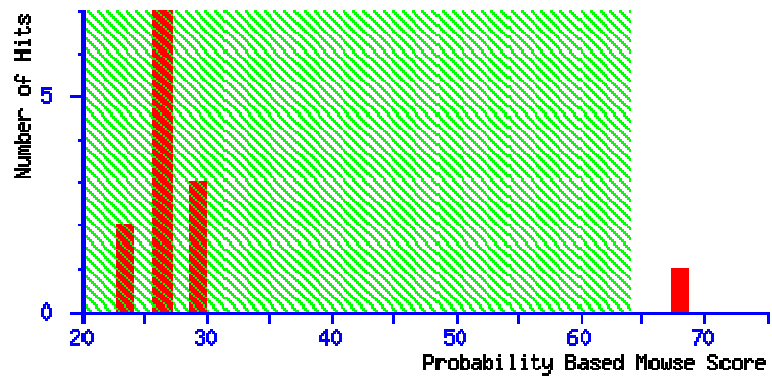
MS peak list

817.1189, 823.1467, 839.0977, 861.1074, 864.5075, 892.5376, 899.5597, **949.4992**, 1022.3511
1028.1499, 1034.1422, 1050.1290, 1102.5670, **1109.5869**, **1149.5951**, 1239.1344, **1268.7734**
1277.1644, 1306.8617, 1738.6869, **2147.1362**, **2233.1077**, **2268.1123**

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss Sequence		
1 - 20	2268.1123	2267.1050	2266.9729	58	1	-.MAAERGAGQQSQEMMEVDR.R	Oxidation (M)
200 - 219	2233.1077	2232.1004	2232.2001	-45	1	R.AIENIDTLTNLESFLGKNK.I	
223 - 241	2147.1362	2146.1289	2146.1052	11	0	K.LQNLDALTNLTVLSMQSNR.L	Oxidation (M)
245 - 255	1268.7734	1267.7661	1267.7248	33	0	K.IEGLQNLVNL.R.E	
276 - 285	1149.5951	1148.5878	1148.5859	2	0	K.LTMLDIASNR.I	Oxidation (M)
322 - 330	1109.5869	1108.5796	1108.5764	3	0	R.SLETVYLER.N	
352 - 359	949.4992	948.4919	948.5029	-12	0	R.QIDATFVR.F	

Probability Based Mowse Score

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 64 are significant ($p < 0.05$).



Match to: **JC5317** Score: **99** Expect: **1.9e-05**
dihydropyrimidinase-related protein 2 - human

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **38**
Number of mass values matched: **12**
Sequence Coverage: **27%**

Mached peptides shown in **Bold Red** in the primary sequence obtained from the NCBI database

1 MSYQGKKNIP RITSDRLLIK GGK**IVNDDQS FYADIYMEDG LIKQIGENLI**
51 **VPGGVK**TIEA HSR**MVIPGGI DVHTR**FQMPD QGMTSADDDFF QGTKAALAGG
101 TTMIIDHVVP EPGTSLAAF DQWREWADSK SCCDYSLHVD ISEWHKGIQE
151 EMEALVKDHG VNSFLVYMAF KDRFQLTDCQ IYEVLSVIRD **IGAIAQVHAE**
201 **NGDIAEEQQ R**ILDLGITGP EGHVLSRPEE VEAEAVNRAI TIANQTNCP
251 YITKVMSK**SS AEVIAQARKK** GTVVYGEPI ASLGTDGSHY WSKNWA
301 FVTSPPLSPD PTPDFLNSL LSCGDLQVTG SAHCTFNTAQ KAVGKDNFTL
351 IPEGTNGTEE RMSVIWDKAV VTGK**MDENQF VAVTSTNAAK VFNLYPRKGR**
401 IAVGSDADLV IWDPDSVKTI SAKTHNSSLE YNIFEGMECR GSPLVVISQ
451 **KIVLEDGTLH VTEGSGRYIP RKPFPDFVYK** RIKARSRLAE LRGVPRGLYD
501 GPVCEVSVTP KTVTPASSAK TSPAK**QQAPP VRNLHQSGFS LSGAQIDDNI**
551 **PRRTTQRIVA PPGGR**ANITS LG

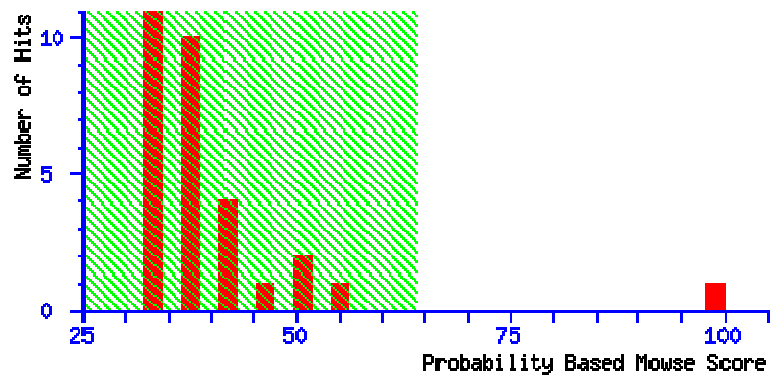
MS peak list

766.4514, 795.4133, 861.1041, 892.5098, 908.5157, 1006.4257, 1031.5680, 1050.0890, 1106.5304, 1126.5518, 1140.6339
1162.6238, 1179.6194, 1232.6132, 1277.7684, **1310.6833, 1323.7286, 1475.7993, 1485.7877, 1497.7633, 1682.9167**
1697.9100, 1716.8810, **1741.8251, 1793.8562, 1837.9352, 1858.7747, 1922.9568, 1962.8965, 1987.0347, 2044.1069, 2169.0754**
2365.0579, 2377.1797, 2399.0532, 2565.2407, 2899.4888, 2949.4438

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss Sequence
24 - 43	2365.0579	2364.0506	2364.0831	-14	0 K.IVNDDQSFYADIYMEDGLIK.Q Oxidation (M)
44 - 56	1323.7286	1322.7213	1322.7558	-26	0 K.QIGENLIVPGGVK.T
64 - 75	1310.6833	1309.6760	1309.6813	-4	0 R.MVIPGGIDVHTR.F Oxidation (M)
190 - 211	2377.1797	2376.1724	2376.1669	2	0 R.DIGAIAQVHAENGDIIEEQQR.I
259 - 268	1031.5680	1030.5607	1030.5407	19	0 K.SSAEVIAQAR.K
375 - 390	1741.8251	1740.8178	1740.7989	11	0 K.MDENQFVAVTSTNAAK.V Oxidation (M)
391 - 397	908.5157	907.5084	907.4916	19	0 K.VFNLYPR.K
452 - 467	1682.9167	1681.9094	1681.8635	27	0 K.IVLEDGTLHVTEGSGR.Y
472 - 480	1140.6339	1139.6266	1139.6015	22	0 R.KPFPDFVYK.R
526 - 532	795.4133	794.4060	794.4399	-43	0 K.QQAPPVR.N
533 - 552	2169.0754	2168.0681	2168.0610	3	0 R.NLHQSGFSLSGAQIDDNIPR.R
558 - 565	766.4514	765.4441	765.4497	-7	0 R.IVAPPGGR.A

Probability Based Mowse Score

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 64 are significant ($p < 0.05$).



Match to: **JC5317** Score: **166** Expect: **3.7e-12**
dihydropyrimidinase-related protein 2 – human

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **41**
Number of mass values matched: **17**
Sequence Coverage: **42%**

Mached peptides shown in **Bold Red** in the primary sequence obtained from the NCBI database

1 MSYQGKKNIP RITSDRLLIK GGK**IVNDDQS FYADIYMEDG LIKQIGENLI**
51 **VPGGVKTIEA HSRMVIPGGI DVHTRFQMPD QGMSADDF QGTKAALAGG**
101 TTMIIDHVVP EPGTSLAAF DQWREWADSK SCCDYSLHVD ISEWHK**GIQE**
151 **EMEALVKDHG VNSFLVYMAF KDRFQLTDCQ IYEVLSVIRD IGAIQVHAE**
201 NGDIIAEEQQ RILDLGITGP EGHVLSRPEE VEAEAVNRAI TIANQTNCP**L**
251 **YITKVMSKSS AEVIAQARKK GTVVYGEPI** ASLGTDGSHY WSKNWA**KAAA**
301 FVTSPPLSPD PTPDFLNSL LSCGDLQVTG SAHCTFN**TAQ** KAVGKDN**FTL**
351 IPEGTNGTEE RMSVIWDKAV VTGK**MDENQF VAVTSTNAAK VFNLYPRKGR**
401 **IAVGSDADLV IWDPDSVKTI** SAKTHNSSLE YNIFEGMECR **GSPLVVISQG**
451 **KIVLEDGTLH VTEGSGRYIP RKPFPDFVYK** RIKARSRLAE LRGVPRGLYD
501 GPVCEVSVTP **KTVTPASSAK TSPAK**QQAPP VRNLHQSGFS LSGAQIDDNI
551 PRRTTQRIVA PPGGRANITS LG

MS peak list

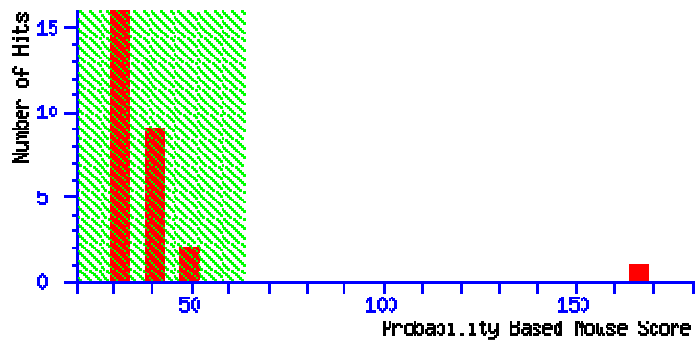
813.4457, 839.0950, 861.1203, 864.5158, 877.1197, 892.5545, 908.5491, 930.5136, 1031.6145, 1050.1189, 1072.0892
1084.6620, 1106.6329, 1140.6595, 1162.6672, 1262.6750, 1277.1160, 1310.7291, 1323.7747, 1332.7139, 1345.8196
1437.7990, 1485.7562, 1682.9391, 1697.9257, 1704.8601, 1719.8932, 1741.8441, 1763.8064, 1815.8148, 1820.9727
1836.9156, 1858.9148, 1899.9850, 1931.9634, 2182.8420, 2233.1248, 2255.0718, 2365.0576, 2378.1682, 2900.4065

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
24 - 43	2365.0576	2364.0503	2364.0831	-14	0	K.IVNDDQSFYADIYMEDGLIK.Q Oxidation (M)
44 - 56	1323.7747	1322.7674	1322.7558	9	0	K.QIGENLIVPGGVK.T

57 - 63	813.4457	812.4384	812.4140	30	0	K.TIEAHSR.M	
64 - 75	1310.7291	1309.7218	1309.6813	31	0	R.MVIPGGIDVHTR.F	Oxidation (M)
76 - 94	2182.8420	2181.8347	2181.8984	-29	0	R.FQMPDQGMTSADDDFFQGTK.A	2 Oxidation (M)
147 - 157	1262.6750	1261.6677	1261.6224	36	0	K.GIQEEMEALVK.D	Oxidation (M)
172 - 189	2255.0718	2254.0645	2254.1416	-34	1	K.DRFQLTDCQIYEVLSVIR.D	
212 - 238	2900.4065	2899.3992	2899.5039	-36	0	R.ILDLGITGPEGHVLSRPEEVEAEAVNR.A	
239 - 254	1820.9727	1819.9654	1819.9502	8	0	R.AITIANQTNCPYITK.V	
259 - 268	1031.6145	1030.6072	1030.5407	65	0	K.SSAEVIAQAR.K	
375 - 390	1741.8441	1740.8368	1740.7989	22	0	K.MDENQFVAVTSTNAAK.V	Oxidation (M)
391 - 397	908.5491	907.5418	907.4916	55	0	K.VFNLYPR.K	
401 - 418	1899.9850	1898.9777	1898.9626	8	0	R.IAVGSDADLVIWDPDSVK.T	
441 - 451	1084.6620	1083.6547	1083.6288	24	0	R.GSPLVVISQGK.I	
452 - 467	1682.9391	1681.9318	1681.8635	41	0	K.IVLEDGTLHVTEGSGR.Y	
472 - 480	1140.6595	1139.6522	1139.6015	44	0	R.KPFPDFVYK.R	
512 - 525	1345.8196	1344.8123	1344.7249	65	1	K.TVTPASSAKTSPAK.Q	

Probability Based Mowse Score

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 64 are significant ($p < 0.05$).



Match to: **A29821** Score: **117** Expect: **3e-07**
dnaK-type molecular chaperone HSPA5 precursor – human
Alternate names: BiP; **glucose-regulated 78K protein**; Ig heavy chain-binding protein

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **40**
Number of mass values matched: **14**
Sequence Coverage: **25%**

Mached peptides shown in **Bold Red** in the primary sequence obtained from the NCBI database

1 MKLSLVAAML LLLSAARAE EDKKEDVGTV VGIDLGTTYS CVGVFKNGRV
51 **EIANDQGNR ITPSYVAFTP EGERLIGDAA** KNQLTSNPEN TVFDAKRLIG
101 RTWNDPSVQQ DIKFLPFKVV EKKTKPYIQV DIGGGQTK**TF APEEISAMVL**
151 **TKMKETA**EAY LGKK**VTHAVV TVPAYFNDAQ** RQATKDAGTI AGLNVMRIIN
201 EPTAAAIAYG LDKREGEKNI LVFDLGGGTF DVSLLTIDNG VFEVVATNGD
251 THLGGEDFDQ RVMEHFILY KKKTGKDVRK DNRAVQKLRR EVEKAK**ALSS**
301 **QHQARIEIES FYEGEDFSET LTRAKFEELN MDLFR**STMKP VQKVLEDSDL
351 **KKSDIDEIVL VGGSTR**IPKI QQLVKEFFNG KEPSRGINPD EAVAYGAAVQ
401 AGVLSGDQDT GDLVLLHVCP LTLGIETVGG VMTKLIPSNT VVPTKNSQIF
451 STASDNQPTV TIK**VYEGERP LTKDNHLLGT FDLTGIPPAP RGVPQIEVTF**
501 **EIDVNGILRV** TAEDKGTGNK NKITITNDQN RLTPEEIERM VNDAEKFAEE
551 DKKLKERIDT RNELESYAYS LKNQIGDKEK LGGKLSSDK ETMEKAVEEK
601 IEWLESHQDA DIEDFKAKKK ELEEIVQPII SKLYGSAGPP PTGEEDTAEK
651 DEL

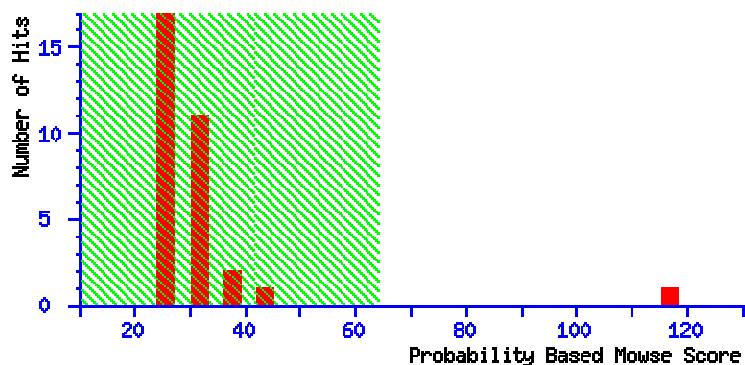
MS peak list

839.1116, 892.5648, 906.8632, 915.9758, 934.8785, 984.1492, 986.6072, **997.5682**, 1019.5576, 1028.1166, 1034.1561
1050.1412, 1072.1046, **1191.7159**, 1213.7026, **1228.7181**, **1233.6962**, 1239.1453, 1250.6979, 1261.1561, 1277.1711, 1283.1226,
1329.6718, 1419.8920, **1460.8563**, **1528.7994**, **1552.7867**, **1566.8448**, **1588.9209**, 1699.9161, 1709.9169, 1858.9907, **1888.0431**
1909.9604, **1934.0532**, 1956.0643, **1999.1542**, **2165.0608**, 2187.0073, 2233.1418

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss Sequence
50 - 60	1228.7181	1227.7108	1227.6207	73	0 R.VEIIANDQGNR.I
61 - 74	1566.8448	1565.8375	1565.7726	41	0 R.ITPSYVAFTPEGER.L
139 - 152	1552.7867	1551.7794	1551.7854	-4	0 K.TFAPEEISAMVLTK.M Oxidation (M)
165 - 181	1888.0431	1887.0358	1886.9639	38	0 K.VTHAVVTVPAYFNDAQR.Q
186 - 197	1233.6962	1232.6889	1232.6183	57	0 K.DAGTIAGLNVMR.I Oxidation (M)
297 - 305	997.5682	996.5609	996.5101	51	0 K.ALSSQHQR.I
306 - 323	2165.0608	2164.0535	2163.9848	32	0 R.IEIESFYEGEDFSETLTR.A
324 - 335	1528.7994	1527.7921	1527.7391	35	1 R.AKFEELNMDLFR.S Oxidation (M)
326 - 335	1329.6718	1328.6645	1328.6071	43	0 K.FEELNMDLFR.S Oxidation (M)
352 - 366	1588.9209	1587.9136	1587.8468	42	1 K.KSDIDEIVLVGGSTR.I
353 - 366	1460.8563	1459.8490	1459.7518	67	0 K.SDIDEIVLVGGSTR.I
464 - 473	1191.7159	1190.7086	1190.6295	66	0 K.VYEGERPLTK.D
474 - 491	1934.0532	1933.0459	1933.0058	21	0 K.DNHLLGTFDLTGIPPAPR.G
492 - 509	1999.1542	1998.1469	1998.0786	34	0 R.GVPQIEVTFEIDVNGILR.V

Probability Based Mowse Score

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 64 are significant ($p < 0.05$).



Match to: **A32936** Score: **187** Expect: **3e-14**
glial fibrillary acidic protein – human

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **42**
Number of mass values matched: **20**
Sequence Coverage: **39%**

Mached peptides shown in **Bold Red** in the primary sequence obtained from the NCBI database

1 MERRRITSAA RRSYVSSGEM MVGGLAPGRR LGPGTRLSLA RMPPPLPTRV
51 DFSLAGALNA GFKETRASER **AEMMELNDRF ASYIEK**VRFL EQQN**KALAAE**
101 **LNQLRAKEPT KLADVYQAE**L REL**RLRLDQL TANSAR**LEVE RDN**LAQDLAT**
151 **VRQKLQDET**N LR**LEAEN**NLA AYRQEADEAT LARLDLER**KI ESLEEE**IRFL
201 **RKIHEEEVRE LQEQLAR**QQV HVELDVAKPD LTAALKEIRT QYEAMASSNM
251 HEAEWYRSK **FADLTDAAR** NAELLRQAKH EANDYRRQLQ SLTCDLESLR
301 GTNESLERQM REQEERHVRE **AASYQEALAR LEEGQSLKD EMARHLQEYQ**
351 **DLLNVKLALD IEIATYRKL**L EGEENRITIP VQTFSNLQIR ETSLDTKSVS
401 EGHLKRNIVV KTVEMRDGEV IKESKQEHKD VM

MS peak list

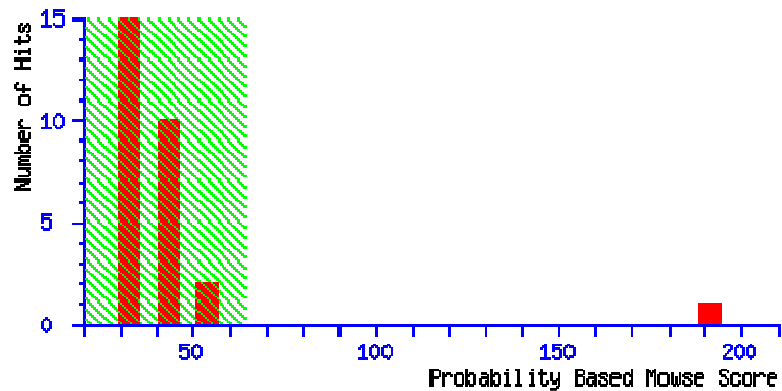
790.4592, 794.0910, 823.1438, 839.1193, 861.1104, 864.5042, 892.5454, 899.5588, **911.4642**, 942.4276, **959.4702**, **986.5663**
988.5643, 1034.1458, **1039.5876**, **1050.5624**, **1087.5906**, **1098.6796**, **1140.5027**, 1160.6162, **1177.6777**, 1199.6578, **1208.6561**
1215.6886, 1235.6555, **1245.7267**, **1263.6997**, **1277.8020**, 1299.7454, 1334.8265, **1357.7761**, 1406.8079, **1499.8199**, 1586.7579
1620.8143, **1650.7798**, 1805.0222, **1962.9731**, 1971.0034, 2044.9465, 2233.1287, 2268.1206

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss Sequence
71 - 79	1140.5027	1139.4954	1139.4587	32	0 R.AEMMELNDR.F 2 Oxidation (M)
71 - 86	1962.9731	1961.9658	1961.8862	41	1 R.AEMMELNDRFASYIEK.V Oxidation (M)
96 - 105	1098.6796	1097.6723	1097.6193	48	0 K.ALAAELNQLR.A
112 - 121	1177.6777	1176.6704	1176.6139	48	0 K.LADVYQAELE.R
125 - 136	1357.7761	1356.7688	1356.7473	16	1 R.LRLDQLTANSAR.L

142 - 152	1215.6886	1214.6813	1214.6255	46	0	R.DNLAQDLATVR.Q
155 - 162	988.5643	987.5570	987.4985	59	0	K.LQDETNR.L
155 - 173	2233.1287	2232.1214	2232.1134	4	1	K.LQDETNRLEAENNLAAYR.Q
163 - 173	1263.6997	1262.6924	1262.6255	53	0	R.LEAENNLAAYR.Q
189 - 198	1245.7267	1244.7194	1244.6612	47	1	R.KIESLEEEIR.F
202 - 209	1039.5876	1038.5803	1038.5458	33	1	R.KIHEEEVR.E
203 - 209	911.4642	910.4569	910.4508	7	0	K.IHEEEVR.E
210 - 217	986.5663	985.5590	985.5192	40	0	R.ELQEQLAR.Q
261 - 270	1050.5624	1049.5551	1049.5142	39	0	K.FADLTDAAAR.N
320 - 330	1208.6561	1207.6488	1207.5833	54	0	R.EAASYQEALAR.L
331 - 344	1650.7798	1649.7725	1649.7566	10	1	R.LEEEGQSLKDEMAR.H Oxidation (M)
345 - 356	1499.8199	1498.8126	1498.7780	23	0	R.HLQEYQDLLNVK.L
357 - 367	1277.8020	1276.7947	1276.7027	72	0	K.LALDIEIATYR.K
368 - 376	1087.5906	1086.5833	1086.5669	15	1	R.KLLEGEENR.I
369 - 376	959.4702	958.4629	958.4719	-9	0	K.LLEGEENR.I

Probability Based Mowse Score

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 64 are significant ($p < 0.05$).



Match to: **Q5VU58_HUMAN** Score: **106** Expect: **3.7e-06**
Tropomyosin 3.- Homo sapiens (Human).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **29**
Number of mass values matched: **11**
Sequence Coverage: **34%**

Mached peptides shown in **Bold Red** in the primary sequence obtained from the NCBI database

1 MAGITTIEAV **KRKIQVLQQQ ADDAEERAER** LQREVEGER AREQAEAEVA
51 SLNRR**IQLVE EELDRA**QERL ATALQKLEEA EK**AADESERG** MKVIENRALK
101 DEEKMELQEI QLKEAKHIAE EADRK**YEEVA RKLVIIEGDL ERTEERAELA**
151 ESRCREMDEQ IRLMDQNLKC LSAAEEKYSQ **KEDKYEEEIK** ILTDKLKEAE
201 TR**AEFAERSV AKLEKTIDDL EDELYAQ**KLK YKAISEELDH ALNDMTSI

MS peak list

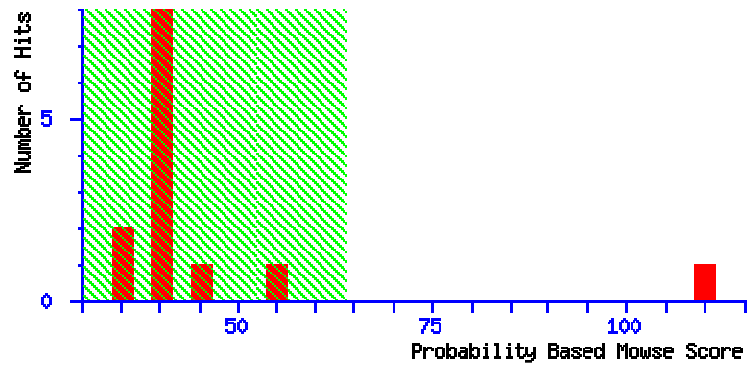
709.3303, **718.3264**, **722.3490**, 741.3730, **777.3282**, 861.0493, 864.4766, **894.4835**, 1050.0704, 1072.0092, 1126.5867, **1156.6956**
1182.6025, **1243.7062**, **1284.8145**, 1314.8544, 1316.7472, 1375.7930, 1442.7357, 1463.8319, **1642.9063**, 1664.8201, **1770.9100**
1816.8038, **1922.9639**, 1962.9540, 2261.1328, 2564.1616, 2839.2000

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss Sequence
13 - 27	1770.9100	1769.9027	1769.8908	7	1 R.KIQVLQQQADDAEER.A
14 - 27	1642.9063	1641.8990	1641.7958	63	0 K.IQVLQQQADDAEER.A
34 - 39	718.3264	717.3191	717.3293	-14	0 R.EVEGER.R
56 - 65	1243.7062	1242.6989	1242.6456	43	0 R.IQLVEEELDR.A
83 - 89	777.3282	776.3209	776.3300	-12	0 K.AADESER.G
126 - 132	894.4835	893.4762	893.4606	17	1 K.YEEVARK.L
132 - 142	1284.8145	1283.8072	1283.7449	49	1 R.KLVIIEGDLER.T
133 - 142	1156.6956	1155.6883	1155.6499	33	0 K.LVIIEGDLER.T
182 - 190	1182.6025	1181.5952	1181.5452	42	1 K.EDKYEEEIK.I
203 - 208	722.3490	721.3417	721.3395	3	0 R.AEFAER.S

213 - 228 1922.9639 1921.9566 1921.9520 2 1 K.LEKTIDDLEDELYAQK.L

Probability Based Mowse Score

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 64 are significant ($p < 0.05$).



Match to: **A32936** Score: **158** Expect: **5.4e-11**
glial fibrillary acidic protein - human

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **18**
Number of mass values matched: **13**
Sequence Coverage: **32%**

Mached peptides shown in **Bold Red** in the primary sequence obtained from the NCBI database

1 MERRRITSAA RRSYVSSGEM MVGGLAPGRR LGPGTRLSLA RMPPPLPTRV
51 DFSLAGALNA GFKETRASER **AEMMELNDRF ASYIEK**VRFL EQQNK**ALAAE**
101 **LNQLRAKEPT KLADVYQ AEL RELRLRLDQL TANSARLEVE RDNLAQDLAT**
151 **VRQKLQDET**N LR**LEAEN**LA **AYRQEA**DEAT LARLDLER**KI ESLEEE**IRFL
201 R**KIH**EEEVRE **LQEQLAR**QQV HVELDVAKPD LTAALKEIRT QYEAMASSNM
251 HEAEWYRSK **FADLTDAAR** NAELLRQAKH EANDYRRQLQ SLTCDLESLR
301 GTNESLERQM REQEERHVRE **AASYQEALAR LEEEGQSLKD EMARHLQEYQ**
351 **DLN**VKLALD **IEIATYR**KLL EGEENRITIP VQTFSNLQIR ETSLDTKSVS
401 EGHLKRNIVV KTVEMRDGEV IKESKQEHKD VM

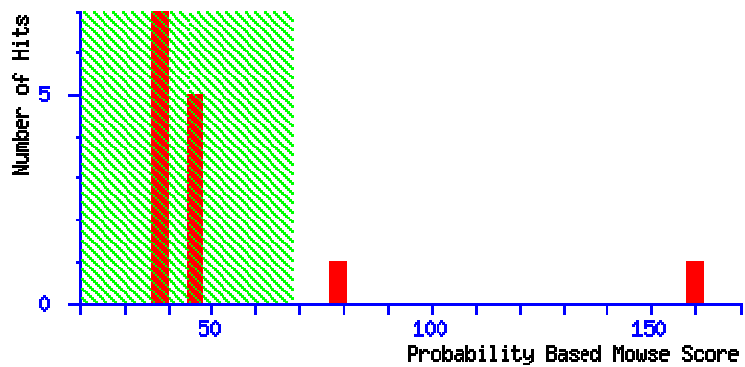
MS peak list

741.3560, **986.5276**, **1039.5798**, **1050.5253**, **1098.6605**, **1177.6804**, 1199.6888, **1208.6344**, **1215.6323**, **1245.6857**, **1263.6831**
1277.7644, **1499.8074**, **1586.7888**, **1650.7819**, 1805.0127, **1962.9745**, 2261.1853

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss Sequence
71 - 86	1962.9745	1961.9672	1961.8862	41	1 R.AEMMELNDRFASYIEK.V Oxidation (M)
96 - 105	1098.6605	1097.6532	1097.6193	31	0 K.ALAAELNQLR.A
112 - 121	1177.6804	1176.6731	1176.6139	50	0 K.LADVYQAELE.R
142 - 152	1215.6323	1214.6250	1214.6255	-0	0 R.DNLAQDLATVR.Q
163 - 173	1263.6831	1262.6758	1262.6255	40	0 R.LEAENNLAAAYR.Q
189 - 198	1245.6857	1244.6784	1244.6612	14	1 R.KIESLEEEIR.F
202 - 209	1039.5798	1038.5725	1038.5458	26	1 R.KIHHEEEVR.E
210 - 217	986.5276	985.5203	985.5192	1	0 R.ELQEQLAR.Q
261 - 270	1050.5253	1049.5180	1049.5142	4	0 K.FADLTDAAR.N
320 - 330	1208.6344	1207.6271	1207.5833	36	0 R.EAASYQEALAR.L
331 - 344	1650.7819	1649.7746	1649.7566	11	1 R.LEEEGQSLKDEMAR.H Oxidation (M)
345 - 356	1499.8074	1498.8001	1498.7780	15	0 R.HLQEYQDLLNVK.L
357 - 367	1277.7644	1276.7571	1276.7027	43	0 K.LALDIEIATYR.K

Probability Based Mowse Score

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 64 are significant ($p < 0.05$).



Match to: **I37082** Score: **83** Expect: **0.0017**
GDP-dissociation inhibitor XAP-4 – human

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **26**
Number of mass values matched: **9**
Sequence Coverage: **25%**

Mached peptides shown in **Bold Red** in the primary sequence obtained from the NCBI database

1 MDEEYDVIVL GTGLTECILS GIMSVNGKKV LHMDRNPYYG GESSITPLE
51 ELYKRFQLE GPPESMGRGR DWNVDLIPKF LMANGQLVKM LLYTEVTRYL
101 DFK**VVEGSFV YKGGKIYKVP STETEALASN LMGMFEKRRF RKFLVFNANF**
151 **DENDPKTFEG VDPQTSMRD** VYRKFDLGQD VIDFTGHALA LYR**TDDYLDQ**
201 **PCLETVNRIG LYSESLARYG** KSPYLYPLYG LGELPQGFAR LSAIYGGTYM
251 LNKPVDDIIM ENKVVGVKS EGEVARCK**QL ICDPSYIPDR** VRKAGQVIRI
301 **ICILSHPIKN TNDANSCQH IPQNQVNRKS** DIYVCMISYA HNVAAQGKYI
351 AIASTTVETT DPEKEVEPAL ELLEPIDQKF VAISDLYEPI DDGCESQVFC
401 SCSYDATTHF ETTCNDIKDI YKR**MAGTAFD FENMKR**KQND VFGAEAEQ

MS peak list

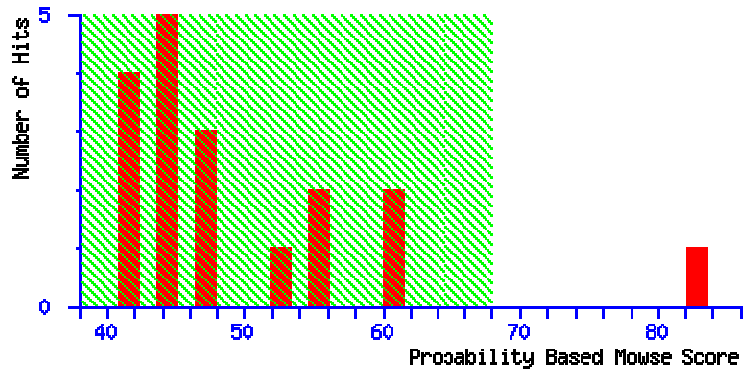
861.0759, **938.5306**, 960.5065, **1027.5658**, 1137.6238, **1193.7241**, 1265.6257, 1287.6805, 1328.7467, 1420.6486
1476.7362, **1484.7094**, 1498.7152, **1549.6688**, 1591.8040, **1654.8220**, 1676.8157, 1816.9070, **1838.8953**, 1935.9507
1941.9634, 1962.9702, 2107.9888, **2198.9829**, 2261.1084, 3442.4966

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss Sequence
104 - 112	1027.5658	1026.5585	1026.5386	19	0 K.VVEGSFVYK.G
143 - 156	1654.8220	1653.8147	1653.8039	7	0 K.FLVFNANFDENDPK.T
157 - 169	1484.7094	1483.7021	1483.6613	27	0 K.TFEGVDPQTSMR.D Oxidation (M)
194 - 208	1838.8953	1837.8880	1837.8152	40	0 R.TDDYLDQPCLETVNR.I
211 - 218	938.5306	937.5233	937.4869	39	0 K.LYSESLAR.Y
279 - 290	1476.7362	1475.7289	1475.7079	14	0 K.QLICDPSYIPDR.V

300 - 309	1193.7241	1192.7168	1192.7002	14	0	R.IICILSHPIK.N
310 - 328	2198.9829	2197.9756	2198.0498	-34	0	K.NTNDANSCQHHPQNQVNR.K
424 - 436	1549.6688	1548.6615	1548.6701	-6	1	R.MAGTAFDFENMKR.K 2 Oxidation (M)

Probability Based Mowse Score

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 64 are significant ($p < 0.05$).



Match to: **I37082** Score: **136** Expect: **8.5e-09**
GDP-dissociation inhibitor XAP-4 - human

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **35**
Number of mass values matched: **14**
Sequence Coverage: **34%**

Matched peptides shown in **Bold Red** in the primary sequence obtained from the NCBI database

1 MDEEYDVIVL GTGLTECILS GIMSVNGKK**V LHMDRNPYYG GESSITPLE**
51 **ELYKRFQ**LE GPPESMGRGR DWNVDLIPKF LMANGQLVK**M LLYTEVTRYL**
101 **DFKVV**EGSFV **YKGGKIYKVP** STETELASN LMGMFEKRRF **RKFLV**FVANF
151 **DENDPKTFEG VDPQ**TSMRD VYRKFDLGQD VIDFTGHALA LYR**TDDYLDQ**
201 **PCLET**VNRIK **LYSESLARYG** KSPYLYPLYG LGELPQGFAR LSAIYGGTYM
251 LNKPVDDIIM ENKVVGVKS EGEVARCK**QL ICDPSYIPDR VRKAGQVIRI**
301 **ICILSHPIKN T**DANSC**QH IPQNQVNRKS** DIYVCMISYA HNVAAQGKYI
351 AIASTTVETT DPEKEVEPAL ELLEPIDQKF VAISDLYEPI DDGCESQVFC
401 SCSYDATTHF ETTCNDIKDI YKR**MAGTAFD FENMKR**KQND VFGEAEQ

MS peak list

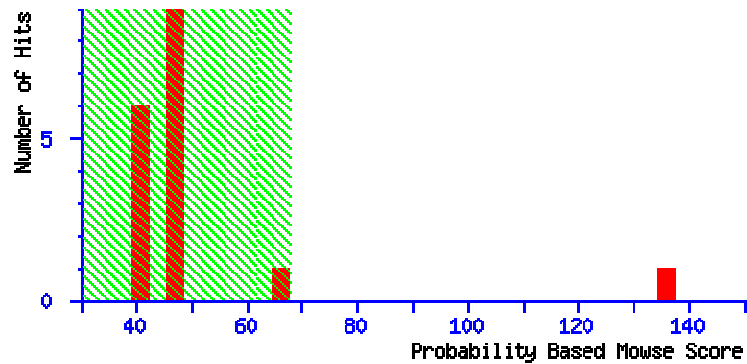
741.3776, **771.4687**, **786.3939**, **861.0937**, **938.5117**, **1027.5422**, 1137.6259, **1141.6056**, **1193.7279**, 1195.6691, 1215.7300
1314.8329, 1328.7288, 1385.7821, **1393.6305**, 1419.6003, 1442.7153, **1476.7178**, **1484.7157**, 1492.7255, 1498.6926
1549.6729, **1654.8267**, 1676.8464, 1816.8745, **1838.8694**, 1962.9518, 1986.9896, 2108.0483, **2146.9690**, **2199.0796**
2221.0967, 2261.1130, 2564.1614, 2839.1399

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss Sequence
30 - 35	786.3939	785.3866	785.3854	2	0 K.VLHMDR.N Oxidation (M)
36 - 54	2146.9690	2145.9617	2146.0106	-23	0 R.NPYYGESSITPLEELYK.R
90 - 98	1141.6056	1140.5983	1140.5849	12	0 K.MLLYTEVTR.Y Oxidation (M)

104 - 112	1027.5422	1026.5349	1026.5386	-4	0	K.VVEGSFVYK.G	
143 - 156	1654.8267	1653.8194	1653.8039	9	0	K.FLVFVANFDENDPK.T	
157 - 169	1484.7157	1483.7084	1483.6613	32	0	K.TFEGVDPQTTSMR.D	Oxidation (M)
194 - 208	1838.8694	1837.8621	1837.8152	26	0	R.TDDYLDQPCLETVNR.I	
211 - 218	938.5117	937.5044	937.4869	19	0	K.LYSESLAR.Y	
279 - 290	1476.7178	1475.7105	1475.7079	2	0	K.QLICDPSYIPDR.V	
293 - 299	771.4687	770.4614	770.4763	-19	1	R.KAGQVIR.I	
300 - 309	1193.7279	1192.7206	1192.7002	17	0	R.IICILSHPIK.N	
310 - 328	2199.0796	2198.0723	2198.0498	10	0	K.NTNDANSCQIIPQNQVNR.K	
424 - 435	1393.6305	1392.6232	1392.5690	39	0	R.MAGTAFDFENMKR.R	2 Oxidation (M)
424 - 436	1549.6729	1548.6656	1548.6701	-3	1	R.MAGTAFDFENMKR.K	2 Oxidation (M)

Probability Based Mowse Score

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 64 are significant ($p < 0.05$).



Match to: **DEHUE** Score: **142** Expect: **2.1e-09**
glutamate dehydrogenase [NAD(P)] (EC 1.4.1.3) precursor - human

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **33**
Number of mass values matched: **15**
Sequence Coverage: **32%**

Mached peptides shown in **Bold Red** in the primary sequence obtained from the NCBI database

1 MYRYLGEALL LSRAGPAALG SASADSAALL GWARGQAAA PQPGLALAAR
51 RHYSEAVADR EDDPNFFKMV EGGFDR**GASI VEDKLVEDLR TRESEEQKRN**
101 RVRGILRIK PCNHVLSLSF PIRRDDGSWE VIEGYRAQHS QHRT**PCKGGI**
151 RYSTDVSVDE **VKALASLMTY KCAVVDVPFG GAKAGVKINP KNYTDNELEK**
201 ITRRFTMELA KKGFIGPID VPAPDMSTGE** REMSWIADTY ASTIGHYDIN**
251 AHACVTGKPI SQGGIHGRIS ATGRGVFHGI ENFINEASYM SILGMTPGFG
301 DKTFVVQGF NVGLHSMRYL** HRFGAKCIAV GESDGSIWNP DGIDPKELED**
351 FKLQHGSILG FPKAKPYEGS** ILEADCILI PAASEKQLTK SNAPRVKAKI**
401 IAEGANGPTT PEADKIFLER NIMVIPDLYL NAGGVTVSYF EWLKNLNHVS****
451 YGRLTFKYER DSNYHLLMSV QESLERKFGK HGGTIPIVPT AEFQDR**ISGA**
501 SEKDIVHSGL AYT**MERSARQ IMRTAMKYNL **GLDLR**TAAYV NAIEK**VFKVY****
551 NEAGVTFT

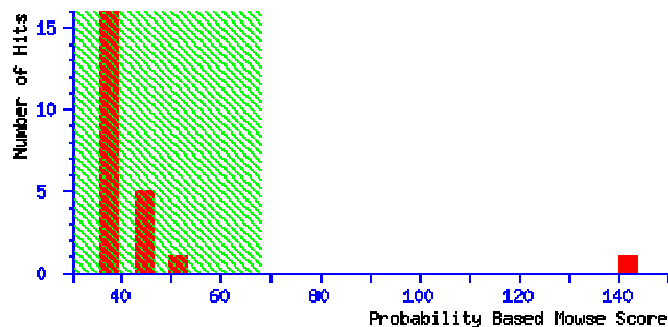
MS peak list

863.4280, 885.4026, **963.5684**, 985.5447, **1011.5289**, **1016.4750**, 1021.5907, 1043.5859, **1059.5807**, 1081.5659, **1196.7139**,
1218.7507, **1241.6593**, 1243.7296, 1282.8613, 1287.8097, 1419.8746, **1425.6869**, 1442.7965, 1452.7366, **1474.7150**, **1507.7788**,
1529.7106, **1584.8340**, 1727.9176, **1737.9697**, 1759.9377, **1764.9347**, **1931.9518**, **1936.9331**, 1953.9659, 1963.0280, 2261.2473

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss Sequence
1 - 13	1584.8340	1583.8267	1583.8493	-14	1 -.MYRYLGEALLSR.A
69 - 76	1016.4750	1015.4677	1015.4433	24	0 K.MVEGFFDR.G Oxidation (M)
125 - 136	1425.6869	1424.6796	1424.6208	41	0 R.DDGSWEVIEGYR.A
137 - 143	863.4280	862.4207	862.4158	6	0 R.AQHSQHR.T
152 - 162	1241.6593	1240.6520	1240.5823	56	0 R.YSTDVSVDEVK.A
204 - 211	1011.5289	1010.5216	1010.5219	-0	1 R.RFTMELAK.K Oxidation (M)
213 - 231	1931.9518	1930.9445	1930.9095	18	0 K.GFIGPGIDVPAPDMSTGER.E Oxidation (M)
303 - 318	1764.9347	1763.9274	1763.8778	28	0 K.TFVVQGFGNVGLHSMR.Y Oxidation (M)
353 - 363	1196.7139	1195.7066	1195.6713	30	0 K.LQHGSILGFPK.A
445 - 453	1059.5807	1058.5734	1058.5257	45	0 K.NLNHVSYGR.L
461 - 476	1936.9331	1935.9258	1935.8996	14	0 R.DSNYHLLMSVQESLER.K Oxidation (M)
481 - 496	1737.9697	1736.9624	1736.8846	45	0 K.HGGTIPIVPTAEFQDR.I
504 - 516	1507.7788	1506.7715	1506.7137	38	0 K.DIVHSGLAYTMER.S Oxidation (M)
528 - 535	963.5684	962.5611	962.5185	44	0 K.YNLGLDLR.T
546 - 558	1474.7150	1473.7077	1473.7504	-29	1 K.VFKVYNEAGVTFT.-

Probability Based Mowse Score

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 64 are significant ($p < 0.05$).



Match to: **HS90A_HUMAN** Score: **128** Expect: **2.3e-08**
Heat shock protein HSP 90-alpha (HSP 86) (NY-REN-38 antigen).- Homo sapiens (Human).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **40**
Number of mass values matched: **19**
Sequence Coverage: **27%**

Mached peptides shown in **Bold Red** in the primary sequence obtained from the NCBI database

1 PEETQTQDQP MEEEEVETFA FQAEIAQLMS LIINTFYNSK EIFLRELISN
51 SSDALDKIRY ESLTDPSKLD SGK**ELHINLI PNK**QDRTLTI VDTGIGMTKA
101 DLINNLGTIA KSGTKAFMEA LQAGADISMI GQFGVGFYSA YLVAEKVTVI
151 TKHNDDEQYA WESSAGGSFT VRT**DTGEPMG** RGTKVILHLK **EDQTEYLEER**
201 RIKEIVKK**HS QFIGYPITLF VEKERD**KEVS DDEAEKEDK EEEKEKEEKE
251 SEDKPEIEDV GSDEEEKGD GK**KKKKKIK EK****YIDQEELN KTKPIWTRNP**
301 **DDITNEEYGE FYKSLTNDWE** DHLAVK**HFSV EGQLEFRALL FVPRRAPFDL**
351 **FENR**KKKNNI KLYVRRVFIM DNCEELIPEY LNFIR**GVVDS EDLPLNISRE**
401 MLQQSKILKV IRKNLVKK**CL ELFTELAEDK ENYK**K**FYEQF SKNIKLGHE**
451 **DSQNR**KKLSE LLR**YYTSASG DEMVSLKDYC** TRMKENQKHI **YYITGETKDQ**
501 **VANS**AFVERL RKHGLEVIYM IEPIDEYCVQ QLKEFEGKTL VSVTKEGLEL
551 PEDEEEKKKQ EEK**TKFENL CKIMKDILEK** KVEKVVVSNR LVTSPCCIVT
601 STYGWTANME RIMKAQALRD NSTMGYMAAK **KHLEINPDHS IETLRQKAE**
651 ADKNDKSVKD LVILLYETAL LSSGFSLEDP QTHANRIYRM IKLGLGIDED
701 DPTADDTSA A VTEEMPPLEG DDDTSRMEEV D

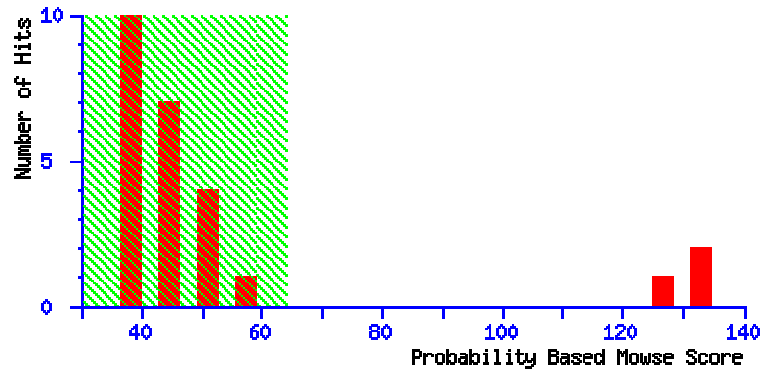
MS peak list

815.4927, 887.4418, **901.4628**, 913.5466, 917.4890, 933.4899, **948.4524**, **979.3931**, 992.5284, 998.5144, 1074.5299
1078.5107, 1097.5565, **1108.5453**, 1126.5645, 1141.5605, **1151.5654**, **1168.5856**, **1190.6272**, 1194.6484, 1211.6158
1224.6273, **1235.6168**, **1264.6488**, 1275.7311, **1311.5942**, **1348.6898**, **1513.8135**, 1559.7168, **1566.7184**, 1722.8606
1778.9429, **1786.9763**, 1794.8567, **1833.8138**, 1922.9309, **2001.9091**, 2564.1680, 2825.2305, 2839.2808

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss Sequence
74 - 83	1190.6272	1189.6199	1189.6819	-52	0 K.ELHINLIPNK.Q
173 - 181	979.3931	978.3858	978.4077	-22	0 R.TDTGEPMGR.G Oxidation (M)
191 - 200	1311.5942	1310.5869	1310.5626	19	0 K.EDQTEYLEER.R
209 - 223	1778.9429	1777.9356	1777.9403	-3	0 K.HSQFIGYPITLFVEK.E
283 - 291	1151.5654	1150.5581	1150.5506	7	0 K.YIDQEELNK.T
292 - 298	901.4628	900.4555	900.5181	-70	0 K.TKPIWTR.N
299 - 313	1833.8138	1832.8065	1832.7741	18	0 R.NPDDITNEEYGEFYK.S
327 - 337	1348.6898	1347.6825	1347.6572	19	0 K.HFSVEGQLEFR.A
338 - 344	815.4927	814.4854	814.5065	-26	0 R.ALLFVPR.R
345 - 354	1264.6488	1263.6415	1263.6360	4	1 R.RAPFDLFENR.K
346 - 354	1108.5453	1107.5380	1107.5349	3	0 R.APFDLFENR.K
386 - 399	1513.8135	1512.8062	1512.7784	18	0 R.GVVDSIDLPLNISR.E
419 - 434	2001.9091	2000.9018	2000.9401	-19	1 K.CLELFTELAEDKENYK.K
436 - 442	948.4524	947.4451	947.4389	7	0 K.FYEQFSK.N
446 - 455	1168.5856	1167.5783	1167.5632	13	0 K.LGIHEDSQNR.K
464 - 477	1566.7184	1565.7111	1565.6919	12	0 R.YYTSASGDEMVSLLK.D Oxidation (M)
489 - 498	1224.6273	1223.6200	1223.6186	1	0 K.HIYYITGETK.D
499 - 509	1235.6168	1234.6095	1234.5942	12	0 K.DQVANSAFVER.L
632 - 646	1786.9763	1785.9690	1785.9373	18	0 K.HLEINPDHSIETLR.Q

Probability Based Mowse Score

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 64 are significant ($p < 0.05$).



Match to: **DEHUE** Score: **147** Expect: **6.8e-10**
glutamate dehydrogenase [NAD(P)] (EC 1.4.1.3) precursor – human

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **26**
Number of mass values matched: **14**
Sequence Coverage: **29%**

Mached peptides shown in **Bold Red** in the primary sequence obtained from the NCBI database

1 MYRYLGEALL LSRAGPAALG SASADSAALL GWARGQPAAA PQPGLALAAR
51 RHYSEAVADR EDDPNFFK**MV EGGFFDR**GASI VEDKLVEDLR TRESEEQKRN
101 RVRGILRIK PCNHVLSLSF PIRR**DDGSWE VIEGYRAQHS QHRT**PCKGGI
151 RYSTDVS**VDE VKALASL**MTY KCAVVDVDPFG GAKAGVKINP KNYTDNELEK
201 ITR**RFTMELA KKG**FIGPGID **VPAPDMSTGE** REMSWIADTY ASTIGHYDIN
251 AHACVTGKPI SQGGIHGRIS ATGRGVFHGI ENFINEASYM SILGMTPGFG
301 DK**TFVVQGF** **NVGLHSMR**YL HRFGAKCIAV GESDGSIWNP DGIDPKELED
351 FK**LQHGSILG** **FPK**AKPYEGS ILEADCILI PAASEKQLTK SNAPRVKAKI
401 IAEGANGPTT PEADKIFLER NIMVIPDLYL NAGGVTVSYF EWLK**NLNHVS**
451 YGRLTFKYER **DSNYHLLMSV QESLER**KFGK **HGGTIPIVPT AEFQDR**ISGA
501 SEK**DIVHSGL AYT**MERSARQ IMRTAMKYNL **GLDLR**TAAYV NAIEKVFKVY
551 NEAGVTFT

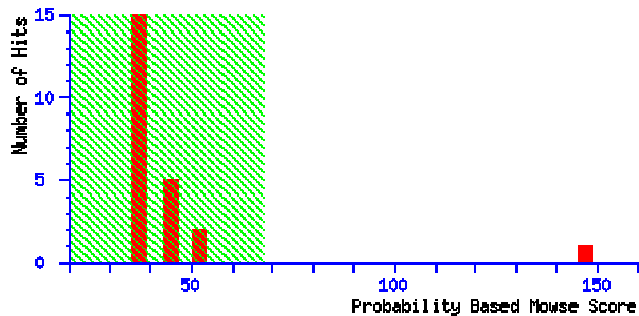
MS peak list

863.4333, 963.5420, 986.4902, 1011.5504, 1016.4686, 1021.5829, 1059.5675, 1196.6880, 1218.6903, 1241.6449, 1314.8014
1420.7192, 1425.7238, 1452.7006, 1507.7491, 1584.8048, 1727.8667, 1737.9376, 1764.9100, 1885.0272, 1931.9064, 1936.8939
1962.9546, 2058.9612, 2261.0847, 2839.1765

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss Sequence
1 - 13	1584.8048	1583.7975	1583.8493	-33	1 -.MYRYLGEALLSR.A
69 - 76	1016.4686	1015.4613	1015.4433	18	0 K.MVEGFFDR.G Oxidation (M)
125 - 136	1425.7238	1424.7165	1424.6208	67	0 R.DDGSWEVIEGYR.A
137 - 143	863.4333	862.4260	862.4158	12	0 R.AQHSQHR.T
152 - 162	1241.6449	1240.6376	1240.5823	45	0 R.YSTDVSVDEVK.A
204 - 211	1011.5504	1010.5431	1010.5219	21	1 R.RFTMELAK.K Oxidation (M)
213 - 231	1931.9064	1930.8991	1930.9095	-5	0 K.GFIGPGIDVPAPDMSTGER.E Oxidation (M)
303 - 318	1764.9100	1763.9027	1763.8778	14	0 K.TFVVQGFQGNVGLHSMR.Y Oxidation (M)
353 - 363	1196.6880	1195.6807	1195.6713	8	0 K.LQHGSILGFPK.A
445 - 453	1059.5675	1058.5602	1058.5257	33	0 K.NLNHVSYGR.L
461 - 476	1936.8939	1935.8866	1935.8996	-7	0 R.DSNYHLLMSVQESLER.K Oxidation (M)
481 - 496	1737.9376	1736.9303	1736.8846	26	0 K.HGGTIPIVPTAEFQDR.I
504 - 516	1507.7491	1506.7418	1506.7137	19	0 K.DIVHSGLAYTMER.S Oxidation (M)
528 - 535	963.5420	962.5347	962.5185	17	0 K.YNLGLDLR.T

Probability Based Mowse Score

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 64 are significant ($p < 0.05$).



Match to: **I37082** Score: **66** Expect: **0.041**
GDP-dissociation inhibitor XAP-4 – human

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **19**
Number of mass values matched: **7**
Sequence Coverage: **18%**

Mached peptides shown in **Bold Red** in the primary sequence obtained from the NCBI database

1 MDEEYDVIVL GTGLTECILS GIMSVNGKKV LHMDRNPYYG GESSITPLE
51 ELYKRFQLE GPPESMGRGR DWNVDLIPKF LMANGQLVK**M LLYTEVTRYL**
101 DFK**VVEGSFV YKGGKIYKVP** STETELASN LMGMFEKRRF RK**FLVVFVANF**
151 **DENDPKTFEG VDPQTSMRD** VYRKFDLGQD VIDFTGHALA LYRTDDYLDQ
201 PCLETVNR**IK LYSESLARYG KSPYLYPLYG LGELPQGFAR** LSAIYGGTYM
251 LNKPVDDIIM ENKVVGVKS EGEVARCK**QL ICDPSYIPDR** VRKAGQVIRI
301 ICILSHPIKN TNDANSCQII IPQNQVNRKS DIYVCMISYA HNVAAQGKYI
351 AIASTTVETT DPEKEVEPAL ELLEPIDQKF VAISDLYEPI DDGCESQVFC
401 SCSYDATTHF ETTCNDIKDI YKRMAGTAFD FENMKRKQND VFGAEAEQ

MS peak list

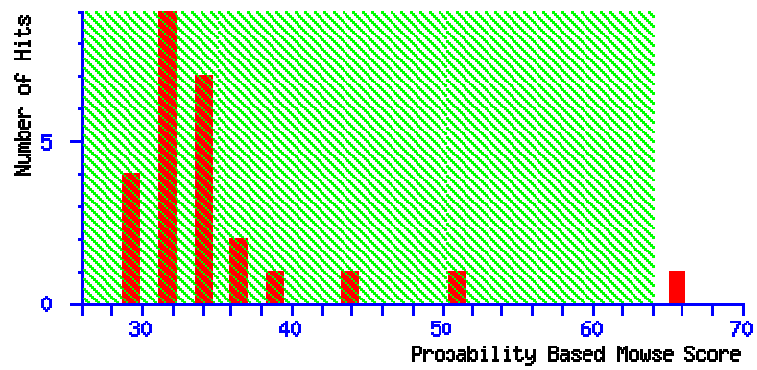
839.0895, 861.0973, 864.4933, **938.5453**, **1027.6019**, 1050.0892, 1137.6372, **1141.6316**, 1157.6376, 1324.7855, **1476.6768**, **1484.7656**
1639.8713, **1654.7717**, 1794.7931, 1826.7345, 1848.8497, 2107.9934, **2141.0549**

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
90 - 98	1141.6316	1140.6243	1140.5849	35	0	K.MLLYTEVTR.Y Oxidation (M)
104 - 112	1027.6019	1026.5946	1026.5386	55	0	K.VVEGSFVYK.G
143 - 156	1654.7717	1653.7644	1653.8039	-24	0	K.FLVVFVANFDENDPK.T
157 - 169	1484.7656	1483.7583	1483.6613	65	0	K.TFEGVDPQTSMR.D Oxidation (M)
211 - 218	938.5453	937.5380	937.4869	55	0	K.LYSESLARY
222 - 240	2141.0549	2140.0476	2140.0993	-24	0	K.SPYLYPLYGLGELPQGFAR.L

279 - 290 1476.6768 1475.6695 1475.7079 -26 0 K.QLICDPSYIPDR.V

Probability Based Mowse Score

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 64 are significant ($p < 0.05$).



Match to: ENOA_HUMAN Score: 69 Expect: 0.018

Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Non- neural enolase) (NNE) (Enolase 1) (Phosphopyruvate hydratase) (C-myc promoter-binding protein) (MBP-1) (MPB-1) (Plasminogen-binding protein).- Homo sapiens (Human).

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 14

Number of mass values matched: 6

Sequence Coverage: 21%

Mached peptides shown in **Bold Red** in the primary sequence obtained from the NCBI database

1 SILKIHAREI FDSR**GNPTVE VDLFTSK**GLF RAAVPSGAST **GIYEALELRD**
51 NDKTRYMGKG VSKAVEHINK TIAPALVSKK LNVTEQEKID KLMIEMDGTE
101 NKSKFGANAI LGVSLAVCKA GAVEKGVPLY RHIADLAGNS EVILPVPFAN
151 VINGGSHAGN **KLAMQEFMIL PVGAANFREA** MRIGAEVYHN LKNVIKEKYG
201 KDATNVGDEG GFAPNILENK EGGLELLKTAI GKAGYTDK**VV IGMDVAASEF**
251 **FRSGKYDLDF** KSPDDPSR**YI SPDQLADLYK** SFIKDYPPVVS IEDPFDQDDW
301 GAWQ**FTASA GIQVVGDDLT VTNPK**RIAKA VNEKSCNCLL LKVNQIGSVT
351 ESLQACKLAQ ANGWGVMVSH RSGETEDTFI ADLVVGLCTG QIKTGAPCRS
401 ERLAKYNQLL RIEEELGSKA KFAGRNFRRNP LAK

MS peak list

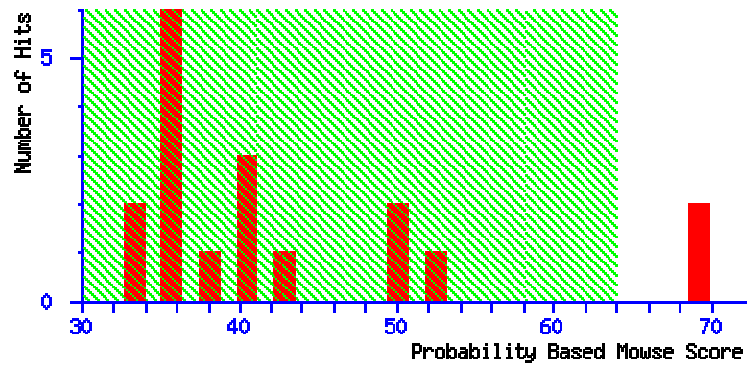
1015.4597, 1140.6727, 1259.5148, **1406.6597**, **1425.7042**, 1480.7976, **1556.7074**, 1639.9264, 1757.0598, **1804.9202**, 1826.8208, **1939.9009**
2033.0331, 2314.1104

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss Sequence
15 - 27	1406.6597	1405.6524	1405.7089	-40	0 R.GNPTVEVDLFTSK.G
32 - 49	1804.9202	1803.9129	1803.9366	-13	0 R.AAVPSGASTGIYEALELR.D
162 - 178	1939.9009	1938.8936	1938.9696	-39	0 K.LAMQEFMILPVGAANFR.E 2 Oxidation (M)
239 - 252	1556.7074	1555.7001	1555.7705	-45	0 K.VVIGMDVAASEFFR.S Oxidation (M)
269 - 280	1425.7042	1424.6969	1424.7187	-15	0 R.YISPDQLADLYK.S

306 - 325 2033.0331 2032.0258 2032.0477 -11 0 K.FTASAGIQVVGDDLTVTNPK.R

Probability Based Mowse Score

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 64 are significant ($p < 0.05$).



Match to: ENOG_HUMAN Score: 175 Expect: 4.7e-13

Gamma-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Neural enolase) (Neuron-specific enolase) (NSE) (Enolase 2).- Homo sapiens (Human).

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 47

Number of mass values matched: 19

Sequence Coverage: 57%

Mached peptides shown in **Bold Red** in the primary sequence obtained from the NCBI database

1 SIEKIWAREI LDSR **GNPTVE VDLYTAKGLF** RAAVPSGAST GIYEALRLD
51 GDKQRYLGKG VLKAVDHINS TIAPALISSG LSVVEQEKLD NLMLELDGTE
101 **NKSKFGANAI LGVSLAVCKA** GAAERELPLY RHIAQLAGNS DLILPVPAFN
151 VINGGSHAGN **KLAMQEFMIL PVGAESFRDA** MRLGAEVYHT LKGVIKDKYG
201 **KDATNVGDEG GFAPNILENS EALELVKEAI** DKAGYTEKIV IGMDVAASEF
251 **YRDGKYDLDF KSPTDPSRYI TGDQLGALYQ** DFVRDYPVVS IEDPFDQDDW
301 AAWSK**FTANV GIQIVGDDLT VTNPKRIERA** VEEKACNCLL LK**VNQIGSVT**
351 **EAIQACKLAQ** ENGWGVMVSH **RSGETEDTFI ADLVVGLCTG QIKTGAPCRS**
401 **ERLAKYNQLM RIEEELGDEA** RFAGHNFRNP SVL

MS peak list

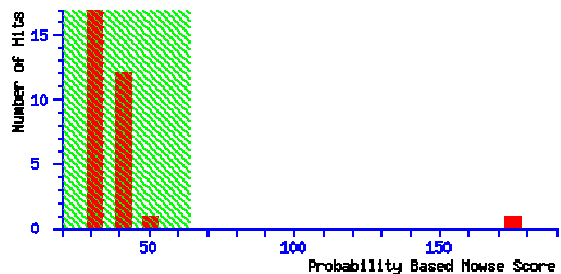
732.4685, 759.4460, 781.4282, 790.5552, **800.4542**, **840.4814**, 848.5466, 905.5366, **1130.7090**, **1152.6849**, **1160.6422**, 1182.6262
1187.7379, 1199.7175, 1235.7294, 1251.7222, 1357.8547, 1379.8485, 1385.6675, **1406.8060**, 1428.8086, **1519.9369**, 1529.5645
1538.8795, 1556.8469, **1570.8927**, **1586.8916**, 1600.8772, **1617.9135**, **1620.8929**, 1642.8730, 1669.0327, **1805.0837**, 1827.0884
1859.0784, 1913.4272, **1955.0912**, **1971.1100**, 1987.1138, **2102.2717**, 2124.3093, 2262.2771, **2353.2725**, **2578.5210**, 2600.5281
2702.3838, 3025.7192

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss Sequence
15 - 27	1406.8060	1405.7987	1405.7089	64	0 R.GNPTVEVDLYTAK.G
32 - 49	1805.0837	1804.0764	1803.9366	77	0 R.AAVPSGASTGIYEALRLR.D

64 - 88	2578.5210	2577.5137	2577.3650	58	0	K.AVDHINSTIAPALISSGLSVVEQEK.L
89 - 102	1620.8929	1619.8856	1619.7712	71	0	K.LDNLMLELDGTENK.S Oxidation (M)
105 - 119	1519.9369	1518.9296	1518.8228	70	0	K.FGANAILGVSLAVCK.A
162 - 178	1955.0912	1954.0839	1953.9692	59	0	K.LAMQEFMILPVGAEFR.D Oxidation (M)
162 - 178	1971.1100	1970.1027	1969.9641	70	0	K.LAMQEFMILPVGAEFR.D 2 Oxidation (M)
183 - 192	1130.7090	1129.7017	1129.6131	78	0	R.LGAEVYHTLK.G
202 - 227	2702.3838	2701.3765	2701.3082	25	0	K.DATNVGDEGGFAPNILENSEALELVK.E
239 - 252	1570.8927	1569.8854	1569.7861	63	0	K.IVIGMDVAASEFYR.D
239 - 252	1586.8916	1585.8843	1585.7810	65	0	K.IVIGMDVAASEFYR.D Oxidation (M)
256 - 261	800.4542	799.4469	799.3752	90	0	K.YDLDFK.S
269 - 284	1859.0784	1858.0711	1857.9261	78	0	R.YITGDQLGALYQDFVR.D
306 - 325	2102.2717	2101.2644	2101.1056	76	0	K.FTANVGIQIVGDDLTVTNPK.R
343 - 357	1617.9135	1616.9062	1616.8192	54	0	K.VNQIGSVTEAIQACK.L
372 - 393	2353.2725	2352.2652	2352.1519	48	0	R.SGETEDTFIADLVVGLCTGQIK.T
403 - 411	1152.6849	1151.6776	1151.6121	57	1	R.LAKYNQLMR.I Oxidation (M)
406 - 411	840.4814	839.4741	839.3959	93	0	K.YNQLMR.I Oxidation (M)
412 - 421	1160.6422	1159.6349	1159.5357	86	0	R.IEEELGDEAR.F

Probability Based Mowse Score

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 64 are significant ($p < 0.05$).



Match to: **S44430** Score: **85** Expect: **0.00051**
synuclein – human

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **39**
Number of mass values matched: **7**
Sequence Coverage: **51%**

Mached peptides shown in **Bold Red** in the primary sequence obtained from the NCBI database

1 MDVFMKGLSM AK**EGVVAAAE KTKQGVTEAA EKTKEGVLYV GSKTREGVVQ**
51 **GVASVAEKTK EQASHLGGAV FSGAGNIAAA TGLVKREEFP** TDLKPEEVAQ
101 EAAEEPLIEP LMEPEGESYE DPPQEYQEY EPEA

823.2022, 861.1762, **873.4603**, 915.4456, **932.4368**, **951.5034**, 973.4697, 1140.4783, **1180.6193**, 1202.5708, **1272.6425**, 1294.6385
1316.5720, 1330.6475, 1351.5885, 1433.6743, 1471.8036, 1479.7554, 1501.6285, 1546.7606, 1576.7793, 1627.8562, 1639.9393
1649.8220, 1730.7390, 1740.8965, 1773.9768, 1880.7982, 1987.9834, 2304.0776, 2315.9878, **2326.1360**, 2338.1221, 2348.1143
2358.0645, 2380.0623, 2533.1401, **2555.2349**, 3754.4050

Start - End	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Sequence
13 - 21	873.4603	872.4530	872.4603	-8	0	K.EGVVAAAEK.T
24 - 32	932.4368	931.4295	931.4611	-34	0	K.QGVTEAAEK.T
33 - 43	1180.6193	1179.6120	1179.6499	-32	1	K.TKEGVLYVGSK.T
35 - 43	951.5034	950.4961	950.5073	-12	0	K.EGVLYVGSK.T
46 - 58	1272.6425	1271.6352	1271.6721	-29	0	R.REGVVQGVASVAEK.T
59 - 85	2555.2349	2554.2276	2554.3503	-48	1	K.TKEQASHLGGAVFSGAGNIAAATGLVK.R
61 - 85	2326.1360	2325.1287	2325.2077	-34	0	K.EQASHLGGAVFSGAGNIAAATGLVK.R

Probability Based Mowse Score

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 64 are significant ($p < 0.05$).

